

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
31 October 2002 (31.10.2002)

PCT

(10) International Publication Number
WO 02/086443 A2

(51) International Patent Classification⁷: G01N

(21) International Application Number: PCT/US02/12476

(22) International Filing Date: 18 April 2002 (18.04.2002)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:

60/284,770	18 April 2001 (18.04.2001)	US
60/290,492	10 May 2001 (10.05.2001)	US
60/339,245	9 November 2001 (09.11.2001)	US
60/350,666	13 November 2001 (13.11.2001)	US
60/334,370	29 November 2001 (29.11.2001)	US
60/372,246	12 April 2002 (12.04.2002)	US

(81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW.

(84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Declaration under Rule 4.17:

— of inventorship (Rule 4.17(iv)) for US only

Published:

— without international search report and to be republished upon receipt of that report

(71) Applicant (*for all designated States except US*): EOS BIOTECHNOLOGY, INC. [US/US]; 225A Gateway Boulevard, South San Francisco, CA 94080 (US).

(72) Inventors; and

(75) Inventors/Applicants (*for US only*): AZIZ, Natasha [US/US]; 411 California Avenue, Palo Alto, CA 94306 (US). MURRAY, Richard [US/US]; 22643 Woodbridge Court, Cupertino, CA 95014 (US).

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(74) Agents: BASTIAN, Kevin, L. et al.; Townsend and Townsend and Crew LLP, Two Embarcadero Center, Eighth Floor, San Francisco, CA 94111-3834 (US).

(54) Title: METHODS OF DIAGNOSIS OF LUNG CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF LUNG CANCER

(57) Abstract: Described herein are methods and compositions that can be used for diagnosis and treatment of lung cancer and similar pathologies. Also described herein are methods that can be used to identify modulators of lung cancer and similar pathologies.



WO 02/086443 A2

METHODS OF DIAGNOSIS OF LUNG CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF LUNG CANCER

5

CROSS-REFERENCES TO RELATED APPLICATIONS

This application is related to USSN 60/284,770, filed April 18, 2001; USSN 60/290,492, filed May 10, 2001; USSN 60/334,370, filed November 29, 2001; USSN 60/339,245, filed November 9, 2001; USSN 60/350,666, filed November 13, 2001; and
10 USSN 60/xxx,xxx, filed April 12, 2002 (Docket OMNI-002P); each of which is incorporated herein by reference in its entirety.

FIELD OF THE INVENTION

The invention relates to the identification of nucleic acid and protein expression
15 profiles and nucleic acids, products, and antibodies thereto that are involved in lung cancer; and to the use of such expression profiles and compositions in diagnosis and therapy of lung cancer. The invention further relates to methods for identifying and using agents and/or targets that inhibit lung cancer or related conditions.

20

BACKGROUND OF THE INVENTION

Lung cancer is the second most commonly occurring cancer in the United States and is the leading cause of cancer-related death. It is estimated that there are over 160,000 new cases of lung cancer in the United States every year. Of those who are diagnosed with lung cancer, 86 percent will die within five years. Lung cancer is the most common visceral
25 cancer in men and accounts for nearly one third of all cancer deaths in both men and women. In fact, lung cancer accounts for 7% of all deaths, due to any cause, in both men and women.

Smoking is the primary cause of lung cancer, with more than 80% of lung cancers resulting from smoking. About 400 to 500 separate gaseous substances are present in the smoke of a non-filter cigarette. The most noteworthy substances include nitrogen oxides,
30 hydrogen cyanide, formaldehyde, benzene, and toluene. The particles present in cigarette smoke contain at least 3,500 individual compounds such as nicotine, tobacco alkaloids (nornicotine, anatabine, anabasine), polycyclic aromatic hydrocarbons (e.g., benzo(a)pyrene, B(a)P), naphthalenes, aromatic amines, phenols, and tobacco-specific nitrosamines.

Tobacco-specific nitrosamines are formed during tobacco curing and processing, and are suspected of causing lung cancer in humans. In rodent studies, regardless of the where or how it is applied, the tobacco-specific nitrosamine known as NNK produces lung adenomas and lung adenocarcinomas. The tobacco-specific nitrosamine known as NNAL also produces lung adenocarcinomas in rodents.

Many of the chemicals found in cigarette smoke also affect the nonsmoker inhaling "secondhand" or sidestream smoke. Indeed, the smoke inhaled by non-smokers has a chemical composition similar to the smoke inhaled by smokers, but, importantly, the concentrations of the carcinogenic tobacco-specific nitrosamines are present in higher concentrations in second hand smoke. For this and other reasons, "passive smoking" is an important cause of lung cancer, causing as many as 3,000 lung cancer deaths in nonsmokers each year.

In addition to smoking, other factors thought to be causes of lung cancer include on-the-job exposure to carcinogens such as asbestos and uranium, exposure to chemical hazards such as radon, polycyclic aromatic hydrocarbons, chromium, nickel, and inorganic arsenic, genetic factors, and diet.

Histological classification of various lung cancers define the types of cancer that begin in the lung. See, e.g., Travis, et al. (1999) Histological Typing of Lung and Pleural Tumours (International Histological Classification of Tumours, No 1. Four major cell types make up more than 88% of all primary lung neoplasms. These are: squamous or epidermoid carcinoma, small cell (also called oat cell) carcinoma, adenocarcinoma, and large cell (also called large cell anaplastic) carcinoma. The remainder include undifferentiated carcinomas, carcinoids, bronchial gland tumors, and other rarer types. The various cell types have different natural histories and responses to therapy, and, thus, a correct histologic diagnosis is the first step of effective treatment.

Small cell lung cancer (SCLC) accounts for 18-25% of all lung cancers, and occurs less frequently than non-small cell lung cancers, and generally spread to distant organs more rapidly than non-small cell lung cancer. In general, at the time of presentation small cell lung cancers have already spread beyond the bounds where surgery and curative intent can be undertaken. However, if identified early enough, these cancers are often responsive to chemotherapy and thoracic radiation treatment.

Non-small cell lung cancers (NSCLC) are the more frequently occurring form of lung cancer. They comprise squamous cell carcinoma, adenocarcinoma, and large cell carcinoma

The screening of asymptomatic persons at high risk for lung cancer has often proven ineffective. In general, only 5 to 15 percent of lung cancer patients have their disease detected while they are asymptomatic. Of course, early detection and treatment are critical factors in the fight against lung cancer. The average survival rate is 49% for those whose cancer is detected early, before the cancer has spread from the lung. Lung cancer often spreads outside of the lung, and it may have spread to the bones or brain by the time it is diagnosed. While the prognosis may be better for lung cancers that are detected early, because of the lack of effective curative treatments, early detection does not necessarily alter the total death rate from lung cancer.

20

20

25

bronchiectasis. Other aspects of the invention will become apparent to the skilled artisan by the following description of the invention.

In one aspect, the present invention provides a method of detecting a lung cancer-associated transcript in a cell from a patient, the method comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16. Alternatively, the sample may be contacted with a specific binding reagent, e.g., antibody.

In one embodiment, the polynucleotide selectively hybridizes to a sequence at least 95% identical to a sequence as shown in Tables 1A-16. In another embodiment, the polynucleotide comprises a sequence as shown in Tables 1A-16.

In one embodiment, the biological sample is a tissue sample, or a body fluid. In another embodiment, the biological sample comprises isolated nucleic acids, e.g., mRNA.

In one embodiment, the polynucleotide is labeled, e.g., with a fluorescent label. In one embodiment, the polynucleotide is immobilized on a solid surface. In one embodiment, the patient is undergoing a therapeutic regimen to treat lung cancer. In another embodiment, the patient is suspected of having lung cancer. In one embodiment, the patient is a primate, e.g., a human.

In one embodiment, the method further comprises the step of amplifying nucleic acids before the step of contacting the biological sample with the polynucleotide.

In another aspect, the present invention provides a method of monitoring the efficacy of a therapeutic treatment of lung cancer, the method comprising the steps of: (i) providing a biological sample from a patient undergoing the therapeutic treatment; and (ii) determining the level of a lung cancer-associated transcript in the biological sample by contacting the biological sample with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16, thereby monitoring the efficacy of the therapy. Or the sample may be evaluated for protein, e.g., contacting the sample with an antibody.

In one embodiment, the method further comprises the step of: (iii) comparing the level of the lung cancer-associated transcript to a level of the lung cancer-associated transcript in a biological sample from the patient prior to, or earlier in, the therapeutic treatment. Or the sample may be evaluated for comparison of protein.

In another aspect, the present invention provides a method of monitoring the efficacy of a therapeutic treatment of lung cancer, the method comprising the steps of: (i) providing a

biological sample from a patient undergoing the therapeutic treatment; and (ii) determining the level of a lung cancer-associated antibody in the biological sample by contacting the biological sample with a polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16, wherein the polypeptide specifically binds to the lung cancer-associated antibody, thereby monitoring the efficacy of the therapy.

In one embodiment, the method further comprises the step of: (iii) comparing the level of the lung cancer-associated antibody to a level of the lung cancer-associated antibody in a biological sample from the patient prior to, or earlier in, the therapeutic treatment.

In another aspect, the present invention provides a method of monitoring the efficacy of a therapeutic treatment of lung cancer, the method comprising the steps of: (i) providing a biological sample from a patient undergoing the therapeutic treatment; and (ii) determining the level of a lung cancer-associated polypeptide in the biological sample by contacting the biological sample with an antibody, wherein the antibody specifically binds to a polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16, thereby monitoring the efficacy of the therapy.

In one embodiment, the method further comprises the step of: (iii) comparing the level of the lung cancer-associated polypeptide to a level of the lung cancer-associated polypeptide in a biological sample from the patient prior to, or earlier in, the therapeutic treatment. In one aspect, the present invention provides an isolated nucleic acid molecule consisting of a polynucleotide sequence as shown in Tables 1A-16. In one embodiment, an expression vector or cell comprises the isolated nucleic acid. In one aspect, the present invention provides an isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1A-16.

In another aspect, the present invention provides an antibody that specifically binds to an isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1A-16. In one embodiment, the antibody is conjugated to an effector component, e.g., a fluorescent label, a radioisotope or a cytotoxic chemical. In one embodiment, the antibody is an antibody fragment. In another embodiment, the antibody is humanized.

In one aspect, the present invention provides a method of detecting lung cancer in a patient, the method comprising contacting a biological sample from the patient with an antibody or protein as described herein.

In another aspect, the present invention provides a method of detecting antibodies specific to a lung cancer gene in a patient, the method comprising contacting a biological sample from the patient with a polypeptide encoded by a nucleic acid comprises a sequence from Tables 1A-16.

5 In another aspect, the present invention provides a method for identifying a compound that modulates a lung cancer-associated polypeptide, the method comprising the steps of: (i) contacting the compound with a lung cancer-associated polypeptide, the polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16; and (ii) determining the functional effect of the
10 compound upon the polypeptide.

In one embodiment, the functional effect is a physical effect, an enzymatic effect, or a chemical effect. In one embodiment, the polypeptide is expressed in a eukaryotic host cell or cell membrane. In another embodiment, the polypeptide is recombinant. In one
15 embodiment, the functional effect is determined by measuring ligand binding to the polypeptide.

In another aspect, the present invention provides a method of inhibiting proliferation or another critical process of a lung cancer-associated cell to treat lung cancer in a patient, the method comprising the step of administering to the subject a therapeutically effective amount of a compound identified as described herein. In one embodiment, the compound is an
20 antibody.

In another aspect, the present invention provides a drug screening assay comprising the steps of: (i) administering a test compound to a mammal having lung cancer or a cell isolated therefrom; (ii) comparing the level of gene expression of a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables
25 1A-16 in a treated cell or mammal with the level of gene expression of the polynucleotide in a control cell or mammal, wherein a test compound that modulates the level of expression of the polynucleotide is a candidate for the treatment of lung cancer.

In one embodiment, the control is a mammal with lung cancer or a cell therefrom that has not been treated with the test compound. In another embodiment, the control is a normal
30 cell or mammal, or a non-malignant lung disease.

In another aspect, the present invention provides a method for treating a mammal having lung cancer comprising administering a compound identified by the assay described herein.

In another aspect, the present invention provides a pharmaceutical composition for treating a mammal having lung cancer, the composition comprising a compound identified by the assay described herein and a physiologically acceptable excipient.

DETAILED DESCRIPTION OF THE INVENTION

In accordance with the objects outlined above, the present invention provides novel methods for diagnosis and treatment of lung disease or cancer, as well as methods for screening for compositions which modulate lung cancer. "Treatment, monitoring, detection or modulation of lung disease or cancer" includes treatment, monitoring, detection, or modulation of lung disease in those patients who have lung disease (whether malignant or non-malignant, e.g., emphysema, bronchitis, or fibrosis) as well as patients with lung cancers in which gene expression from a gene in Tables 1A-16 is increased or decreased, indicating that the subject is more likely to have disease. In particular, while these targets are identified primarily from lung cancer samples, these same targets are likely to be similarly found in analyses of other medical conditions. These other conditions may result from similar pathological processes which affect similar tissues, e.g., lung cancer, small cell lung carcinoma (oat cell carcinoma), non-small cell carcinomas (e.g., squamous cell carcinoma, adenocarcinoma, large cell lung carcinoma, carcinoid, granulomatous), fibrosis (idiopathic pulmonary fibrosis (IPF), hypersensitivity pneumonitis (HP), interstitial pneumonitis, nonspecific idiopathic pneumonitis (NSIP)), chronic obstructive pulmonary disease (COPD, e.g., emphysema, chronic bronchitis), asthma, bronchiectasis, and esophageal cancer. See, e.g., the NCI webpage and USSN 60/347,349 and USSN 60/xxx,xxx (docket LFBR-001-1P, filed March 29, 2002), each of which is incorporated herein by reference. The treatment may be of lung cancer or related condition itself, or treatment of metastasis.

In particular, identification of markers selectively expressed on these cancers allows for use of that expression in diagnostic, prognostic, or therapeutic methods. As such, the invention defines various compositions, e.g., nucleic acids, polypeptides, antibodies, and small molecule agonists/antagonists, which will be useful to selectively identify those markers. For example, therapeutic methods may take the form of protein therapeutics which use the marker expression for selective localization or modulation of function (for those markers which have a causative disease effect), for vaccines, identification of binding partners, or antagonism, e.g., using antisense or RNAi. The markers may be useful for molecular characterization of subsets of lung diseases, which subsets may actually require

very different treatments. Moreover, the markers may also be important in related diseases to the specific cancers, e.g., which affect similar tissues in non-malignant diseases, or have similar mechanisms of induction/maintenance. Metastatic processes or characteristics may also be targeted. Diagnostic and prognostic uses are made available, e.g., to subset related but distinct diseases, or to determine treatment strategy. The detection methods may be based upon nucleic acid, e.g., PCR or hybridization techniques, or protein, e.g., ELISA, imaging, IHC, etc. The diagnosis may be qualitative or quantitative, and may detect increases or decreases in expression levels.

Tables 1A-16 provide unigene cluster identification numbers for the nucleotide sequence of genes that exhibit increased or decreased expression in lung cancer samples. The tables also provide an exemplar accession number that provides a nucleotide sequence that is part of the unigene cluster. In Table 1A, genes marked as "target 1" or "target 2" are particularly useful as therapeutic targets. Genes marked as "target 3" are particularly useful as diagnostic markers. Genes marked as "chron" are upregulated in chronically diseased lung (e.g., emphysema, bronchitis, fibrosis) relative to lung tumors and normal tissue. In certain analyses, the ratio for the "chron" category was determined using the 70th percentile of chronically diseased lung samples divided by the 90th percentile of normal lung samples. The ratio for the targets was determined using the 70th percentile of lung tumor samples divided by the 90th percentile of normal lung samples.

Definitions

The term "lung cancer protein" or "lung cancer polynucleotide" or "lung cancer-associated transcript" refers to nucleic acid and polypeptide polymorphic variants, alleles, mutants, and interspecies homologs that: (1) have a nucleotide sequence that has greater than about 60% nucleotide sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% or greater nucleotide sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more nucleotides, to a nucleotide sequence of or associated with a unigene cluster of Tables 1A-16; (2) bind to antibodies, e.g., polyclonal antibodies, raised against an immunogen comprising an amino acid sequence encoded by a nucleotide sequence of or associated with a unigene cluster of Tables 1A-16, and conservatively modified variants thereof; (3) specifically hybridize under stringent hybridization conditions to a nucleic acid sequence, or the complement thereof of Tables 1A-16 and conservatively modified variants thereof; or (4)

have an amino acid sequence that has greater than about 60% amino acid sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% or greater amino sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more amino acid, to an amino acid sequence

5 encoded by a nucleotide sequence of or associated with a unigene cluster of Tables 1A-16. A polynucleotide or polypeptide sequence is typically from a mammal including, but not limited to, primate, e.g., human; rodent, e.g., rat, mouse, hamster; cow, pig, horse, sheep, or other mammal. A "lung cancer polypeptide" and a "lung cancer polynucleotide," include both naturally occurring or recombinant forms.

10 A "full length" lung cancer protein or nucleic acid refers to a lung cancer polypeptide or polynucleotide sequence, or a variant thereof, that contains the elements normally contained in one or more naturally occurring, wild type lung cancer polynucleotide or polypeptide sequences. The "full length" may be prior to, or after, various stages of post-translational processing or splicing, including alternative splicing.

15 "Biological sample" as used herein is a sample of biological tissue or fluid that contains nucleic acids or polypeptides, e.g., of a lung cancer protein, polynucleotide, or transcript. Such samples include, but are not limited to, tissue isolated from primates, e.g., humans, or rodents, e.g., mice, and rats. Biological samples may also include sections of tissues such as biopsy and autopsy samples, frozen sections taken for histologic purposes, 20 archival materials, blood, plasma, serum, sputum, stool, tears, mucus, hair, skin, etc. Biological samples also include explants and primary and/or transformed cell cultures derived from patient tissues. A biological sample is typically obtained from a eukaryotic organism, most preferably a mammal such as a primate, e.g., chimpanzee or human; cow; dog; cat; a rodent, e.g., guinea pig, rat, mouse; rabbit; or other mammal; or a bird; reptile; 25 fish. Livestock and domestic animals are of interest.

"Providing a biological sample" means to obtain a biological sample for use in methods described in this invention. Most often, this will be done by removing a sample of cells from an animal, but can also be accomplished by using previously isolated cells (e.g., isolated by another person, at another time, and/or for another purpose), or by performing the 30 methods of the invention in vivo. Archival tissues or materials, having treatment or outcome history, will be particularly useful.

The terms "identical" or percent "identity," in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the

same or have a specified percentage of amino acid residues or nucleotides that are the same (e.g., about 60% identity, preferably 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or higher identity over a specified region, when compared and aligned for maximum correspondence over a comparison window or designated region) as measured using, e.g., a BLAST or BLAST 2.0 sequence comparison algorithms with default parameters described below, or by manual alignment and visual inspection (see, e.g., NCBI web site <http://www.ncbi.nlm.nih.gov/BLAST/> or the like). Such sequences are then said to be "substantially identical." This definition also refers to, or may be applied to, the complement of a test sequence. The definition also includes sequences that have deletions and/or insertions, substitutions, and naturally occurring, e.g., polymorphic or allelic variants, and man-made variants. As described below, the preferred algorithms can account for gaps and the like. Preferably, identity exists over a region that is at least about 25 amino acids or nucleotides in length, or more preferably over a region that is 50-100 amino acids or nucleotides in length.

For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Preferably, default program parameters can be used, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

A "comparison window", as used herein, includes reference to a segment of contiguous positions selected from the group consisting typically of from 20 to 600, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well-known in the art. Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith and Waterman (1981) Adv. Appl. Math. 2:482, by the homology alignment algorithm of Needleman and Wunsch (1970) J. Mol. Biol. 48:443, by the search for similarity method of Pearson and Lipman (1988) Proc. Nat'l. Acad. Sci. USA 85:2444, by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer

WO 02/086443 PCT/US02/12476
Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection (see, e.g., Ausubel, et al. (eds. 1995 and supplements) Current Protocols in Molecular Biology.

Preferred examples of algorithms that are suitable for determining percent sequence identity and sequence similarity include the BLAST and BLAST 2.0 algorithms, which are described in Altschul, et al. (1977) Nuc. Acids Res. 25:3389-3402 and Altschul, et al. (1990) J. Mol. Biol. 215:403-410. BLAST and BLAST 2.0 are used, with the parameters described herein, to determine percent sequence identity for the nucleic acids and proteins of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul, et al., *supra*). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, e.g., for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff and Henikoff (1989) Proc. Natl. Acad. Sci. USA 89:10915) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

The BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, e.g., Karlin and Altschul (1993) Proc. Nat'l. Acad. Sci. USA 90:5873-5787). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between

two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.2, more preferably less than about 0.01, and most preferably less than about 0.001. Log values may be negative large numbers, e.g., 5, 10, 20, 30, 40, 40, 70, 90, 110, 150, 170, etc.

An indication that two nucleic acid sequences are substantially identical is that the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the antibodies raised against the polypeptide encoded by the second nucleic acid. Thus, a polypeptide is typically substantially identical to a second polypeptide, e.g., where the two peptides differ only by conservative substitutions. Another indication that two nucleic acid sequences are substantially identical is that the two molecules or their complements hybridize to each other under stringent conditions. Yet another indication that two nucleic acid sequences are substantially identical is that the same primers can be used to amplify the sequences.

A "host cell" is a naturally occurring cell or a transformed cell that contains an expression vector and supports the replication or expression of the expression vector. Host cells may be cultured cells, explants, cells *in vivo*, and the like. Host cells may be prokaryotic cells such as *E. coli*, or eukaryotic cells such as yeast, insect, amphibian, or mammalian cells such as CHO, HeLa, and the like (see, e.g., the American Type Culture Collection catalog or web site, www.atcc.org).

The terms "isolated," "purified," or "biologically pure" refer to material that is substantially or essentially free from components that normally accompany it as found in its native state. Purity and homogeneity are typically determined using analytical chemistry techniques such as polyacrylamide gel electrophoresis or high performance liquid chromatography. A protein or nucleic acid that is the predominant species present in a preparation is substantially purified. In particular, an isolated nucleic acid is separated from some open reading frames that naturally flank the gene and encode proteins other than protein encoded by the gene. The term "purified" in some embodiments denotes that a nucleic acid or protein gives rise to essentially one band in an electrophoretic gel. Preferably, it means that the nucleic acid or protein is at least about 85% pure, more preferably at least 95% pure, and most preferably at least 99% pure. "Purify" or "purification" in other embodiments means removing at least one contaminant or component from the composition to be purified.

In this sense, purification does not require that the purified compound be homogeneous, e.g., 100% pure.

The terms "polypeptide," "peptide" and "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid polymers in which one or more amino acid residue is an artificial chemical mimetic of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers, those containing modified residues, and non-naturally occurring amino acid polymer.

The term "amino acid" refers to naturally occurring and synthetic amino acids, as well as amino acid analogs and amino acid mimetics that function similarly to the naturally occurring amino acids. Naturally occurring amino acids are those encoded by the genetic code, as well as those amino acids that are later modified, e.g., hydroxyproline, γ -carboxyglutamate, and O-phosphoserine. Amino acid analogs refer to compounds that have the same basic chemical structure as a naturally occurring amino acid, e.g., an α carbon that is bound to a hydrogen, a carboxyl group, an amino group, and an R group, e.g., homoserine, norleucine, methionine sulfoxide, methionine methyl sulfonium. Such analogs may have modified R groups (e.g., norleucine) or modified peptide backbones, but retain some basic chemical structure as a naturally occurring amino acid. Amino acid mimetics refer to chemical compounds that have a structure that is different from the general chemical structure of an amino acid, but that function similarly to another amino acid.

Amino acids may be referred to herein by either their commonly known three letter symbols or by the one-letter symbols recommended by the IUPAC-IUB Biochemical Nomenclature Commission. Nucleotides, likewise, may be referred to by their commonly accepted single-letter codes.

"Conservatively modified variants" applies to both amino acid and nucleic acid sequences. With respect to particular nucleic acid sequences, conservatively modified variants refers to those nucleic acids which encode identical or essentially identical amino acid sequences, or where the nucleic acid does not encode an amino acid sequence, to essentially identical or associated, e.g., naturally contiguous, sequences. Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids encode most proteins. For instance, the codons GCA, GCC, GCG, and GCU each encode the amino acid alanine. Thus, at each position where an alanine is specified by a codon, the codon can be altered to another of the corresponding codons described without altering the encoded polypeptide. Such nucleic acid variations are "silent variations," which are one species of

conservatively modified variations. Every nucleic acid sequence herein which encodes a polypeptide also describes silent variations of the nucleic acid. In certain contexts each codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine, and TGG, which is ordinarily the only codon for tryptophan) can be modified to yield a functionally similar molecule. Accordingly, a silent variation of a nucleic acid which encodes a polypeptide is implicit in a described sequence with respect to the expression product, but not necessarily with respect to actual probe sequences.

As to amino acid sequences, one of skill will recognize that individual substitutions, deletions or additions to a nucleic acid, peptide, polypeptide, or protein sequence which alters, adds or deletes a single amino acid or a small percentage of amino acids in the encoded sequence is a "conservatively modified variant" where the alteration results in the substitution of an amino acid with a chemically similar amino acid. Conservative substitution tables providing functionally similar amino acids are well known in the art. Such conservatively modified variants are in addition to and do not exclude polymorphic variants, interspecies homologs, and alleles of the invention. Typically conservative substitutions include for one another: 1) Alanine (A), Glycine (G); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (K); 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V); 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W); 7) Serine (S), Threonine (T); and 8) Cysteine (C), Methionine (M) (see, e.g., Creighton, Proteins (1984)).

Macromolecular structures such as polypeptide structures can be described in terms of various levels of organization. For a general discussion of this organization, see, e.g., Alberts, et al. (1994) Molecular Biology of the Cell (3rd ed.) and Cantor and Schimmel (1980) Biophysical Chemistry Part I: The Conformation of Biological Macromolecules. "Primary structure" refers to the amino acid sequence of a particular peptide. "Secondary structure" refers to locally ordered, three dimensional structures within a polypeptide. These structures are commonly known as domains. Domains are portions of a polypeptide that often form a compact unit of the polypeptide and are typically 25 to approximately 500 amino acids long. Typical domains are made up of sections of lesser organization such as stretches of β -sheet and α -helices. "Tertiary structure" refers to the complete three dimensional structure of a polypeptide monomer. "Quaternary structure" refers to the three dimensional structure formed, usually by the noncovalent association of independent tertiary units. Anisotropic terms are also known as energy terms.

"Nucleic acid" or "oligonucleotide" or "polynucleotide" or grammatical equivalents used herein means at least two nucleotides covalently linked together. Oligonucleotides are typically from about 5, 6, 7, 8, 9, 10, 12, 15, 25, 30, 40, 50 or more nucleotides in length, up to about 100 nucleotides in length. Nucleic acids and polynucleotides are a polymers of any length, including longer lengths, e.g., 200, 300, 500, 1000, 2000, 3000, 5000, 7000, 10,000, etc. A nucleic acid of the present invention will generally contain phosphodiester bonds, although in some cases, nucleic acid analogs are included that may have at least one different linkage, e.g., phosphoramidate, phosphorothioate, phosphorodithioate, or O-methylphosphoroamidite linkages (see Eckstein (1992) Oligonucleotides and Analogues: A Practical Approach Oxford University Press); and peptide nucleic acid backbones and linkages. Other analog nucleic acids include those with positive backbones; non-ionic backbones, and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7, in Sanghui and Cook, eds. Carbohydrate Modifications in Antisense Research, ASC Symposium Series 580. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids. Modifications of the ribose-phosphate backbone may be done for a variety of reasons, e.g., to increase the stability and half-life of such molecules in physiological environments or as probes on a biochip. Mixtures of naturally occurring nucleic acids and analogs can be made; alternatively, mixtures of different nucleic acid analogs, and mixtures of naturally occurring nucleic acids and analogs may be made.

Particularly preferred are peptide nucleic acids (PNA) which includes peptide nucleic acid analogs. These backbones are substantially non-ionic under neutral conditions, in contrast to the highly charged phosphodiester backbone of naturally occurring nucleic acids. This results in two advantages. First, the PNA backbone exhibits improved hybridization kinetics. PNAs have larger changes in the melting temperature (T_m) for mismatched versus perfectly matched basepairs. DNA and RNA typically exhibit a 2-4° C drop in T_m for an internal mismatch. With the non-ionic PNA backbone, the drop is closer to 7-9° C. Similarly, due to their non-ionic nature, hybridization of the bases attached to these backbones is relatively insensitive to salt concentration. In addition, PNAs are not degraded by cellular enzymes, and thus can be more stable.

The nucleic acids may be single stranded or double stranded, as specified, or contain portions of both double stranded or single stranded sequence. As will be appreciated by those in the art, the depiction of a single strand also defines the sequence of the complementary

strand; thus the sequences described herein also provide the complement of the sequence.

The nucleic acid may be DNA, both genomic and cDNA, RNA, or a hybrid, where the nucleic acid may contain combinations of deoxyribo- and ribo-nucleotides, and combinations of bases, including uracil, adenine, thymine, cytosine, guanine, inosine, xanthine

5 hypoxanthine, isocytosine, isoguanine, etc. "Transcript" typically refers to a naturally occurring RNA, e.g., a pre-mRNA, hnRNA, or mRNA. As used herein, the term "nucleoside" includes nucleotides and nucleoside and nucleotide analogs, and modified nucleosides such as amino modified nucleosides. In addition, "nucleoside" includes non-naturally occurring analog structures. Thus, e.g., the individual units of a peptide nucleic
10 acid, each containing a base, are referred to herein as a nucleoside.

A "label" or a "detectable moiety" is a composition detectable by spectroscopic, photochemical, biochemical, immunochemical, physiological, chemical, or other physical means. For example, useful labels include ^{32}P , fluorescent dyes, electron-dense reagents, enzymes (e.g., as commonly used in an ELISA), biotin, digoxigenin, or haptens and proteins
15 or other entities which can be made detectable, e.g., by incorporating a radiolabel into the peptide or used to detect antibodies specifically reactive with the peptide. The labels may be incorporated into the cancer nucleic acids, proteins, and antibodies. Many methods known in the art for conjugating the antibody to the label may be employed, including those methods described by Hunter, et al. (1962) Nature 144:945; David, et al. (1974) Biochemistry
20 13:1014-1021; Pain, et al. (1981) J. Immunol. Meth., 40:219-230; and Nygren (1982) J. Histochem. and Cytochem. 30:407-412.

An "effector" or "effector moiety" or "effector component" is a molecule that is bound (or linked, or conjugated), either covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds, to an antibody.
25 The "effector" can be a variety of molecules including, e.g., detection moieties including radioactive compounds, fluorescent compounds, an enzyme or substrate, tags such as epitope tags, a toxin; activatable moieties, a chemotherapeutic agent; a lipase; an antibiotic; or a radioisotope emitting "hard" e.g., beta radiation.

A "labeled nucleic acid probe or oligonucleotide" is one that is bound, either
30 covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds to a label such that the presence of the probe may be detected by detecting the presence of the label bound to the probe. Alternatively, method

using high affinity interactions may achieve the same results where one of a pair of binding partners binds to the other, e.g., biotin, streptavidin.

As used herein a "nucleic acid probe or oligonucleotide" is a nucleic acid capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, e.g., through hydrogen bond formation. As used herein, a probe may include natural (i.e., A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in a probe may be joined by a linkage other than a phosphodiester bond, preferably one that does not functionally interfere with hybridization. Thus, e.g., probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages. Probes may bind target sequences lacking complete complementarity with the probe sequence depending upon the stringency of the hybridization conditions. The probes are preferably directly labeled, e.g., with isotopes, chromophores, lumiphores, chromogens, or indirectly labeled, e.g., with biotin to which a streptavidin complex may later bind. By assaying for the presence or absence of the probe, one can detect the presence or absence of the select sequence or subsequence. Diagnosis or prognosis may be based at the genomic level, or at the level of RNA or protein expression.

The term "recombinant" when used with reference, e.g., to a cell, or nucleic acid, protein, or vector, indicates that the cell, nucleic acid, protein or vector, has been modified by the introduction of a heterologous nucleic acid or protein or the alteration of a native nucleic acid or protein, or that the cell is derived from a cell so modified. Thus, e.g., recombinant cells express genes that are not found within the native (non-recombinant) form of the cell or express native genes that are otherwise abnormally expressed, under expressed or not expressed at all. By the term "recombinant nucleic acid" herein is meant nucleic acid, originally formed *in vitro*, in general, by the manipulation of nucleic acid, e.g., using polymerases and endonucleases, in a form not normally found in nature. In this manner, operably linkage of different sequences is achieved. Thus an isolated nucleic acid, in a linear form, or an expression vector formed *in vitro* by ligating DNA molecules that are not normally joined, are both considered recombinant for the purposes of this invention. It is understood that once a recombinant nucleic acid is made and reintroduced into a host cell or organism, it will replicate non-recombinantly, i.e., using the *in vivo* cellular machinery of the host cell rather than *in vitro* manipulations; however, such nucleic acids, once produced recombinantly, although subsequently replicated non-recombinantly, are still considered

recombinant for the purposes of the invention. Similarly, a “recombinant protein” is a protein made using recombinant techniques, i.e., through the expression of a recombinant nucleic acid as depicted above.

The term “heterologous” when used with reference to portions of a nucleic acid indicates that the nucleic acid comprises two or more subsequences that are not normally found in the same relationship to each other in nature. For instance, the nucleic acid is typically recombinantly produced, having two or more sequences, e.g., from unrelated genes arranged to make a new functional nucleic acid, e.g., a promoter from one source and a coding region from another source. Similarly, a heterologous protein will often refer to two or more subsequences that are not found in the same relationship to each other in nature (e.g., a fusion protein).

A “promoter” is typically an array of nucleic acid control sequences that direct transcription of a nucleic acid. As used herein, a promoter includes necessary nucleic acid sequences near the start site of transcription, such as, in the case of a polymerase II type promoter, a TATA element. A promoter also optionally includes distal enhancer or repressor elements, which can be located as much as several thousand base pairs from the start site of transcription. A “constitutive” promoter is a promoter that is active under most environmental and developmental conditions. An “inducible” promoter is a promoter that is active under environmental or developmental regulation. The term “operably linked” refers to a functional linkage between a nucleic acid expression control sequence (such as a promoter, or array of transcription factor binding sites) and a second nucleic acid sequence, e.g., wherein the expression control sequence directs transcription of the nucleic acid corresponding to the second sequence.

An “expression vector” is a nucleic acid construct, generated recombinantly or synthetically, with a series of specified nucleic acid elements that permit transcription of a particular nucleic acid in a host cell. The expression vector can be part of a plasmid, virus, or nucleic acid fragment. Typically, the expression vector includes a nucleic acid to be transcribed in operable linkage to a promoter.

The phrase “selectively (or specifically) hybridizes to” refers to the binding, duplexing, or hybridizing of a molecule selectively to a particular nucleotide sequence under stringent hybridization conditions when that sequence is present in a complex mixture (e.g., total cellular or library DNA or RNA).

The phrase "stringent hybridization conditions" refers to conditions under which a probe will hybridize to its target subsequence, typically in a complex mixture of nucleic acids, but to essentially no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in "Overview of principles of hybridization and the strategy of nucleic acid assays" in Tijssen (1993) Techniques in Biochemistry and Molecular Biology--Hybridization with Nucleic Probes (vol. 24) Elsevier. Generally, stringent conditions are selected to be about 5-10° C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. The T_m is the temperature (under defined ionic strength, pH, and nucleic concentration) at which 50% of the probes complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at T_m , 50% of the probes are occupied at equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30° C for short probes (e.g., 10 to 50 nucleotides) and at least about 60° C for long probes (e.g., greater than 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. For selective or specific hybridization, a positive signal is typically at least two times background, preferably 10 times background hybridization. Exemplary stringent hybridization conditions are often: 50% formamide, 5x SSC, and 1% SDS, incubating at 42° C, or, 5x SSC, 1% SDS, incubating at 65° C, with wash in 0.2x SSC, and 0.1% SDS at 65° C. For PCR, a temperature of about 36° C is typical for low stringency amplification, although annealing temperatures may vary between about 32° C and 48° C depending on primer length. For high stringency PCR amplification, a temperature of about 62° C is typical, although high stringency annealing temperatures can range from about 50° C to about 65° C, depending on the primer length and specificity. Typical cycle conditions for both high and low stringency amplifications include a denaturation phase of 90° C - 95° C for 0.5 - 2 min., an annealing phase lasting 0.5 - 2 min., and an extension phase of about 72° C for 1 - 2 min. Protocols and guidelines for low and high stringency amplification reactions are provided, e.g., in Innis, et al.(1990) PCR Protocols, A Guide to Methods and Applications.

Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides which they encode are substantially identical. This

occurs, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. In such cases, the nucleic acids typically hybridize under moderately stringent hybridization conditions. Exemplary "moderately stringent hybridization conditions" include a hybridization in a buffer of 40% formamide, 1 M NaCl, 1% SDS at 37° C, and a wash in 1X SSC at 45° C. A positive hybridization is at least twice background. Alternative hybridization and wash conditions can be utilized to provide conditions of similar stringency. Additional guidelines for determining hybridization parameters are provided in numerous reference, e.g., Ausubel, et al. (ed.) Current Protocols in Molecular Biology Lippincott.

The phrase "functional effects" in the context of assays for testing compounds that modulate activity of a lung cancer protein includes the determination of a parameter that is indirectly or directly under the influence of the lung cancer protein or nucleic acid, e.g., a physiological, enzymatic, functional, physical, or chemical effect, such as the ability to decrease lung cancer. It includes ligand binding activity; cell viability, cell growth on soft agar; anchorage dependence; contact inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis *in vivo*; mRNA and protein expression in cells undergoing metastasis, and other characteristics of lung cancer cells. "Functional effects" include *in vitro*, *in vivo*, and *ex vivo* activities.

By "determining the functional effect" is meant assaying for a compound that increases or decreases a parameter that is indirectly or directly under the influence of a lung cancer protein sequence, e.g., physiological, functional, enzymatic, physical, or chemical effects. Such functional effects can be measured by many means known to those skilled in the art, e.g., changes in spectroscopic characteristics (e.g., fluorescence, absorbance, refractive index), hydrodynamic (e.g., shape), chromatographic, or solubility properties for the protein, measuring inducible markers or transcriptional activation of the lung cancer protein; measuring binding activity or binding assays, e.g., binding to antibodies or other ligands, and measuring cellular proliferation. Determination of the functional effect of a compound on lung cancer can also be performed using lung cancer assays known to those of skill in the art such as an *in vitro* assays, e.g., cell growth on soft agar; anchorage dependence; contact inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis *in vivo*; mRNA and protein

expression in cells undergoing metastasis, and other characteristics of lung cancer cells. The functional effects can be evaluated by many means known to those skilled in the art, e.g., microscopy for quantitative or qualitative measures of alterations in morphological features, measurement of changes in RNA or protein levels for lung cancer-associated sequences, measurement of RNA stability, identification of downstream or reporter gene expression (CAT, luciferase, β -gal, GFP, and the like), e.g., via chemiluminescence, fluorescence, colorimetric reactions, antibody binding, inducible markers, and ligand binding assays.

"Inhibitors", "activators", and "modulators" of lung cancer polynucleotide and polypeptide sequences are used to refer to activating, inhibitory, or modulating molecules or compounds identified using *in vitro* and *in vivo* assays of lung cancer polynucleotide and polypeptide sequences. Inhibitors are compounds that, e.g., bind to, partially or totally block activity, decrease, prevent, delay activation, inactivate, desensitize, or down regulate the activity or expression of lung cancer proteins, e.g., antagonists. Antisense or inhibitory nucleic acids may seem to inhibit expression and subsequent function of the protein.

"Activators" are compounds that increase, open, activate, facilitate, enhance activation, sensitize, agonize, or up regulate lung cancer protein activity. Inhibitors, activators, or modulators also include genetically modified versions of lung cancer proteins, e.g., versions with altered activity, as well as naturally occurring and synthetic ligands, antagonists, agonists, antibodies, small chemical molecules and the like. Such assays for inhibitors and activators include, e.g., expressing the lung cancer protein *in vitro*, in cells, or cell membranes, applying putative modulator compounds, and then determining the functional effects on activity, as described above. Activators and inhibitors of lung cancer can also be identified by incubating lung cancer cells with the test compound and determining increases or decreases in the expression of 1 or more lung cancer proteins, e.g., 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 40, 50 or more lung cancer proteins, such as lung cancer proteins encoded by the sequences set out in Tables 1A-16.

Samples or assays comprising lung cancer proteins that are treated with a potential activator, inhibitor, or modulator are compared to control samples without the inhibitor, activator, or modulator to examine the extent of inhibition. Control samples (untreated with inhibitors) are assigned a relative protein activity value of 100%. Inhibition of a polypeptide is achieved when the activity value relative to the control is about 80%, preferably 50%, more preferably 25-0%. Activation of a lung cancer polypeptide is achieved when the activity value relative to the control (untreated with activators) is 110%, more preferably 150%, more

preferably 200-500% (i.e., two to five fold higher relative to the control), more preferably 1000-3000% higher.

The phrase "changes in cell growth" refers to any change in cell growth and proliferation characteristics *in vitro* or *in vivo*, such as cell viability, formation of foci, anchorage independence, semi-solid or soft agar growth, changes in contact inhibition and density limitation of growth, loss of growth factor or serum requirements, changes in cell morphology, gaining or losing immortalization, gaining or losing tumor specific markers, ability to form or suppress tumors when injected into suitable animal hosts, and/or immortalization of the cell. See, e.g., Freshney (1994) Culture of Animal Cells a Manual of Basic Technique pp. 231-241 (3rd ed.).

"Tumor cell" refers to precancerous, cancerous, and normal cells in a tumor.

"Cancer cells," "transformed" cells, or "transformation" in tissue culture, refers to spontaneous or induced phenotypic changes that do not necessarily involve the uptake of new genetic material. Although transformation can arise from infection with a transforming virus and incorporation of new genomic DNA, or uptake of exogenous DNA, it can also arise spontaneously or following exposure to a carcinogen, thereby mutating an endogenous gene. Transformation is associated with phenotypic changes, such as immortalization of cells, aberrant growth control, nonmorphological changes, and/or malignancy (see, Freshney (1994) Culture of Animal Cells a Manual of Basic Technique (3rd ed.)).

"Antibody" refers to a polypeptide comprising a framework region from an immunoglobulin gene or fragments thereof that specifically binds and recognizes an antigen. The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta, epsilon, and mu constant region genes, as well as the myriad immunoglobulin variable region genes. Light chains are classified as either kappa or lambda. Heavy chains are classified as gamma, mu, alpha, delta, or epsilon, which in turn define the immunoglobulin classes, IgG, IgM, IgA, IgD, and IgE, respectively. Typically, the antigen-binding region of an antibody or its functional equivalent will be most critical in specificity and affinity of binding. See Paul, Fundamental Immunology.

An exemplary immunoglobulin (antibody) structural unit comprises a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair having one "light" (about 25 kD) and one "heavy" chain (about 50-70 kD). The N-terminus of each chain defines a variable region of about 100 to 110 or more amino acids primarily responsible

for antigen recognition. The terms variable light chain (V_L) and variable heavy chain (V_H) refer to these light and heavy chains respectively.

Antibodies exist, e.g., as intact immunoglobulins or as a number of well-characterized fragments produced by digestion with various peptidases. Thus, e.g., pepsin digests an antibody below the disulfide linkages in the hinge region to produce $F(ab)'_2$, a dimer of Fab which itself is a light chain joined to V_H - C_H1 by a disulfide bond. The $F(ab)'_2$ may be reduced under mild conditions to break the disulfide linkage in the hinge region, thereby converting the $F(ab)'_2$ dimer into an Fab' monomer. The Fab' monomer is essentially Fab with part of the hinge region (see Paul (ed. 1999) Fundamental Immunology (4th ed.)). While various antibody fragments are defined in terms of the digestion of an intact antibody, one of skill will appreciate that such fragments may be synthesized *de novo* either chemically or by using recombinant DNA methodology. Thus, the term antibody, as used herein, also includes antibody fragments either produced by the modification of whole antibodies, or those synthesized *de novo* using recombinant DNA methodologies (e.g., single chain Fv) or those identified using phage display libraries (see, e.g., McCafferty, et al. (1990) Nature 348:552-554).

For preparation of antibodies, e.g., recombinant, monoclonal, or polyclonal antibodies, many technique known in the art can be used (see, e.g., Kohler and Milstein (1975) Nature 256:495-497; Kozbor, et al. (1983) Immunology Today 4:72; Cole, et al. (1985), pp. 77-96 in Monoclonal Antibodies and Cancer Therapy; Coligan (1991 and supplements) Current Protocols in Immunology; Harlow and Lane (1988) Antibodies, A Laboratory Manual; and Goding (1986) Monoclonal Antibodies: Principles and Practice (2d ed.)). Techniques for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce antibodies to polypeptides of this invention. Also, transgenic mice, or other organisms such as other mammals, may be used to express humanized antibodies. Alternatively, phage display technology can be used to identify antibodies and heteromeric Fab fragments that specifically bind to selected antigens (see, e.g., McCafferty, et al. (1990) Nature 348:552-554; Marks, et al. (1992) Biotechnology 10:779-783).

A "chimeric antibody" is an antibody molecule in which, e.g., (a) the constant region, or a portion thereof, is altered, replaced, or exchanged so that the antigen binding site (variable region) is linked to a constant region of a different or altered class, effector function, and/or species, or an entirely different molecule which confers new properties to the chimeric antibody, e.g., an enzyme, toxin, hormone, growth factor, drug, etc.; or (b) the

variable region, or a portion thereof, is altered, replaced, or exchanged with a variable region having a different or altered antigen specificity.

Identification of lung cancer-associated sequences

5 In one aspect, the expression levels of genes are determined in different patient samples for which diagnosis information is desired, to provide expression profiles. An expression profile of a particular sample is essentially a "fingerprint" of the state of the sample; while two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is
10 characteristic of the state of the cell. That is, normal tissue may be distinguished from cancerous or metastatic cancerous tissue, or metastatic cancerous tissue can be compared with tissue from surviving cancer patients. By comparing expression profiles of tissue in known different lung cancer states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained.
15 Molecular profiling may distinguish subtypes of a currently collective disease designation, e.g., different forms of lung cancer (chronic disease, adenocarcinoma, etc.)

 The identification of sequences that are differentially expressed in lung cancer versus non-lung cancer tissue allows the use of this information in a number of ways. For example, a particular treatment regime may be evaluated: does a chemotherapeutic drug act to down-
20 regulate lung cancer, and thus tumor growth or recurrence, in a particular patient. Alternatively, a treatment step may induce other markers which may be used as targets to destroy tumor cells. Similarly, diagnosis and treatment outcomes may be done or confirmed by comparing patient samples with the known expression profiles. Malignant disease may be compared to non-malignant conditions. Metastatic tissue can also be analyzed to determine
25 the stage of lung cancer in the tissue, or origin of primary tumor, e.g., metastasis from a remote primary site. Furthermore, these gene expression profiles (or individual genes) allow screening of drug candidates with an eye to mimicking or altering a particular expression profile; e.g., screening can be done for drugs that suppress the lung cancer expression profile. This may be done by making biochips comprising sets of the important lung cancer genes,
30 which can then be used in these screens. PCR methods may be applied with selected primer pairs, and analysis may be of RNA or of genomic sequences. These methods can also be done on the protein basis; that is, protein expression levels of the lung cancer proteins can be evaluated for diagnostic purposes or to screen candidate agents. In addition, the lung cancer

nucleic acid sequences can be administered for gene therapy purposes, including the administration of antisense nucleic acids, or the lung cancer proteins (including antibodies and other modulators thereof) administered as therapeutic drugs or as protein or DNA vaccines.

5 Thus the present invention provides nucleic acid and protein sequences that are differentially expressed in lung cancer relative to normal tissues and/or non-malignant lung disease, or in different types of lung disease, herein termed "lung cancer sequences." As outlined below, lung cancer sequences include those that are up-regulated (i.e., expressed at a higher level) in lung cancer, as well as those that are down-regulated (i.e., expressed at a lower level). In a preferred embodiment, the lung cancer sequences are from humans;
10 however, as will be appreciated by those in the art, lung cancer sequences from other organisms may be useful in animal models of disease and drug evaluation; thus, other lung cancer sequences are provided, from vertebrates, including mammals, including rodents (rats, mice, hamsters, guinea pigs, etc.), primates, farm animals (including sheep, goats, pigs, cows, horses, etc.) and pets (dogs, cats, etc.). Lung cancer sequences from other organisms may be
15 obtained using the techniques outlined below.

 Lung cancer sequences can include both nucleic acid and amino acid sequences. As will be appreciated by those in the art and is more fully outlined below, lung cancer nucleic acid sequences are useful in a variety of applications, including diagnostic applications,
20 which will detect naturally occurring nucleic acids, as well as screening applications; e.g., biochips comprising nucleic acid probes or PCR microtiter plates with selected probes to the lung cancer sequences can be generated.

 A lung cancer sequence can be initially identified by substantial nucleic acid and/or amino acid sequence homology to the lung cancer sequences outlined herein. Such
25 homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, e.g., using homology programs or hybridization conditions.

 For identifying lung cancer-associated sequences, the lung cancer screen typically includes comparing genes identified in different tissues, e.g., normal and cancerous tissues,
30 cancer and non-malignant conditions, non-malignant conditions and normal tissues, or tumor tissue samples from patients who have metastatic disease vs. non metastatic tissue. Other suitable tissue comparisons include comparing lung cancer samples with metastatic cancer samples from other cancers, such as, breast, other gastrointestinal cancers, prostate, ovarian,

etc. Samples of, non metastatic disease tissue and tissue undergoing metastasis are applied to biochips comprising nucleic acid probes. The samples are first microdissected, if applicable, and treated as is known in the art for the preparation of mRNA. Suitable biochips are commercially available, e.g., from Affymetrix, Santa Clara, CA. Gene expression profiles as described herein are generated and the data analyzed.

In one embodiment, the genes showing changes in expression as between normal and disease states are compared to genes expressed in other normal tissues, preferably normal lung, but also including, and not limited to colon, heart, brain, liver, breast, kidney, muscle, prostate, small intestine, large intestine, spleen, bone, and/or placenta. In a preferred embodiment, those genes identified during the lung cancer screen that are expressed in significant amounts in other tissues (e.g., essential organs) are removed from the profile, although in some embodiments, this is not necessary (e.g., where organs may be dispensable at a later stage of life). That is, when screening for drugs, it is usually preferable that the target expression be disease specific, to minimize possible side effects on other organs.

In a preferred embodiment, lung cancer sequences are those that are up-regulated in lung cancer; that is, the expression of these genes is higher in cancerous tissue than in normal lung or other tissue. "Up-regulation" as used herein means, when the ratio is presented as a number greater than one, that the ratio is greater than one, preferably 1.5 or greater, more preferably 2.0 or greater. Another embodiment is directed to sequences up-regulated in non-malignant conditions relative to normal. Unigene cluster identification numbers and accession numbers herein are for the GenBank sequence database and the sequences of the accession numbers are hereby expressly incorporated by reference. GenBank is known in the art, see, e.g., Benson, DA, et al (1998) *Nucleic Acids Research* 26:1-7 and <http://www.ncbi.nlm.nih.gov/>. Sequences are also available in other databases, e.g., European Molecular Biology Laboratory (EMBL) and DNA Database of Japan (DDBJ). Another embodiment is directed to sequences up-regulated in non-malignant conditions relative to normal. In some situations, the sequences may be derived from assembly of available sequences or be predicted from genomic DNA using exon prediction algorithms, such as FGENESH (Salamov and Solovyev (2000) *Genome Res.* 10:516-522). In other situations, sequences have been derived from cloning and sequencing of isolated nucleic acids.

In another preferred embodiment, lung cancer sequences are those that are down-regulated in the lung cancer; that is, the expression of these genes is lower in cancerous tissue

or normal lung or other tissue. "Down-regulation" as used herein means, when the ratio is presented as a number greater than one, that the ratio is greater than one, preferably 1.5 or greater, more preferably 2.0 or greater, or, when the ratio is presented as a number less than one, that the ratio is less than one, preferably 0.5 or less, more preferably 0.25 or less.

5

Informatics

The ability to identify genes that are over or under expressed in lung cancer can additionally provide high-resolution, high-sensitivity datasets which can be used in the areas of diagnostics, therapeutics, drug development, pharmacogenetics, protein structure, biosensor development, and other related areas. For example, the expression profiles can be used in diagnostic or prognostic evaluation of patients with lung cancer. Or as another example, subcellular toxicological information can be generated to better direct drug structure and activity correlation (see Anderson (1998) Pharmaceutical Proteomics: Targets, Mechanism, and Function, paper presented at the IBC Proteomics conference, Coronado, CA (June 11-12, 1998)). Subcellular toxicological information can also be utilized in a biological sensor device to predict the likely toxicological effect of chemical exposures and likely tolerable exposure thresholds (see U.S. Patent No. 5,811,231). Similar advantages accrue from datasets relevant to other biomolecules and bioactive agents (e.g., nucleic acids, saccharides, lipids, drugs, and the like).

10

15

20

25

Thus, in another embodiment, the present invention provides a database that includes at least one set of assay data. The data contained in the database is acquired, e.g., using array analysis either singly or in a library format. The database can be in a form in which data can be maintained and transmitted, but is preferably an electronic database. The electronic database of the invention can be maintained on any electronic device allowing for the storage of and access to the database, such as a personal computer, but is preferably distributed on a wide area network, such as the World Wide Web.

The focus of the present section on databases that include peptide sequence data is for clarity of illustration only. It will be apparent to those of skill in the art that similar databases can be assembled for assay data acquired using an assay of the invention.

30

The compositions and methods for identifying and/or quantitating the relative and/or absolute abundance of a variety of molecular and macromolecular species from a biological sample representing lung cancer, i.e., the identification of lung cancer-associated sequences described herein, provide an abundance of information, which can be correlated with

pathological conditions, predisposition to disease, drug testing, therapeutic monitoring, gene-disease causal linkages, identification of correlates of immunity and physiological status, among others. Although the data generated from the assays of the invention is suited for manual review and analysis, in a preferred embodiment, data processing using high-speed computers is utilized.

An array of methods for indexing and retrieving biomolecular information is known in the art. For example, U.S. Patents 6,023,659 and 5,966,712 disclose a relational database system for storing biomolecular sequence information in a manner that allows sequences to be catalogued and searched according to one or more protein function hierarchies. U.S. Patent 5,953,727 discloses a relational database having sequence records containing information in a format that allows a collection of partial-length DNA sequences to be catalogued and searched according to association with one or more sequencing projects for obtaining full-length sequences from the collection of partial length sequences. U.S. Patent 5,706,498 discloses a gene database retrieval system for making a retrieval of a gene sequence similar to a sequence data item in a gene database based on the degree of similarity between a key sequence and a target sequence. U.S. Patent 5,538,897 discloses a method using mass spectroscopy fragmentation patterns of peptides to identify amino acid sequences in computer databases by comparison of predicted mass spectra with experimentally-derived mass spectra using a closeness-of-fit measure. U.S. Patent 5,926,818 discloses a multi-dimensional database comprising a functionality for multi-dimensional data analysis described as on-line analytical processing (OLAP), which entails the consolidation of projected and actual data according to more than one consolidation path or dimension. U.S. Patent 5,295,261 reports a hybrid database structure in which the fields of each database record are divided into two classes, navigational and informational data, with navigational fields stored in a hierarchical topological map which can be viewed as a tree structure or as the merger of two or more such tree structures.

See also Mount, et al. (2001) Bioinformatics; Durbin, et al. (eds., 1999) Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids (; Baxeavanis and Oeullette (eds., 1998) Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins); Rashidi and Buehler (1999) Bioinformatics: Basic Applications in Biological Science and Medicine; Setubal, et al. (eds 1997) Introduction to Computational Molecular Biology; Misener and Krawetz (eds, 2000) Bioinformatics: Methods and Protocols; Higgins and Taylor (eds., 2000) Bioinformatics: Sequence, Structure, and Databanks: A Practical

Approach; Brown (2001) Bioinformatics: A Biologist's Guide to Biocomputing and the Internet; Han and Kamber (2000) Data Mining: Concepts and Techniques (2000); and Waterman (1995) Introduction to Computational Biology: Maps, Sequences, and Genomes.

5 The present invention provides a computer database comprising a computer and software for storing in computer-retrievable form assay data records cross-tabulated, e.g., with data specifying the source of the target-containing sample from which each sequence specificity record was obtained.

10 In an exemplary embodiment, at least one of the sources of target-containing sample is from a control tissue sample known to be free of pathological disorders. In a variation, at least one of the sources is a known pathological tissue specimen, e.g., a neoplastic lesion or another tissue specimen to be analyzed for lung cancer. In another variation, the assay records cross-tabulate one or more of the following parameters for each target species in a sample: (1) a unique identification code, which can include, e.g., a target molecular structure and/or characteristic separation coordinate (e.g., electrophoretic coordinates); (2) sample
15 source; and (3) absolute and/or relative quantity of the target species present in the sample.

The invention also provides for the storage and retrieval of a collection of target data in a computer data storage apparatus, which can include magnetic disks, optical disks, magneto-optical disks, DRAM, SRAM, SGRAM, SDRAM, RDRAM, DDR RAM, magnetic bubble memory devices, and other data storage devices, including CPU registers and on-CPU
20 data storage arrays. Typically, the target data records are stored as a bit pattern in an array of magnetic domains on a magnetizable medium or as an array of charge states or transistor gate states, such as an array of cells in a DRAM device (e.g., each cell comprised of a transistor and a charge storage area, which may be on the transistor). In one embodiment, the invention provides such storage devices, and computer systems built therewith, comprising a bit pattern
25 encoding a protein expression fingerprint record comprising unique identifiers for at least 10 target data records cross-tabulated with target source.

When the target is a peptide or nucleic acid, the invention preferably provides a method for identifying related peptide or nucleic acid sequences, comprising performing a computerized comparison between a peptide or nucleic acid sequence assay record stored in
30 or retrieved from a computer storage device or database and at least one other sequence. The comparison can include a sequence analysis or comparison algorithm or computer program embodiment thereof (e.g., FASTA, TFASTA, GAP, BESTFIT) and/or the comparison may

be of the relative amount of a peptide or nucleic acid sequence in a pool of sequences determined from a polypeptide or nucleic acid sample of a specimen.

The invention also preferably provides a magnetic disk, such as an IBM-compatible (DOS, Windows, Windows95/98/2000, Windows NT, OS/2) or other format (e.g., Linux,
5 SunOS, Solaris, AIX, SCO Unix, VMS, MV, Macintosh, etc.) floppy diskette or hard (fixed, Winchester) disk drive, comprising a bit pattern encoding data from an assay of the invention in a file format suitable for retrieval and processing in a computerized sequence analysis, comparison, or relative quantitation method.

The invention also provides a network, comprising a plurality of computing devices
10 linked via a data link, such as an Ethernet cable (coax or 10BaseT), telephone line, ISDN line, wireless network, optical fiber, or other suitable signal transmission medium, whereby at least one network device (e.g., computer, disk array, etc.) comprises a pattern of magnetic domains (e.g., magnetic disk) and/or charge domains (e.g., an array of DRAM cells) composing a bit pattern encoding data acquired from an assay of the invention.

15 The invention also provides a method for transmitting assay data that includes generating an electronic signal on an electronic communications device, such as a modem, ISDN terminal adapter, DSL, cable modem, ATM switch, or the like, wherein the signal includes (in native or encrypted format) a bit pattern encoding data from an assay or a database comprising a plurality of assay results obtained by the method of the invention.

20 In a preferred embodiment, the invention provides a computer system for comparing a query target to a database containing an array of data structures, such as an assay result obtained by the method of the invention, and ranking database targets based on the degree of identity and gap weight to the target data. A central processor is preferably initialized to load and execute the computer program for alignment and/or comparison of the assay results.

25 Data for a query target is entered into the central processor via an I/O device. Execution of the computer program results in the central processor retrieving the assay data from the data file, which comprises a binary description of an assay result.

The target data or record and the computer program can be transferred to secondary
30 memory, which is typically random access memory (e.g., DRAM, SRAM, SGRAM, or SDRAM). Targets are ranked according to the degree of correspondence between a selected assay characteristic (e.g., binding to a selected affinity moiety) and the same characteristic of the query target and results are output via an I/O device. For example, a central processor can be a conventional computer (e.g., Intel Pentium, PowerPC, Alpha, PA-8000, SPARC,

MIPS 4400, MIPS 10000, VAX, etc.); a program can be a commercial or public domain molecular biology software package (e.g., UWGCG Sequence Analysis Software, Darwin); a data file can be an optical or magnetic disk, a data server, a memory device (e.g., DRAM, SRAM, SGRAM, SDRAM, EPROM, bubble memory, flash memory, etc.); an I/O device can be a terminal comprising a video display and a keyboard, a modem, an ISDN terminal adapter, an Ethernet port, a punched card reader, a magnetic strip reader, or other suitable I/O device.

The invention also preferably provides the use of a computer system, such as that described above, which comprises: (1) a computer; (2) a stored bit pattern encoding a collection of peptide sequence specificity records obtained by the methods of the invention, which may be stored in the computer; (3) a comparison target, such as a query target; and (4) a program for alignment and comparison, typically with rank-ordering of comparison results on the basis of computed similarity values.

Characteristics of lung cancer-associated proteins

Lung cancer proteins of the present invention may be classified as secreted proteins, transmembrane proteins or intracellular proteins. In one embodiment, the lung cancer protein is an intracellular protein. Intracellular proteins may be found in the cytoplasm and/or in the nucleus. Intracellular proteins are involved in all aspects of cellular function and replication (including, e.g., signaling pathways); aberrant expression of such proteins often results in unregulated or dysregulated cellular processes (see, e.g., Alberts (ed. 1994) Molecular Biology of the Cell (3d ed.)). For example, many intracellular proteins have enzymatic activity such as protein kinase activity, protein phosphatase activity, protease activity, nucleotide cyclase activity, polymerase activity and the like. Intracellular proteins also serve as docking proteins that are involved in organizing complexes of proteins, or targeting proteins to various subcellular localizations, and are involved in maintaining the structural integrity of organelles.

An increasingly appreciated concept in characterizing proteins is the presence in the proteins of one or more structural motifs for which defined functions have been attributed. In addition to the highly conserved sequences found in the enzymatic domain of proteins, highly conserved sequences have been identified in proteins that are involved in protein-protein interaction. For example, Src-homology-2 (SH2) domains bind tyrosine-phosphorylated targets in a sequence dependent manner. PTB domains, which are distinct from SH2

domains, also bind tyrosine phosphorylated targets. SH3 domains bind to proline-rich targets. In addition, PH domains, tetratricopeptide repeats and WD domains to name only a few, have been shown to mediate protein-protein interactions. Some of these may also be involved in binding to phospholipids or other second messengers. As will be appreciated by one of ordinary skill in the art, these motifs can be identified on the basis of amino acid sequence; thus, an analysis of the sequence of proteins may provide insight into both the enzymatic potential of the molecule and/or molecules with which the protein may associate. One useful database is Pfam (protein families), which is a large collection of multiple sequence alignments and hidden Markov models covering many common protein domains. Versions are available via the internet from Washington University in St. Louis, the Sanger Center in England, and the Karolinska Institute in Sweden (see, e.g., Bateman, et al (2000) *Nuc. Acids Res.* 28:263-266; Sonnhammer, et al. (1997) *Proteins* 28:405-420; Bateman, et al. (1999) *Nuc. Acids Res.* 27:260-262; and Sonnhammer, et al. (1998) *Nuc. Acids Res.* 26:320-322).

In another embodiment, the lung cancer sequences are transmembrane proteins. Transmembrane proteins are molecules that span a phospholipid bilayer of a cell. They may have an intracellular domain, an extracellular domain, or both. The intracellular domains of such proteins may have a number of functions including those already described for intracellular proteins. For example, the intracellular domain may have enzymatic activity and/or may serve as a binding site for additional proteins. Frequently the intracellular domain of transmembrane proteins serves both roles. For example certain receptor tyrosine kinases have both protein kinase activity and SH2 domains. In addition, autophosphorylation of tyrosines on the receptor molecule itself, creates binding sites for additional SH2 domain containing proteins.

Transmembrane proteins may contain from one to many transmembrane domains. For example, receptor tyrosine kinases, certain cytokine receptors, receptor guanylyl cyclases and receptor serine/threonine protein kinases contain a single transmembrane domain. However, various other proteins including channels, pumps, and adenylyl cyclases contain numerous transmembrane domains. Many important cell surface receptors such as G protein coupled receptors (GPCRs) are classified as "seven transmembrane domain" proteins, as they contain 7 membrane spanning regions. Characteristics of transmembrane domains include approximately 17 consecutive hydrophobic amino acids that may be followed by charged amino acids. Therefore, upon analysis of the amino acid sequence of a particular protein, the

localization and number of transmembrane domains within the protein may be predicted (see, e.g., PSORT web site <http://psort.nibb.ac.jp/>).

The extracellular domains of transmembrane proteins are diverse; however, conserved motifs are found repeatedly among various extracellular domains. Conserved structure and/or functions have been ascribed to different extracellular motifs. Many extracellular domains are involved in binding to other molecules. In one aspect, extracellular domains are found on receptors. Factors that bind the receptor domain include circulating ligands, which may be peptides, proteins, or small molecules such as adenosine and the like. For example, growth factors such as EGF, FGF, and PDGF are circulating growth factors that bind to their cognate receptors to initiate a variety of cellular responses. Other factors include cytokines, mitogenic factors, hormones, neurotrophic factors and the like. Extracellular domains also bind to cell-associated molecules. In this respect, they may mediate cell-cell interactions. Cell-associated ligands can be tethered to the cell, e.g., via a glycosylphosphatidylinositol (GPI) anchor, or may themselves be transmembrane proteins. Extracellular domains may also associate with the extracellular matrix and contribute to the maintenance of the cell structure.

Lung cancer proteins that are transmembrane are particularly preferred in the present invention as they are readily accessible targets for extracellular immunotherapeutics, as are described herein. In addition, as outlined below, transmembrane proteins can be also useful in imaging modalities. Antibodies may be used to label such readily accessible proteins *in situ* or in histological analysis. Alternatively, antibodies can also label intracellular proteins, in which case analytical samples are typically permeabilized to provide access to intracellular proteins. In addition, some membrane proteins can be processed to release a soluble protein, or to expose a residual fragment. Released soluble proteins may be useful diagnostic markers, processed residual protein fragments may be useful lung markers of disease.

It will also be appreciated by those in the art that a transmembrane protein can be made soluble by removing transmembrane sequences, e.g., through recombinant methods. Furthermore, transmembrane proteins that have been made soluble can be made to be secreted through recombinant means by adding an appropriate signal sequence.

In another embodiment, the lung cancer proteins are secreted proteins; the secretion of which can be either constitutive or regulated. These proteins may have a signal peptide or signal sequence that targets the molecule to the secretory pathway. Secreted proteins are involved in numerous physiological events; e.g., if circulating, they often serve to transmit

signals to various other cell types. The secreted protein may function in an autocrine manner (acting on the cell that secreted the factor), a paracrine manner (acting on cells in close proximity to the cell that secreted the factor), an endocrine manner (acting on cells at a distance, e.g., secretion into the blood stream), or exocrine (secretion, e.g., through a duct or to adjacent epithelial surface as sweat glands, sebaceous glands, pancreatic ducts, lacrimal glands, mammary glands, wax producing glands of the ear, etc.). Thus secreted molecules often find use in modulating or altering numerous aspects of physiology. Lung cancer proteins that are secreted proteins are particularly preferred in the present invention as they serve as good targets for diagnostic markers, e.g., for blood, plasma, serum, or stool tests. Those which are enzymes may be antibody or small molecule targets. Others may be useful as vaccine targets, e.g., via CTL mechanisms.

Use of lung cancer nucleic acids

As described above, lung cancer sequence is initially identified by substantial nucleic acid and/or amino acid sequence homology or linkage to the lung cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions. Typically, linked sequences on a mRNA are found on the same molecule.

The lung cancer nucleic acid sequences of the invention, e.g., the sequences in Tables 1A-16, can be fragments of larger genes, i.e., they are nucleic acid segments. "Genes" in this context includes coding regions, non-coding regions, and mixtures of coding and non-coding regions. Accordingly, as will be appreciated by those in the art, using the sequences provided herein, extended sequences, in either direction, of the lung cancer genes can be obtained, using techniques well known in the art for cloning either longer sequences or the full length sequences; see Ausubel, et al., *supra*. Much can be done by informatics and many sequences can be clustered to include multiple sequences corresponding to a single gene, e.g., systems such as UniGene (see, <http://www.ncbi.nlm.nih.gov/UniGene/>).

Once a lung cancer nucleic acid is identified, it can be cloned and, if necessary, its constituent parts recombined to form the entire lung cancer nucleic acid coding regions or the entire mRNA sequence. Once isolated from its natural source, e.g., contained within a plasmid or other vector or excised therefrom as a linear nucleic acid segment, the recombinant lung cancer nucleic acid can be further-used as a probe to identify and isolate

other lung cancer nucleic acids, e.g., extended coding regions. It can also be used as a “precursor” nucleic acid to make modified or variant lung cancer nucleic acids and proteins.

The lung cancer nucleic acids of the present invention are used in several ways. In a first embodiment, nucleic acid probes to the lung cancer nucleic acids are made and attached to biochips to be used in screening and diagnostic methods, as outlined below, or for administration, e.g., for gene therapy, RNAi, vaccine, and/or antisense applications. Alternatively, the lung cancer nucleic acids that include coding regions of lung cancer proteins can be put into expression vectors for the expression of lung cancer proteins, again for screening purposes or for administration to a patient.

In a preferred embodiment, nucleic acid probes to lung cancer nucleic acids (both the nucleic acid sequences outlined in the figures and/or the complements thereof) are made. The nucleic acid probes attached to the biochip are designed to be substantially complementary to the lung cancer nucleic acids, i.e., the target sequence (either the target sequence of the sample or to other probe sequences, e.g., in sandwich assays), such that hybridization of the target sequence and the probes of the present invention occurs. As outlined below, this complementarity need not be perfect; there may be any number of base pair mismatches which will interfere with hybridization between the target sequence and the single stranded nucleic acids of the present invention. However, if the number of mutations is so great that no hybridization can occur under even the least stringent of hybridization conditions, the sequence is not a complementary target sequence. Thus, by “substantially complementary” herein is meant that the probes are sufficiently complementary to the target sequences to hybridize under appropriate reaction conditions, particularly high stringency conditions, as outlined herein.

A nucleic acid probe is generally single stranded but can be partially single and partially double stranded. The strandedness of the probe is dictated by the structure, composition, and properties of the target sequence. In general, the nucleic acid probes range from about 8 to about 100 bases long, with from about 10 to about 80 bases being preferred, and from about 30 to about 50 bases being particularly preferred. That is, generally complements of ORFs or whole genes are not used. In some embodiments, nucleic acids of lengths up to hundreds of bases can be used.

In a preferred embodiment, more than one probe per sequence is used, with either overlapping probes or probes to different sections of the target being used. That is, two, three, four or more probes, with three being preferred, are used to build in a redundancy for a

particular target. The probes can be overlapping (i.e., have some sequence in common), or separate. In some cases, PCR primers may be used to amplify signal for higher sensitivity.

As will be appreciated by those in the art, nucleic acids can be attached or immobilized to a solid support in a wide variety of ways. By "immobilized" and grammatical
5 equivalents herein is meant the association or binding between the nucleic acid probe and the solid support is sufficient to be stable under the conditions of binding, washing, analysis, and removal as outlined below. The binding can typically be covalent or non-covalent. By "non-covalent binding" and grammatical equivalents herein is typically meant one or more of electrostatic, hydrophilic, and hydrophobic interactions. Included in non-covalent binding is
10 the covalent attachment of a molecule, such as, streptavidin to the support and the non-covalent binding of the biotinylated probe to the streptavidin. By "covalent binding" and grammatical equivalents herein is meant that the two moieties, the solid support and the probe, are attached by at least one bond, including sigma bonds, pi bonds and coordination bonds. Covalent bonds can be formed directly between the probe and the solid support or can
15 be formed by a cross linker or by inclusion of a specific reactive group on either the solid support or the probe or both molecules. Immobilization may also involve a combination of covalent and non-covalent interactions.

In general, the probes are attached to a biochip in a wide variety of ways, as will be appreciated by those in the art. As described herein, the nucleic acids can either be
20 synthesized first, with subsequent attachment to the biochip, or can be directly synthesized on the biochip.

The biochip comprises a suitable solid substrate. By "substrate" or "solid support" or other grammatical equivalents herein is meant a material that can be modified for the attachment or association of the nucleic acid probes and is amenable to at least one detection
25 method. Often the substrate may contain discrete individual sites appropriate for individual partitioning and identification. As will be appreciated by those in the art, the number of possible substrates are very large, and include, but are not limited to, glass and modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, Teflon, etc.),
30 polysaccharides, nylon or nitrocellulose, resins, silica or silica-based materials including silicon and modified silicon, carbon, metals, inorganic glasses, plastics, etc. In general, the substrates allow optical detection and do not appreciably fluoresce. A preferred substrate is described in US application entitled Reusable Low Fluorescent Plastic Biochip, U.S.

Application Serial No. 09/270,214, filed March 15, 1999, herein incorporated by reference in its entirety.

Generally the substrate is planar, although as will be appreciated by those in the art, other configurations of substrates may be used as well. For example, the probes may be placed on the inside surface of a tube, for flow-through sample analysis to minimize sample volume. Similarly, the substrate may be flexible, such as a flexible foam, including closed cell foams made of particular plastics.

In a preferred embodiment, the surface of the biochip and the probe may be derivatized with chemical functional groups for subsequent attachment of the two. Thus, e.g., the biochip is derivatized with a chemical functional group including, but not limited to, amino groups, carboxy groups, oxo groups and thiol groups, with amino groups being particularly preferred. Using these functional groups, the probes can be attached using functional groups on the probes. For example, nucleic acids containing amino groups can be attached to surfaces comprising amino groups, e.g., using linkers as are known in the art; e.g., homo-or hetero-bifunctional linkers as are well known (see 1994 Pierce Chemical Company catalog, technical section on cross-linkers, pages 155-200). In addition, in some cases, additional linkers, such as alkyl groups (including substituted and heteroalkyl groups) may be used.

In this embodiment, oligonucleotides are synthesized, and then attached to the surface of the solid support. Either the 5' or 3' terminus may be attached to the solid support, or attachment may be via linkage to an internal nucleoside.

In another embodiment, the immobilization to the solid support may be very strong, yet non-covalent. For example, biotinylated oligonucleotides can be made, which bind to surfaces covalently coated with streptavidin, resulting in attachment.

Alternatively, the oligonucleotides may be synthesized on the surface, as is known in the art. For example, photoactivation techniques utilizing photopolymerization compounds and techniques are used. In a preferred embodiment, the nucleic acids can be synthesized *in situ*, using known photolithographic techniques, such as those described in WO 95/25116; WO 95/35505; U.S. Patent Nos. 5,700,637 and 5,445,934; and references cited within, all of which are expressly incorporated by reference; these methods of attachment form the basis of the Affymetrix GeneChip™ technology.

Often, amplification-based assays are performed to measure the expression level of lung cancer-associated sequences. These assays are typically performed in conjunction with

reverse transcription. In such assays, a lung cancer-associated nucleic acid sequence acts as a template in an amplification reaction (e.g., Polymerase Chain Reaction, or PCR). In a quantitative amplification, the amount of amplification product will be proportional to the amount of template in the original sample. Comparison to appropriate controls provides a measure of the amount of lung cancer-associated RNA. Methods of quantitative amplification are well known to those of skill in the art. Detailed protocols for quantitative PCR are provided, e.g., in Innis, et al. (1990) PCR Protocols, A Guide to Methods and Applications.

In some embodiments, a TaqMan based assay is used to measure expression. TaqMan based assays use a fluorogenic oligonucleotide probe that contains a 5' fluorescent dye and a 3' quenching agent. The probe hybridizes to a PCR product, but cannot itself be extended due to a blocking agent at the 3' end. When the PCR product is amplified in subsequent cycles, the 5' nuclease activity of the polymerase, e.g., AmpliTaq, results in the cleavage of the TaqMan probe. This cleavage separates the 5' fluorescent dye and the 3' quenching agent, thereby resulting in an increase in fluorescence as a function of amplification (see, e.g., literature provided by Perkin-Elmer, e.g., www2.perkin-elmer.com).

Other suitable amplification methods include, but are not limited to, ligase chain reaction (LCR) (see Wu and Wallace (1989) Genomics 4:560, Landegren, et al. (1988) Science 241:1077, and Barringer, et al. (1990) Gene 89:117), transcription amplification (Kwoh, et al. (1989) Proc. Natl. Acad. Sci. USA 86:1173), self-sustained sequence replication (Guatelli, et al. (1990) Proc. Nat. Acad. Sci. USA 87:1874), dot PCR, and linker adapter PCR, etc.

Expression of lung cancer proteins from nucleic acids

In a preferred embodiment, lung cancer nucleic acids, e.g., encoding lung cancer proteins, are used to make a variety of expression vectors to express lung cancer proteins which can then be used in screening assays, as described below. Expression vectors and recombinant DNA technology are well known to those of skill in the art (see, e.g., Ausubel, *supra*, and Fernandez and Hoeffler (eds 1999) Gene Expression Systems) and are used to express proteins. The expression vectors may be either self-replicating extrachromosomal vectors or vectors which integrate into a host genome. Generally, these expression vectors include transcriptional and translational regulatory nucleic acid operably linked to the nucleic acid encoding the lung cancer protein. The term "control sequences" refers to DNA

sequences used for the expression of an operably linked coding sequence in a particular host organism. Control sequences that are suitable for prokaryotes, e.g., include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

5 Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding
10 sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is typically accomplished by ligation at convenient restriction
15 sites. If such sites do not exist, synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice. Transcriptional and translational regulatory nucleic acid will generally be appropriate to the host cell used to express the lung cancer protein. Numerous types of appropriate expression vectors, and suitable regulatory sequences are known in the art for a variety of host cells.

In general, transcriptional and translational regulatory sequences may include, but are
20 not limited to, promoter sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and stop sequences, and enhancer or activator sequences. In a preferred embodiment, the regulatory sequences include a promoter and transcriptional start and stop sequences.

Promoter sequences may be either constitutive or inducible promoters. The promoters
25 may be either naturally occurring promoters or hybrid promoters. Hybrid promoters, which combine elements of more than one promoter, are also known in the art, and are useful in the present invention.

In addition, an expression vector may comprise additional elements. For example, the
30 expression vector may have two replication systems, thus allowing it to be maintained in two organisms, e.g., in mammalian or insect cells for expression and in a prokaryotic host for cloning and amplification. Furthermore, for integrating expression vectors, the expression vector often contains at least one sequence homologous to the host cell genome, and preferably two homologous sequences which flank the expression construct. The integrating

vector may be directed to a specific locus in the host cell by selecting the appropriate homologous sequence for inclusion in the vector. Constructs for integrating vectors are well known in the art (e.g., Fernandez and Hoeffler, *supra*).

In addition, in a preferred embodiment, the expression vector contains a selectable
5 marker gene to allow the selection of transformed host cells. Selection genes are well known in the art and will vary with the host cell used.

The lung cancer proteins of the present invention are usually produced by culturing a host cell transformed with an expression vector containing nucleic acid encoding a lung cancer protein, under the appropriate conditions to induce or cause expression of the lung
10 cancer protein. Conditions appropriate for lung cancer protein expression will vary with the choice of the expression vector and the host cell, and will be easily ascertained by one skilled in the art through routine experimentation or optimization. For example, the use of constitutive promoters in the expression vector will require optimizing the growth and proliferation of the host cell, while the use of an inducible promoter requires the appropriate
15 growth conditions for induction. In addition, in some embodiments, the timing of the harvest is important. For example, the baculoviral systems used in insect cell expression are lytic viruses, and thus harvest time selection can be crucial for product yield.

Appropriate host cells include yeast, bacteria, archaeobacteria, fungi, and insect and animal cells, including mammalian cells. Of particular interest are *Saccharomyces cerevisiae*
20 and other yeasts, *E. coli*, *Bacillus subtilis*, Sf9 cells, C129 cells, 293 cells, *Neurospora*, BHK, CHO, COS, HeLa cells, HUVEC (human umbilical vein endothelial cells), THP1 cells (a macrophage cell line) and various other human cells and cell lines.

In a preferred embodiment, the lung cancer proteins are expressed in mammalian cells. Mammalian expression systems are also known in the art, and include retroviral and
25 adenoviral systems. Of particular use as mammalian promoters are the promoters from mammalian viral genes, since the viral genes are often highly expressed and have a broad host range. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter, herpes simplex virus promoter, and the CMV promoter (see, e.g., Fernandez and Hoeffler, *supra*). Typically, transcription termination and
30 polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. Examples of transcription terminator and polyadenylation signals include those derived from SV40.

The methods of introducing exogenous nucleic acid into mammalian hosts, as well as other hosts, is well known in the art, and will vary with the host cell used. Techniques include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, viral infection, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

In a preferred embodiment, lung cancer proteins are expressed in bacterial systems. Promoters from bacteriophage may also be used and are known in the art. In addition, synthetic promoters and hybrid promoters are also useful; e.g., the tac promoter is a hybrid of the trp and lac promoter sequences. Furthermore, a bacterial promoter can include naturally occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. In addition to a functioning promoter sequence, an efficient ribosome binding site is desirable. The expression vector may also include a signal peptide sequence that provides for secretion of the lung cancer protein in bacteria. The protein is either secreted into the growth media (gram-positive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). The bacterial expression vector may also include a selectable marker gene to allow for the selection of bacterial strains that have been transformed. Suitable selection genes include genes which render the bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin, neomycin and tetracycline. Selectable markers also include biosynthetic genes, such as those in the histidine, tryptophan and leucine biosynthetic pathways. These components are assembled into expression vectors. Expression vectors for bacteria are well known in the art, and include vectors for *Bacillus subtilis*, *E. coli*, *Streptococcus cremoris*, and *Streptococcus lividans*, among others (e.g., Fernandez and Hoeffler, *supra*). The bacterial expression vectors are transformed into bacterial host cells using techniques well known in the art, such as calcium chloride treatment, electroporation, and others.

In one embodiment, lung cancer proteins are produced in insect cells. Expression vectors for the transformation of insect cells, and in particular, baculovirus-based expression vectors, are well known in the art.

In a preferred embodiment, lung cancer protein is produced in yeast cells. Yeast expression systems are well known in the art, and include expression vectors for *Saccharomyces cerevisiae*, *Candida albicans* and *C. maltosa*, *Hansenula polymorpha*,

Kluyveromyces fragilis and *K. lactis*, *Pichia guillermondii*, and *P. pastoris*, *Schizosaccharomyces pombe*, and *Yarrowia lipolytica*.

The lung cancer protein may also be made as a fusion protein, using techniques well known in the art. Thus, e.g., for the creation of monoclonal antibodies, if the desired epitope is small, the lung cancer protein may be fused to a carrier protein to form an immunogen. Alternatively, the lung cancer protein may be made as a fusion protein to increase expression for affinity purification purposes, or for other reasons. For example, when the lung cancer protein is a lung cancer peptide, the nucleic acid encoding the peptide may be linked to other nucleic acid for expression purposes.

In a preferred embodiment, the lung cancer protein is purified or isolated after expression. Lung cancer proteins may be isolated or purified in a variety of appropriate ways. Standard purification methods include electrophoretic, molecular, immunological and chromatographic techniques, including ion exchange, hydrophobic, affinity, and reverse-phase HPLC chromatography, and chromatofocusing. For example, the lung cancer protein may be purified using a standard anti-lung cancer protein antibody column. Ultrafiltration and diafiltration techniques, in conjunction with protein concentration, are also useful. For general guidance in suitable purification techniques, see Scopes (1982) Protein Purification. The degree of purification necessary will vary depending on the use of the lung cancer protein. In some instances no purification will be necessary.

Once expressed and purified if necessary, the lung cancer proteins and nucleic acids are useful in a number of applications. They may be used as immunoselection reagents, as vaccine reagents, as screening agents, therapeutic entities, for production of antibodies, as transcription or translation inhibitors, etc.

Variants of lung cancer proteins

In one embodiment, the lung cancer proteins are derivative or variant lung cancer proteins as compared to the wild-type sequence. That is, as outlined more fully below, the derivative lung cancer peptide will often contain at least one amino acid substitution, deletion or insertion, with amino acid substitutions being particularly preferred. The amino acid substitution, insertion or deletion may occur at a particular residue within the lung cancer peptide.

Also included within one embodiment of lung cancer proteins of the present invention are amino acid sequence variants. These variants typically fall into one or more of three

classes: substitutional, insertional or deletional variants. These variants ordinarily are prepared by site specific mutagenesis of nucleotides in the DNA encoding the lung cancer protein, using cassette or PCR mutagenesis or other techniques, to produce DNA encoding the variant, and thereafter expressing the DNA in recombinant cell culture as outlined above.

5 However, variant lung cancer protein fragments having up to about 100-150 residues may be prepared by *in vitro* synthesis. Amino acid sequence variants are characterized by the predetermined nature of the variation, a feature that sets them apart from naturally occurring allelic or interspecies variation of the lung cancer protein amino acid sequence. The variants typically exhibit a similar qualitative biological activity as the naturally occurring analogue,
10 although variants can also be selected which have modified characteristics as will be more fully outlined below.

While the site or region for introducing an amino acid sequence variation is often predetermined, the mutation per se need not be predetermined. For example, in order to optimize the performance of a mutation at a given site, random mutagenesis may be
15 conducted at the target codon or region and the expressed lung cancer variants screened for the optimal combination of desired activity. Techniques exist for making substitution mutations at predetermined sites in DNA having a known sequence, e.g., M13 primer mutagenesis and PCR mutagenesis. Screening of mutants is often done using assays of lung cancer protein activities.

20 Amino acid substitutions are typically of single residues; insertions usually will be on the order of from about 1 to 20 amino acids, although considerably larger insertions may be occasionally tolerated. Deletions generally range from about 1 to about 20 residues, although in some cases deletions may be much larger.

Substitutions, deletions, insertions or any combination thereof may be used to arrive
25 at a final derivative. Generally these changes are done on a few amino acids to minimize the alteration of the molecule. Larger changes may be tolerated in certain circumstances. When small alterations in the characteristics of a lung cancer protein are desired, substitutions are generally made in accordance with the amino acid substitution chart provided in the definition section.

30 Variants typically exhibit essentially the same qualitative biological activity and will elicit the same immune response as a naturally-occurring analog, although variants also are selected to modify the characteristics of lung cancer proteins as needed. Alternatively, the

variant may be designed or reorganized such that a biological activity of the lung cancer protein is altered. For example, glycosylation sites may be added, altered, or removed.

Covalent modifications of lung cancer polypeptides are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid
5 residues of a lung cancer polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N-or C-terminal residues of a lung cancer polypeptide. Derivatization with bifunctional agents is useful, for instance, for crosslinking lung cancer polypeptides to a water-insoluble support matrix or surface for use in a method for purifying anti-lung cancer polypeptide antibodies or screening assays, as is more fully
10 described below. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, e.g., esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-((p-azidophenyl)dithio)propioimide.

15 Other modifications include deamidation of glutamyl and asparagyl residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of serinyl, threonyl or tyrosyl residues, methylation of the γ -amino groups of lysine, arginine, and histidine side chains (Creighton (1983) Proteins: Structure and Molecular Properties, pp. 79-86), acetylation of the N-terminal
20 amine, and amidation of any C-terminal carboxyl group.

Another type of covalent modification of the lung cancer polypeptide encompassed by this invention is an altered native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended herein to mean adding to or deleting one or more carbohydrate moieties of a native sequence lung cancer polypeptide. Glycosylation patterns
25 can be altered in many ways. For example the use of different cell types to express lung cancer-associated sequences can result in different glycosylation patterns.

Addition of glycosylation sites to lung cancer polypeptides may also be accomplished by altering the amino acid sequence thereof. The alteration may be made, e.g., by the addition of, or substitution by, one or more serine or threonine residues to the native sequence
30 lung cancer polypeptide (for O-linked glycosylation sites). The lung cancer amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the lung cancer polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the lung cancer polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. Such methods are described in the art, e.g., in WO 87/05330, and in Aplin and Wriston (1981) CRC Crit. Rev. Biochem., pp. 259-306.

- 5 Removal of carbohydrate moieties present on the lung cancer polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are known in the art and described, for instance, by Hakimuddin, et al. (1987) Arch. Biochem. Biophys., 259:52 and by Edge, et al. (1981) Anal. Biochem., 118:131.
- 10 Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo-and exo-glycosidases as described by Thotakura, et al. (1987) Meth. Enzymol., 138:350.

- Another type of covalent modification of lung cancer comprises linking the lung cancer polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol, polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent
- 15 Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192, or 4,179,337.

- Lung cancer polypeptides of the present invention may also be modified in a way to form chimeric molecules comprising a lung cancer polypeptide fused to another, heterologous polypeptide or amino acid sequence. In one embodiment, such a chimeric
- 20 molecule comprises a fusion of a lung cancer polypeptide with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino-or carboxyl-terminus of the lung cancer polypeptide. The presence of such epitope-tagged forms of a lung cancer polypeptide can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the lung
- 25 cancer polypeptide to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. In an alternative embodiment, the chimeric molecule may comprise a fusion of a lung cancer polypeptide with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule, such a fusion could be to the Fc region of an IgG molecule.

- 30 Various tag polypeptides and their respective antibodies are well known and examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; HIS6 and metal chelation tags, the flu HA tag polypeptide and its antibody 12CA5 (Field, et al. (1988) Mol. Cell. Biol. 8:2159-2165); the c-myc tag and the 8F9, 3C7, 6E10, G4, B7 and 9E10 antibodies

thereto (Evan, et al. (1985) Molecular and Cellular Biology 5:3610-3616); and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody (Paborsky, et al. (1990) Protein Engineering 3(6):547-553). Other tag polypeptides include the Flag-peptide (Hopp, et al. (1988) BioTechnology 6:1204-1210); the KT3 epitope peptide (Martin, et al. (1992) Science 255:192-194); tubulin epitope peptide (Skinner, et al. (1991) J. Biol. Chem. 266:15163-15166); and the T7 gene 10 protein peptide tag (Lutz-Freyermuth, et al. (1990) Proc. Nat'l Acad. Sci. USA 87:6393-6397).

Also included are other lung cancer proteins of the lung cancer family, and lung cancer proteins from other organisms, which are cloned and expressed as outlined below.

Thus, probe or degenerate polymerase chain reaction (PCR) primer sequences may be used to find other related lung cancer proteins from primates or other organisms. As will be appreciated by those in the art, particularly useful probe and/or PCR primer sequences include unique areas of the lung cancer nucleic acid sequence. As is generally known in the art, preferred PCR primers are from about 15 to about 35 nucleotides in length, with from about 20 to about 30 being preferred, and may contain inosine as needed. PCR reaction conditions are well known in the art (e.g., Innis, PCR Protocols, *supra*).

Antibodies to lung cancer proteins

In a preferred embodiment, when a lung cancer protein is to be used to generate antibodies, e.g., for immunotherapy or immunodiagnosis, the lung cancer protein should share at least one epitope or determinant with the full length protein. By "epitope" or "determinant" herein is typically meant a portion of a protein which will generate and/or bind an antibody or T-cell receptor in the context of MHC. Thus, in most instances, antibodies made to a smaller lung cancer protein will be able to bind to the full-length protein, particularly linear epitopes. In a preferred embodiment, the epitope is unique; that is, antibodies generated to a unique epitope show little or no cross-reactivity.

Methods of preparing polyclonal antibodies are well known (e.g., Coligan, *supra*; and Harlow and Lane, *supra*). Polyclonal antibodies can be raised in a mammal, e.g., by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include a protein encoded by a nucleic acid of Tables 1A-16 or fragment thereof or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal

being immunized. Immunogenic proteins include, e.g., keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Adjuvants include, e.g., Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be selected by one skilled in the art.

The antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein (1975) Nature 256:495. In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized *in vitro*. The immunizing agent will typically include a polypeptide encoded by a nucleic acid of the tables, or fragment thereof, or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding (1986) Monoclonal Antibodies: Principles and Practice, pp. 59-103). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovin, or primate origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

In one embodiment, the antibodies are bispecific antibodies. Bispecific antibodies are typically monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens or that have binding specificities for two epitopes on the same antigen. In one embodiment, one of the binding specificities is for a protein encoded by a nucleic acid of the tables or a fragment thereof, the other one is for any other antigen, and preferably for a cell-surface protein or receptor or receptor subunit, preferably one that is tumor specific. Alternatively, tetramer-type technology may create multivalent reagents.

In a preferred embodiment, the antibodies to lung cancer protein are capable of reducing or eliminating a biological function of a lung cancer protein, in a naked form or conjugated to an effector moiety. That is, the addition of anti-lung cancer protein antibodies (either polyclonal or preferably monoclonal) to lung cancer tissue (or cells containing lung cancer) may reduce or eliminate the lung cancer. Generally, at least a 25% decrease in activity, growth, size or the like is preferred, with at least about 50% being particularly preferred and about a 95-100% decrease being especially preferred.

In a preferred embodiment the antibodies to the lung cancer proteins are humanized antibodies (e.g., Xenex Biosciences, Medarex, Inc., Abgenix, Inc., Protein Design Labs, Inc.) Humanized forms of non-human (e.g., murine) antibodies are chimeric molecules of immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of a human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, a humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework (FR) regions are those of a human immunoglobulin consensus sequence. A humanized antibody optimally also will typically comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones, et al. (1986) Nature 321:522-525; Riechmann, et al. (1988) Nature 332:323-329; and Presta (1992) Curr. Op. Struct. Biol. 2:593-596). Humanization can be performed following the method of Winter and co-workers (Jones, et al. (1986) Nature 321:522-525; Riechmann, et al. (1988) Nature 332:323-327; Verhoeven, et al. (1988) Science 239:1534-1536), by substituting rodent CDRs or CDR sequences for corresponding sequences of a human antibody. Accordingly, such humanized antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by corresponding sequence from a non-human species.

Human-like antibodies can also be produced using various techniques known in the art, including phage display libraries (Hoogenboom and Winter (1991) J. Mol. Biol. 227:381; Marks, et al. (1991) J. Mol. Biol. 222:581). The techniques of Cole, et al. and Boerner, et al. are also available for the preparation of human monoclonal antibodies (Cole, et al. (1985) Monoclonal Antibodies and Cancer Therapy, p. 77 and Boerner, et al. (1991) J. Immunol. 147(1):86-95). Similarly, human antibodies can be made by introducing human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in nearly all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, e.g., in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in the following scientific publications: Marks, et al. (1992) Bio/Technology 10:779-783; Lonberg, et al. (1994) Nature 368:856-859; Morrison (1994) Nature 368:812-13; Fishwild, et al. (1996) Nature Biotechnology 14:845-51; Neuberger (1996) Nature Biotechnology 14:826; and Lonberg and Huszar (1995) Intern. Rev. Immunol. 13:65-93.

By immunotherapy is meant treatment of lung cancer with an antibody raised against a lung cancer proteins. As used herein, immunotherapy can be passive or active. Passive immunotherapy as defined herein is the passive transfer of antibody to a recipient (patient). Active immunization is the induction of antibody and/or T-cell responses in a recipient (patient). Induction of an immune response is the result of providing the recipient with an antigen to which antibodies are raised. The antigen may be provided by injecting a polypeptide against which antibodies are desired to be raised into a recipient, or contacting the recipient with a nucleic acid capable of expressing the antigen and under conditions for expression of the antigen, leading to an immune response.

In a preferred embodiment the lung cancer proteins against which antibodies are raised are secreted proteins as described above. Without being bound by theory, antibodies used for treatment, may bind and prevent the secreted protein from binding to its receptor, thereby inactivating the secreted lung cancer protein.

In another preferred embodiment, the lung cancer protein to which antibodies are raised is a transmembrane protein. Without being bound by theory, antibodies used for treatment may bind the extracellular domain of the lung cancer protein and prevent it from binding to other proteins, such as circulating ligands or cell-associated molecules. The

antibody may cause down-regulation of the transmembrane lung cancer protein. The antibody may be a competitive, non-competitive or uncompetitive inhibitor of protein binding to the extracellular domain of the lung cancer protein. The antibody may be an antagonist of the lung cancer protein or may prevent activation of a transmembrane lung cancer protein, or
5 may induce or suppress a particular cellular pathway. In some embodiments, when the antibody prevents the binding of other molecules to the lung cancer protein, the antibody prevents growth of the cell. The antibody may also be used to target or sensitize the cell to cytotoxic agents, including, but not limited to TNF- α , TNF- β , IL-1, INF- γ , and IL-2, or
10 chemotherapeutic agents including 5FU, vinblastine, actinomycin D, cisplatin, methotrexate, and the like. In some instances the antibody may belong to a sub-type that activates serum complement when complexed with the transmembrane protein thereby mediating cytotoxicity or antigen-dependent cytotoxicity (ADCC). Thus, lung cancer may be treated by administering to a patient antibodies directed against the transmembrane lung cancer protein. Antibody-labeling may activate a co-toxin, localize a toxin payload, or otherwise provide
15 means to locally ablate cells.

In another preferred embodiment, the antibody is conjugated to an effector moiety. The effector moiety can be various molecules, including labeling moieties such as radioactive labels or fluorescent labels, or can be a therapeutic moiety. In one aspect the therapeutic moiety is a small molecule that modulates the activity of a lung cancer protein. In another
20 aspect the therapeutic moiety may modulate an activity of molecules associated with or in close proximity to a lung cancer protein. The therapeutic moiety may inhibit enzymatic or signaling activity such as protease or collagenase activity associated with lung cancer.

In a preferred embodiment, the therapeutic moiety can also be a cytotoxic agent. In this method, targeting the cytotoxic agent to lung cancer tissue or cells results in a reduction
25 in the number of afflicted cells, thereby reducing symptoms associated with lung cancer. Cytotoxic agents are numerous and varied and include, but are not limited to, cytotoxic drugs or toxins or active fragments of such toxins. Suitable toxins and their corresponding fragments include diphtheria A chain, exotoxin A chain, ricin A chain, abrin A chain, curcin, crotin, phenomycin, enomycin, saporin, auristatin, and the like. Cytotoxic agents also include
30 radiochemicals made by conjugating radioisotopes to antibodies raised against lung cancer proteins, or binding of a radionuclide to a chelating agent that has been covalently attached to the antibody. Targeting the therapeutic moiety to transmembrane lung cancer proteins not only serves to increase the local concentration of therapeutic moiety in the lung cancer

afflicted area, but also serves to reduce deleterious side effects that may be associated with the untargeted therapeutic moiety.

In another preferred embodiment, the lung cancer protein against which the antibodies are raised is an intracellular protein. In this case, the antibody may be conjugated to a protein or other entity which facilitates entry into the cell. In one case, the antibody enters the cell by endocytosis. In another embodiment, a nucleic acid encoding the antibody is administered to the individual or cell. Moreover, wherein the lung cancer protein can be targeted within a cell, i.e., the nucleus, an antibody theretomay contain a signal for that target localization, i.e., a nuclear localization signal.

The lung cancer antibodies of the invention specifically bind to lung cancer proteins. By "specifically bind" herein is meant that the antibodies bind to the protein with a K_d of at least about 0.1 mM, more usually at least about 1 μ M, preferably at least about 0.1 μ M or better, and most preferably, 0.01 μ M or better. Selectivity of binding to the specific target and not to related other sequences is also important.

Detection of lung cancer sequence for diagnostic and therapeutic applications

In one aspect, the RNA expression levels of genes are determined for different cellular states in the lung cancer phenotype. Expression levels of genes in normal tissue (e.g., not undergoing lung cancer), in lung cancer tissue (and in some cases, for varying severities of lung cancer that relate to prognosis, as outlined below), or in non-malignant disease are evaluated to provide expression profiles. A gene expression profile of a particular cell state or point of development is essentially a "fingerprint" of the state of the cell. While two states may have a particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is reflective of the state of the cell. By comparing expression profiles of cells in different states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Then, diagnosis may be performed or confirmed to determine whether a tissue sample has the gene expression profile of normal or cancerous tissue. This will provide for molecular diagnosis of related conditions.

"Differential expression," or grammatical equivalents as used herein, refers to qualitative or quantitative differences in the temporal and/or cellular gene expression patterns within and among cells and tissue. Thus, a differentially expressed gene can qualitatively have its expression altered, including an activation or inactivation, in, e.g.,

normal versus lung cancer tissue. Genes may be turned on or turned off in a particular state, relative to another state thus permitting comparison of two or more states. A qualitatively regulated gene will exhibit an expression pattern within a state or cell type which is detectable by standard techniques. Some genes will be expressed in one state or cell type, but not in both. Alternatively, the difference in expression may be quantitative, e.g., in that expression is increased or decreased; i.e., gene expression is either upregulated, resulting in an increased amount of transcript, or downregulated, resulting in a decreased amount of transcript. The degree to which expression differs need only be large enough to quantify via standard characterization techniques as outlined below, such as by use of Affymetrix GeneChip™ expression arrays, Lockhart (1996) Nature Biotechnology 14:1675-1680, hereby expressly incorporated by reference. Other techniques include, but are not limited to, quantitative reverse transcriptase PCR, northern analysis and RNase protection. As outlined above, preferably the change in expression (i.e., upregulation or downregulation) is typically at least about 50%, more preferably at least about 100%, more preferably at least about 150%, more preferably at least about 200%, with from 300 to at least 1000% being especially preferred.

Evaluation may be at the gene transcript or the protein level. The amount of gene expression may be monitored using nucleic acid probes to the RNA or DNA equivalent of the gene transcript, and the quantification of gene expression levels, or, alternatively, the final gene product itself (protein) can be monitored, e.g., with antibodies to the lung cancer protein and standard immunoassays (ELISAs, etc.) or other techniques, including mass spectroscopy assays, 2D gel electrophoresis assays, etc. Proteins corresponding to lung cancer genes, e.g., those identified as being important in a lung cancer or disease phenotype, can be evaluated in a lung cancer diagnostic test. In a preferred embodiment, gene expression monitoring is performed simultaneously on a number of genes.

The lung cancer nucleic acid probes may be attached to biochips as outlined herein for the detection and quantification of lung cancer sequences in a particular cell. The assays are further described below in the example. PCR techniques can be used to provide greater sensitivity. Multiple protein expression monitoring can be performed as well. Similarly, these assays may be performed on an individual basis as well.

In a preferred embodiment nucleic acids encoding the lung cancer protein are detected. Although DNA or RNA encoding the lung cancer protein may be detected, of particular interest are methods wherein an mRNA encoding a lung cancer protein is detected.

Probes to detect mRNA can be a nucleotide/deoxynucleotide probe that is complementary to and hybridizes with the mRNA and includes, but is not limited to, oligonucleotides, cDNA or RNA. Probes also should contain a detectable label, as defined herein. In one method the mRNA is detected after immobilizing the nucleic acid to be examined on a solid support such as nylon membranes and hybridizing the probe with the sample. Following washing to remove the non-specifically bound probe, the label is detected. In another method detection of the mRNA is performed *in situ*. In this method permeabilized cells or tissue samples are contacted with a detectably labeled nucleic acid probe for sufficient time to allow the probe to hybridize with the target mRNA. Following washing to remove the non-specifically bound probe, the label is detected. For example a digoxigenin labeled riboprobe (RNA probe) that is complementary to the mRNA encoding a lung cancer protein is detected by binding the digoxigenin with an anti-digoxigenin secondary antibody and developed with nitro blue tetrazolium and 5-bromo-4-chloro-3-indoyl phosphate.

In a preferred embodiment, various proteins from the three classes of proteins as described herein (secreted, transmembrane or intracellular proteins) are used in diagnostic assays. The lung cancer proteins, antibodies, nucleic acids, modified proteins and cells containing lung cancer sequences are used in diagnostic assays. This can be performed on an individual gene or corresponding polypeptide level. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes and/or corresponding polypeptides.

As described and defined herein, lung cancer proteins, including intracellular, transmembrane, or secreted proteins, find use as markers of lung cancer, e.g., for prognostic or diagnostic purposes. Detection of these proteins in putative lung cancer tissue allows for detection, prognosis, or diagnosis of lung cancer or similar disease, and perhaps for selection of therapeutic strategy. In one embodiment, antibodies are used to detect lung cancer proteins. A preferred method separates proteins from a sample by electrophoresis on a gel (typically a denaturing and reducing protein gel, but may be another type of gel, including isoelectric focusing gels and the like). Following separation of proteins, the lung cancer protein is detected, e.g., by immunoblotting with antibodies raised against the lung cancer protein. Methods of immunoblotting are well known to those of ordinary skill in the art.

In another preferred method, antibodies to the lung cancer protein find use in *in situ* imaging techniques, e.g., in histology (e.g., Asai (ed. 1993) Methods in Cell Biology:

Antibodies in Cell Biology, volume 37. In this method cells are contacted with from one to many antibodies to the lung cancer protein(s). Following washing to remove non-specific antibody binding, the presence of the antibody or antibodies is detected. In one embodiment the antibody is detected by incubating with a secondary antibody that contains a detectable label, e.g., multicolor fluorescence or confocal imaging. In another method the primary antibody to the lung cancer protein(s) contains a detectable label, e.g., an enzyme marker that can act on a substrate. In another preferred embodiment each one of multiple primary antibodies contains a distinct and detectable label. This method finds particular use in simultaneous screening for a plurality of lung cancer proteins. Many other histological imaging techniques are also provided by the invention.

In a preferred embodiment the label is detected in a fluorometer which has the ability to detect and distinguish emissions of different wavelengths. In addition, a fluorescence activated cell sorter (FACS) can be used in the method.

In another preferred embodiment, antibodies find use in diagnosing lung cancer from blood, serum, plasma, stool, and other samples. Such samples, therefore, are useful as samples to be probed or tested for the presence of lung cancer proteins. Antibodies can be used to detect a lung cancer protein by previously described immunoassay techniques including ELISA, immunoblotting (western blotting), immunoprecipitation, BIACORE technology and the like. Conversely, the presence of antibodies may indicate an immune response against an endogenous lung cancer protein or vaccine.

In a preferred embodiment, *in situ* hybridization of labeled lung cancer nucleic acid probes to tissue arrays is done. For example, arrays of tissue samples, including lung cancer tissue and/or normal tissue, are made. *In situ* hybridization (see, e.g., Ausubel, *supra*) is then performed. When comparing the fingerprints between an individual and a standard, the skilled artisan can make a diagnosis, a prognosis, or a prediction based on the findings. It is further understood that the genes which indicate the diagnosis may differ from those which indicate the prognosis and molecular profiling of the condition of the cells may lead to distinctions between responsive or refractory conditions or may be predictive of outcomes.

In a preferred embodiment, the lung cancer proteins, antibodies, nucleic acids, modified proteins and cells containing lung cancer sequences are used in prognosis assays. As above, gene expression profiles can be generated that correlate to lung cancer, clinical, pathological, or other information, in terms of long term prognosis. Again, this may be done on either a protein or gene level, with the use of genes being preferred. Single or multiple

genes may be useful in various combinations. As above, lung cancer probes may be attached to biochips for the detection and quantification of lung cancer sequences in a tissue or patient. The assays proceed as outlined above for diagnosis. PCR method may provide more sensitive and accurate quantification.

5

Assays for therapeutic compounds

In a preferred embodiment, the proteins, nucleic acids, and antibodies as described herein are used in drug screening assays. The lung cancer proteins, antibodies, nucleic acids, modified proteins and cells containing lung cancer sequences are used in drug screening
10 assays or by evaluating the effect of drug candidates on a "gene expression profile" or expression profile of polypeptides. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent (e.g., Zlokarnik, et al. (1998) Science 279:84-8; Heid (1996) Genome Res. 6:986-94.

15

In a preferred embodiment, the lung cancer proteins, antibodies, nucleic acids, modified proteins and cells containing the native or modified lung cancer proteins are used in screening assays. That is, the present invention provides novel methods for screening for compositions which modulate the lung cancer phenotype or an identified physiological function of a lung cancer protein. As above, this can be done on an individual gene level or
20 by evaluating the effect of drug candidates on a "gene expression profile". In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent, see Zlokarnik, *supra*.

25

Having identified differentially expressed genes herein, a variety of assays may be performed. In a preferred embodiment, assays may be run on an individual gene or protein level. That is, having identified a particular gene with altered regulation in lung cancer, test compounds can be screened for the ability to modulate gene expression or for binding to the lung cancer protein. "Modulation" thus includes an increase or a decrease in gene expression. The preferred amount of modulation will depend on the original change of the
30 gene expression in normal versus tissue undergoing lung cancer, with changes of at least 10%, preferably 50%, more preferably 100-300%, and in some embodiments 300-1000% or greater. Thus, if a gene exhibits a 4-fold increase in lung cancer tissue compared to normal tissue, a decrease of about four-fold is often desired; similarly, a 10-fold decrease in lung

cancer tissue compared to normal tissue often provides a target value of a 10-fold increase in expression to be induced by the test compound.

The amount of gene expression may be monitored using nucleic acid probes and the quantification of gene expression levels, or, alternatively, the gene product itself can be monitored, e.g., through the use of antibodies to the lung cancer protein and standard immunoassays. Proteomics and separation techniques may also allow quantification of expression.

In a preferred embodiment, gene or protein expression monitoring of a number of entities, i.e., an expression profile, is monitored simultaneously. Such profiles will typically involve a plurality of those entities described herein.

In this embodiment, the lung cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of lung cancer sequences in a particular cell. Alternatively, PCR may be used. Thus, a series, e.g., of microtiter plate, may be used with dispensed primers in desired wells. A PCR reaction can then be performed and analyzed for each well.

Expression monitoring can be performed to identify compounds that modify the expression of one or more lung cancer-associated sequences, e.g., a polynucleotide sequence set out in the tables. Generally, in a preferred embodiment, a test compound is added to the cells prior to analysis. Moreover, screens are also provided to identify agents that modulate lung cancer, modulate lung cancer proteins, bind to a lung cancer protein, or interfere with the binding of a lung cancer protein and an antibody, substrate, or other binding partner.

The term "test compound" or "drug candidate" or "modulator" or grammatical equivalents as used herein describes a molecule, e.g., protein, oligopeptide, small organic molecule, polysaccharide, polynucleotide, etc., to be tested for the capacity to directly or indirectly alter the lung cancer phenotype or the expression of a lung cancer sequence, e.g., a nucleic acid or protein sequence. In preferred embodiments, modulators alter expression profiles of nucleic acids or proteins provided herein. In one embodiment, the modulator suppresses a lung cancer phenotype, e.g., to a normal or non-malignant tissue fingerprint. In another embodiment, a modulator induces a lung cancer phenotype. Generally, a plurality of assay mixtures are run in parallel with different agent concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, i.e., at zero concentration or below the level of detection.

In one aspect, a modulator will neutralize the effect of a lung cancer protein. By “neutralize” is meant that activity of a protein and the consequent effect on the cell is inhibited or blocked.

In certain embodiments, combinatorial libraries of potential modulators will be screened for an ability to bind to a lung cancer polypeptide or to modulate activity. Conventionally, new chemical entities with useful properties are generated by identifying a chemical compound (called a “lead compound”) with some desirable property or activity, e.g., inhibiting activity, creating variants of the lead compound, and evaluating the property and activity of those variant compounds. Often, high throughput screening (HTS) methods are employed for such an analysis.

In one preferred embodiment, high throughput screening methods involve providing a library containing a large number of potential therapeutic compounds (candidate compounds). Such “combinatorial chemical libraries” are then screened in one or more assays to identify those library members (particular chemical species or subclasses) that display a desired characteristic activity. The compounds thus identified can serve as conventional “lead compounds” or can themselves be used as potential or actual therapeutics.

A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis by combining a number of chemical “building blocks” such as reagents. For example, a linear combinatorial chemical library, such as a polypeptide (e.g., mutein) library, is formed by combining a set of chemical building blocks called amino acids in every possible way for a given compound length (i.e., the number of amino acids in a polypeptide compound). Millions of chemical compounds can be synthesized through such combinatorial mixing of chemical building blocks (Gallop, et al. (1994) J. Med. Chem. 37(9):1233-1251).

Preparation and screening of combinatorial chemical libraries is well known to those of skill in the art. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (see, e.g., U.S. Patent No. 5,010,175, Furka (1991) Pept. Prot. Res. 37:487-493, Houghton, et al. (1991) Nature, 354:84-88), peptoids (PCT Publication No WO 91/19735), encoded peptides (PCT Publication WO 93/20242), random bio-oligomers (PCT Publication WO 92/00091), benzodiazepines (U.S. Pat. No. 5,288,514), diversomers such as hydantoins, benzodiazepines and dipeptides (Hobbs, et al. (1993) Proc. Nat. Acad. Sci. USA 90:6909-6913), vinylogous polypeptides (Hagihara, et al. (1992) J. Amer. Chem. Soc. 114:6568), nonpeptidal peptidomimetics with a Beta-D-Glucose scaffolding (Hirschmann, et

al. (1992) J. Amer. Chem. Soc. 114:9217-9218), analogous organic syntheses of small compound libraries (Chen, et al. (1994) J. Amer. Chem. Soc. 116:2661), oligocarbamates (Cho, et al. (1993) Science 261:1303), and/or peptidyl phosphonates (Campbell, et al. (1994) J. Org. Chem. 59:658). See, generally, Gordon, et al. (1994) J. Med. Chem. 37:1385, nucleic acid libraries (see, e.g., Stratagene, Corp.), peptide nucleic acid libraries (see, e.g., U.S. Patent 5,539,083), antibody libraries (see, e.g., Vaughn, et al. (1996) Nature Biotechnology 14(3):309-314, and PCT/US96/10287), carbohydrate libraries (see, e.g., Liang, et al. (1996) Science 274:1520-1522, and U.S. Patent No. 5,593,853), and small organic molecule libraries (see, e.g., benzodiazepines, Baum (1993) C&EN, Jan 18, page 33; isoprenoids, U.S. Patent No. 5,569,588; thiazolidinones and metathiazanones, U.S. Patent No. 5,549,974; pyrrolidines, U.S. Patent Nos. 5,525,735 and 5,519,134; morpholino compounds, U.S. Patent No. 5,506,337; benzodiazepines, U.S. Patent No. 5,288,514; and the like).

Devices for the preparation of combinatorial libraries are commercially available (see, e.g., 357 MPS, 390 MPS, Advanced Chem Tech, Louisville KY, Symphony, Rainin, Woburn, MA, 433A Applied Biosystems, Foster City, CA, 9050 Plus, Millipore, Bedford, MA).

A number of well known robotic systems have also been developed for solution phase chemistries. These systems include automated workstations like the automated synthesis apparatus developed by Takeda Chemical Industries, LTD. (Osaka, Japan) and many robotic systems utilizing robotic arms (Zymate II, Zymark Corporation, Hopkinton, Mass.; Orca, Hewlett-Packard, Palo Alto, Calif.), which mimic the manual synthetic operations performed by a chemist. The above devices, with appropriate modification, are suitable for use with the present invention. In addition, numerous combinatorial libraries are themselves commercially available (see, e.g., ComGenex, Princeton, N.J., Asinex, Moscow, Ru, Tripos, Inc., St. Louis, MO, ChemStar, Ltd, Moscow, RU, 3D Pharmaceuticals, Exton, PA, Martek Biosciences, Columbia, MD, etc.).

The assays to identify modulators are amenable to high throughput screening. Preferred assays thus detect modulation of lung cancer gene transcription, polypeptide expression, and polypeptide activity.

High throughput assays for evaluating the presence, absence, quantification, or other properties of particular nucleic acids or protein products are well known to those of skill in the art. Similarly, binding assays and reporter gene assays are similarly well known. Thus, e.g., U.S. Patent No. 5,559,410 discloses high throughput screening methods for proteins,

U.S. Patent No. 5,585,639 discloses high throughput screening methods for nucleic acid binding (i.e., in arrays), while U.S. Patent Nos. 5,576,220 and 5,541,061 disclose high throughput methods of screening for ligand/antibody binding.

In addition, high throughput screening systems are commercially available (see, e.g.,
5 Zymark Corp., Hopkinton, MA; Air Technical Industries, Mentor, OH; Beckman
Instruments, Inc. Fullerton, CA; Precision Systems, Inc., Natick, MA, etc.). These systems
typically automate procedures, including sample and reagent pipetting, liquid dispensing,
timed incubations, and final readings of the microplate in detector(s) appropriate for the
assay. These configurable systems provide high throughput and rapid start up as well as a
10 high degree of flexibility and customization. The manufacturers of such systems provide
detailed protocols for various high throughput systems. Thus, e.g., Zymark Corp. provides
technical bulletins describing screening systems for detecting the modulation of gene
transcription, ligand binding, and the like.

In one embodiment, modulators are proteins, often naturally occurring proteins or
15 fragments of naturally occurring proteins. Thus, e.g., cellular extracts containing proteins, or
random or directed digests of proteinaceous cellular extracts, may be used. In this way
libraries of proteins may be made for screening in the methods of the invention. Particularly
preferred in this embodiment are libraries of bacterial, fungal, viral, and mammalian proteins,
with the latter being preferred, and human proteins being especially preferred. Particularly
20 useful test compound will be directed to the class of proteins to which the target belongs, e.g.,
substrates for enzymes or ligands and receptors.

In a preferred embodiment, modulators are peptides of from about 5 to about 30
amino acids, with from about 5 to about 20 amino acids being preferred, and from about 7 to
about 15 being particularly preferred. The peptides may be digests of naturally occurring
25 proteins, random peptides, or "biased" random peptides. By "randomized" or grammatical
equivalents herein is meant that the nucleic acid or peptide consists of essentially random
sequences of nucleotides and amino acids, respectively. Since these random peptides (or
nucleic acids, discussed below) are often chemically synthesized, they may incorporate a
nucleotide or amino acid at any position. The synthetic process can be designed to generate
30 randomized proteins or nucleic acids, to allow the formation of all or most of the possible
combinations over the length of the sequence, thus forming a library of randomized candidate
bioactive proteinaceous agents.

In one embodiment, the library is fully randomized, with no sequence preferences or constants at any position. In a preferred embodiment, the library is biased. That is, some positions within the sequence are either held constant, or are selected from a limited number of possibilities. In a preferred embodiment, the nucleotides or amino acid residues are randomized within a defined class, e.g., of hydrophobic amino acids, hydrophilic residues, 5 sterically biased (either small or large) residues, towards the creation of nucleic acid binding domains, the creation of cysteines, for cross-linking, prolines for SH-3 domains, serines, threonines, tyrosines or histidines for phosphorylation sites, etc.

Modulators of lung cancer can also be nucleic acids, as defined above.

10 As described above generally for proteins, nucleic acid modulating agents may be naturally occurring nucleic acids, random nucleic acids, or "biased" random nucleic acids. Digests of procaryotic or eucaryotic genomes may be used as is outlined above for proteins.

In a preferred embodiment, the candidate compounds are organic chemical moieties, a wide variety of which are available in the literature.

15 After a candidate agent has been added and the cells allowed to incubate for some period of time, the sample containing a target sequence is analyzed. If required, the target sequence is prepared using known techniques. For example, the sample may be treated to lyse the cells, using known lysis buffers, electroporation, etc., with purification and/or amplification such as PCR performed as appropriate. For example, an *in vitro* transcription 20 with labels covalently attached to the nucleotides is performed. Generally, the nucleic acids are labeled with biotin-FITC or PE, or with cy3 or cy5.

In a preferred embodiment, the target sequence is labeled with, e.g., a fluorescent, a chemiluminescent, a chemical, or a radioactive signal, to provide a means of detecting the target sequence's specific binding to a probe. The label also can be an enzyme, such as, 25 alkaline phosphatase or horseradish peroxidase, which when provided with an appropriate substrate produces a product that can be detected. Alternatively, the label can be a labeled compound or small molecule, such as an enzyme inhibitor, that binds but is not catalyzed or altered by the enzyme. The label also can be a moiety or compound, such as, an epitope tag or biotin which specifically binds to streptavidin. For the example of biotin, the streptavidin 30 is labeled as described above, thereby, providing a detectable signal for the bound target sequence. Unbound labeled streptavidin is typically removed prior to analysis.

Nucleic acid assays can be direct hybridization assays or can comprise "sandwich assays", which include the use of multiple probes, as is generally outlined in U.S. Patent Nos.

5,681,702, 5,597,909, 5,545,730, 5,594,117, 5,591,584, 5,571,670, 5,580,731, 5,571,670, 5,591,584, 5,624,802, 5,635,352, 5,594,118, 5,359,100, 5,124,246 and 5,681,697, all of which are hereby incorporated by reference. In this embodiment, in general, the target nucleic acid is prepared as outlined above, and then added to the biochip comprising a plurality of
5 nucleic acid probes, under conditions that allow the formation of a hybridization complex.

A variety of hybridization conditions may be used in the present invention, including high, moderate and low stringency conditions as outlined above. The assays are generally run under stringency conditions which allow formation of the label probe hybridization complex only in the presence of target. Stringency can be controlled by altering a step
10 parameter that is a thermodynamic variable, including, but not limited to, temperature, formamide concentration, salt concentration, chaotropic salt concentration, pH, organic solvent concentration, etc.

These parameters may also be used to control non-specific binding, as is generally outlined in U.S. Patent No. 5,681,697. Thus it may be desirable to perform certain steps at
15 higher stringency conditions to reduce non-specific binding.

The reactions outlined herein may be accomplished in a variety of ways. Components of the reaction may be added simultaneously, or sequentially, in different orders, with preferred embodiments outlined below. In addition, the reaction may include a variety of other reagents. These include salts, buffers, neutral proteins, e.g., albumin, detergents, etc.
20 which may be used to facilitate optimal hybridization and detection, and/or reduce non-specific or background interactions. Reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may also be used as appropriate, depending on the sample preparation methods and purity of the target.

The assay data are analyzed to determine the expression levels, and changes in
25 expression levels as between states, of individual genes, forming a gene expression profile.

Screens are performed to identify modulators of the lung cancer phenotype. In one embodiment, screening is performed to identify modulators that can induce or suppress a particular expression profile, thus preferably generating the associated phenotype. In another embodiment, e.g., for diagnostic applications, having identified differentially expressed genes
30 important in a particular state, screens can be performed to identify modulators that alter expression of individual genes. In an another embodiment, screening is performed to identify modulators that alter a biological function of the expression product of a differentially expressed gene. Again, having identified the importance of a gene in a particular state,

screens are performed to identify agents that bind and/or modulate the biological activity of the gene product, or evaluate genetic polymorphisms.

Genes can be screened for those that are induced in response to a candidate agent. After identifying a modulator based upon its ability to suppress a lung cancer expression pattern leading to a normal expression pattern, or to modulate a single lung cancer gene expression profile so as to mimic the expression of the gene from normal tissue, a screen as described above can be performed to identify genes that are specifically modulated in response to the agent. Comparing expression profiles between normal tissue and agent treated lung cancer tissue reveals genes that are not expressed in normal tissue or lung cancer tissue, but are expressed in agent treated tissue. These agent-specific sequences can be identified and used by methods described herein for lung cancer genes or proteins. In particular these sequences and the proteins they encode find use in marking or identifying agent treated cells. In addition, antibodies can be raised against the agent induced proteins and used to target novel therapeutics to the treated lung cancer tissue sample.

Thus, in one embodiment, a test compound is administered to a population of lung cancer cells, that have an associated lung cancer expression profile. By "administration" or "contacting" herein is meant that the candidate agent is added to the cells in such a manner as to allow the agent to act upon the cell, whether by uptake and intracellular action, or by action at the cell surface. In some embodiments, nucleic acid encoding a proteinaceous candidate agent (i.e., a peptide) may be put into a viral construct such as an adenoviral or retroviral construct, and added to the cell, such that expression of the peptide agent is accomplished, e.g., PCT US97/01019. Regulatable gene therapy systems can also be used.

Once a test compound has been administered to the cells, the cells can be washed if desired and are allowed to incubate under preferably physiological conditions for some period of time. The cells are then harvested and a new gene expression profile is generated, as outlined herein.

Thus, e.g., lung cancer or non-malignant tissue may be screened for agents that modulate, e.g., induce or suppress a lung cancer phenotype. A change in at least one gene, preferably many, of the expression profile indicates that the agent has an effect on lung cancer activity. By defining such a signature for the lung cancer phenotype, screens for new drugs that alter the phenotype can be devised. With this approach, the drug target need not be known and need not be represented in the original expression screening platform, nor does the level of transcript for the target protein need to change.

Measure of lung cancer polypeptide activity, or of lung cancer or the lung cancer phenotype can be performed using a variety of assays. For example, the effects of the test compounds upon the function of the metastatic polypeptides can be measured by examining parameters described above. A suitable physiological change that affects activity can be used to assess the influence of a test compound on the polypeptides of this invention. When the functional consequences are determined using intact cells or animals, one can also measure a variety of effects such as, in the case of lung cancer associated with tumors, tumor growth, tumor metastasis, neovascularization, hormone release, transcriptional changes to both known and uncharacterized genetic markers (e.g., northern blots), changes in cell metabolism such as cell growth or pH changes, and changes in intracellular second messengers such as cGMP. In the assays of the invention, mammalian lung cancer polypeptide is typically used, e.g., mouse, preferably human.

Assays to identify compounds with modulating activity can be performed *in vitro*. For example, a lung cancer polypeptide is first contacted with a potential modulator and incubated for a suitable amount of time, e.g., from 0.5 to 48 hours. In one embodiment, the lung cancer polypeptide levels are determined *in vitro* by measuring the level of protein or mRNA. The level of protein is typically measured using immunoassays such as western blotting, ELISA and the like with an antibody that selectively binds to the lung cancer polypeptide or a fragment thereof. For measurement of mRNA, amplification, e.g., using PCR, LCR, or hybridization assays, e.g., northern hybridization, RNase protection, dot blotting, are preferred. The level of protein or mRNA is typically detected using directly or indirectly labeled detection agents, e.g., fluorescently or radioactively labeled nucleic acids, radioactively or enzymatically labeled antibodies, and the like, as described herein.

Alternatively, a reporter gene system can be devised using a lung cancer protein promoter operably linked to a reporter gene such as luciferase, green fluorescent protein, CAT, or β -gal. The reporter construct is typically transfected into a cell. After treatment with a potential modulator, the amount of reporter gene transcription, translation, or activity is measured according to standard techniques known to those of skill in the art.

In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of the expression of the gene or the gene product itself can be done. The gene products of differentially expressed

genes are sometimes referred to herein as "lung cancer proteins." The lung cancer protein may be a fragment, or alternatively, be the full length protein to a fragment shown herein.

In one embodiment, screening for modulators of expression of specific genes is performed. Typically, the expression of only one or a few genes are evaluated. In another
5 embodiment, screens are designed to first find compounds that bind to differentially expressed proteins. These compounds are then evaluated for the ability to modulate differentially expressed activity. Moreover, once initial candidate compounds are identified, variants can be further screened to better evaluate structure activity relationships.

In a preferred embodiment, binding assays are done. In general, purified or isolated
10 gene product is used; that is, the gene products of one or more differentially expressed nucleic acids are made. For example, antibodies are generated to the protein gene products, and standard immunoassays are run to determine the amount of protein present. Alternatively, cells comprising the lung cancer proteins can be used in the assays.

Thus, in a preferred embodiment, the methods comprise combining a lung cancer
15 protein and a candidate compound, and determining the binding of the compound to the lung cancer protein. Preferred embodiments utilize the human lung cancer protein, although other mammalian proteins may also be used, e.g., for the development of animal models of human disease. In some embodiments, as outlined herein, variant or derivative lung cancer proteins may be used.

20 Generally, in a preferred embodiment of the methods herein, the lung cancer protein or the candidate agent is non-diffusably bound to an insoluble support, preferably having isolated sample receiving areas (e.g., a microtiter plate, an array, etc.). The insoluble supports may be made of a composition to which the compositions can be bound, is readily separated from soluble material, and is otherwise compatible with the overall method of
25 screening. The surface of such supports may be solid or porous and of a convenient shape. Examples of suitable insoluble supports include microtiter plates, arrays, membranes and beads. These are typically made of glass, plastic (e.g., polystyrene), polysaccharides, nylon or nitrocellulose, teflon™, etc. Microtiter plates and arrays are especially convenient because a large number of assays can be carried out simultaneously, using small amounts of reagents
30 and samples. The particular manner of binding of the composition is typically not crucial so long as it is compatible with the reagents and overall methods of the invention, maintains the activity of the composition, and is nondiffusable. Preferred methods of binding include the use of antibodies (which do not sterically block either the ligand binding site or activation

sequence when the protein is bound to the support), direct binding to "sticky" or ionic supports, chemical crosslinking, the synthesis of the protein or agent on the surface, etc. Following binding of the protein or agent, excess unbound material is removed by washing. The sample receiving areas may then be blocked through incubation with bovine serum albumin (BSA), casein or other innocuous protein or other moiety.

In a preferred embodiment, the lung cancer protein is bound to the support, and a test compound is added to the assay. Alternatively, the candidate agent is bound to the support and the lung cancer protein is added. Novel binding agents include specific antibodies, non-natural binding agents identified in screens of chemical libraries, peptide analogs, etc. Of particular interest are screening assays for agents that have a low toxicity for human cells. A wide variety of assays may be used for this purpose, including labeled *in vitro* protein-protein binding assays, electrophoretic mobility shift assays, immunoassays for protein binding, functional assays (phosphorylation assays, etc.) and the like.

The determination of the binding of the test modulating compound to the lung cancer protein may be done in a number of ways. In a preferred embodiment, the compound is labeled, and binding determined directly, e.g., by attaching all or a portion of the lung cancer protein to a solid support, adding a labeled candidate agent (e.g., a fluorescent label), washing off excess reagent, and determining whether the label is present on the solid support. Various blocking and washing steps may be utilized as appropriate.

In some embodiments, only one of the components is labeled, e.g., the proteins (or proteinaceous candidate compounds) can be labeled. Alternatively, more than one component can be labeled with different labels, e.g., ^{125}I for the proteins and a fluorophor for the compound. Proximity reagents, e.g., quenching or energy transfer reagents are also useful.

In one embodiment, the binding of the test compound is determined by competitive binding assay. The competitor may be a binding moiety known to bind to the target molecule (i.e., a lung cancer protein), such as an antibody, peptide, binding partner, ligand, etc. Under certain circumstances, there may be competitive binding between the compound and the binding moiety, with the binding moiety displacing the compound. In one embodiment, the test compound is labeled. Either the compound, or the competitor, or both, is added first to the protein for a time sufficient to allow binding, if present. Incubations may be performed at a temperature which facilitates optimal activity, typically between 4 and 40° C. Incubation periods are typically optimized, e.g., to facilitate rapid high throughput screening. Typically

between 0.1 and 1 hour will be sufficient. Excess reagent is generally removed or washed away. The second component is then added, and the presence or absence of the labeled component is followed, to indicate binding.

In a preferred embodiment, the competitor is added first, followed by a test compound. Displacement of the competitor is an indication that the test compound is binding to the lung cancer protein and thus is capable of binding to, and potentially modulating, the activity of the lung cancer protein. In this embodiment, either component can be labeled. Thus, e.g., if the competitor is labeled, the presence of label in the wash solution indicates displacement by the agent. Alternatively, if the test compound is labeled, the presence of the label on the support indicates displacement.

In an alternative embodiment, the test compound is added first, with incubation and washing, followed by the competitor. The absence of binding by the competitor may indicate that the test compound is bound to the lung cancer protein with a higher affinity. Thus, if the test compound is labeled, the presence of the label on the support, coupled with a lack of competitor binding, may indicate that the test compound is capable of binding to the lung cancer protein.

In a preferred embodiment, the methods comprise differential screening to identify agents that are capable of modulating the activity of the lung cancer proteins. In one embodiment, the methods comprise combining a lung cancer protein and a competitor in a first sample. A second sample comprises a test compound, a lung cancer protein, and a competitor. The binding of the competitor is determined for both samples, and a change, or difference in binding between the two samples indicates the presence of an agent capable of binding to the lung cancer protein and potentially modulating its activity. That is, if the binding of the competitor is different in the second sample relative to the first sample, the agent is capable of binding to the lung cancer protein.

Alternatively, differential screening is used to identify drug candidates that bind to the native lung cancer protein, but cannot bind to modified lung cancer proteins. The structure of the lung cancer protein may be modeled, and used in rational drug design to synthesize agents that interact with that site. Drug candidates that affect the activity of a lung cancer protein are also identified by screening drugs for the ability to either enhance or reduce the activity of the protein.

Positive controls and negative controls may be used in the assays. Preferably control and test samples are performed in at least triplicate to obtain statistically significant results.

Incubation of all samples is for a time sufficient for the binding of the agent to the protein. Following incubation, samples are washed free of non-specifically bound material and the amount of bound, generally labeled agent determined. For example, where a radiolabel is employed, the samples may be counted in a scintillation counter to determine the amount of bound compound.

A variety of other reagents may be included in the screening assays. These include reagents like salts, neutral proteins, e.g., albumin, detergents, etc. which may be used to facilitate optimal protein-protein binding and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used. The mixture of components may be added in an order that provides for the requisite binding.

In a preferred embodiment, the invention provides methods for screening for a compound capable of modulating the activity of a lung cancer protein. The methods comprise adding a test compound, as defined above, to a cell comprising lung cancer proteins. Preferred cell types include almost any cell. The cells contain a recombinant nucleic acid that encodes a lung cancer protein. In a preferred embodiment, a library of candidate agents are tested on a plurality of cells.

In one aspect, the assays are evaluated in the presence or absence or previous or subsequent exposure of physiological signals, e.g., hormones, antibodies, peptides, antigens, cytokines, growth factors, action potentials, pharmacological agents including chemotherapeutics, radiation, carcinogenics, or other cells (e.g., cell-cell contacts). In another example, the determinations are determined at different stages of the cell cycle process.

In this way, compounds that modulate lung cancer agents are identified. Compounds with pharmacological activity are able to enhance or interfere with the activity of the lung cancer protein. Once identified, similar structures are evaluated to identify critical structural feature of the compound.

In one embodiment, a method of inhibiting lung cancer cell division is provided. The method comprises administration of a lung cancer inhibitor. In another embodiment, a method of inhibiting lung cancer is provided. The method may comprise administration of a lung cancer inhibitor. In a further embodiment, methods of treating cells or individuals with lung cancer are provided, e.g., comprising administration of a lung cancer inhibitor.

In one embodiment, a lung cancer inhibitor is an antibody as discussed above. In another embodiment, the lung cancer inhibitor is an antisense molecule.

A variety of cell growth, proliferation, viability, and metastasis assays are known to those of skill in the art, as described below.

Soft agar growth or colony formation in suspension

5 Normal cells require a solid substrate to attach and grow. When the cells are transformed, they lose this phenotype and grow detached from the substrate. For example, transformed cells can grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft agar. The transformed cells, when transfected with tumor suppressor genes, regenerate normal phenotype and require a solid substrate to attach and
10 grow. Soft agar growth or colony formation in suspension assays can be used to identify modulators of lung cancer sequences, which when expressed in host cells, inhibit abnormal cellular proliferation and transformation. A therapeutic compound would reduce or eliminate the host cells' ability to grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft.

15 Techniques for soft agar growth or colony formation in suspension assays are described in Freshney (1994) Culture of Animal Cells a Manual of Basic Technique (3rd ed.), herein incorporated by reference. See also, the methods section of Garkavtsev, et al. (1996), *supra*, herein incorporated by reference.

20 *Contact inhibition and density limitation of growth*

Normal cells typically grow in a flat and organized pattern in a petri dish until they touch other cells. When the cells touch one another, they are contact inhibited and stop growing. When cells are transformed, however, the cells are not contact inhibited and continue to grow to high densities in disorganized foci. Thus, the transformed cells grow to a
25 higher saturation density than normal cells. This can be detected morphologically by the formation of a disoriented monolayer of cells or rounded cells in foci within the regular pattern of normal surrounding cells. Alternatively, labeling index with (³H)-thymidine at saturation density can be used to measure density limitation of growth. See Freshney (1994), *supra*. The transformed cells, when transfected with tumor suppressor genes, regenerate a
30 normal phenotype and become contact inhibited and would grow to a lower density.

In this assay, labeling index with (³H)-thymidine at saturation density is a preferred method of measuring density limitation of growth. Transformed host cells are transfected with a lung cancer-associated sequence and are grown for 24 hours at saturation density in

non-limiting medium conditions. The percentage of cells labeling with (^3H)-thymidine is determined autoradiographically. See, Freshney (1994), *supra*.

Growth factor or serum dependence

5 Transformed cells typically have a lower serum dependence than their normal counterparts (see, e.g., Temin (1966) J. Natl. Cancer Inst. 37:167-175; Eagle, et al. (1970) J. Exp. Med. 131:836-879); Freshney, *supra*. This is in part due to release of various growth factors by the transformed cells. Growth factor or serum dependence of transformed host cells can be compared with that of control.

10

Tumor specific markers levels

Tumor cells release an increased amount of certain factors (hereinafter "tumor specific markers") than their normal counterparts. For example, plasminogen activator (PA) is released from human glioma at a higher level than from normal brain cells (see, e.g.,
15 Gullino, "Angiogenesis, tumor vascularization, and potential interference with tumor growth" in Mihich (ed. 1985) Biological Responses in Cancer, pp. 178-184). Similarly, Tumor angiogenesis factor (TAF) is released at a higher level in tumor cells than their normal counterparts. See, e.g., Folkman (1992) "Angiogenesis and Cancer" in Sem Cancer Biol.

Various techniques which measure the release of these factors are described in
20 Freshney (1994), *supra*. Also, see, Unkeless, et al. (1974) J. Biol. Chem. 249:4295-4305; Strickland and Beers (1976) J. Biol. Chem. 251:5694-5702; Whur, et al. (1980) Br. J. Cancer 42:305-312; Gullino, "Angiogenesis, tumor vascularization, and potential interference with tumor growth" in Mihich (ed. 1985) Biological Responses in Cancer, pp. 178-184; Freshney Anticancer Res. 5:111-130 (1985).

25

Invasiveness into Matrigel

The degree of invasiveness into Matrigel or some other extracellular matrix constituent can be used as an assay to identify compounds that modulate lung cancer-associated sequences. Tumor cells exhibit a good correlation between malignancy and
30 invasiveness of cells into Matrigel or some other extracellular matrix constituent. In this assay, tumorigenic cells are typically used as host cells. Expression of a tumor suppressor gene in these host cells would decrease invasiveness of the host cells.

Techniques described in Freshney (1994), *supra*, can be used. Briefly, the level of invasion of host cells can be measured by using filters coated with Matrigel or some other extracellular matrix constituent. Penetration into the gel, or through to the distal side of the filter, is rated as invasiveness, and rated histologically by number of cells and distance
5 moved, or by prelabeling the cells with ^{125}I and counting the radioactivity on the distal side of the filter or bottom of the dish. See, e.g., Freshney (1984), *supra*.

Tumor growth in vivo

Effects of lung cancer-associated sequences on cell growth can be tested in transgenic
10 or immune-suppressed mice. Knock-out transgenic mice can be made, in which the lung cancer gene is disrupted or in which a lung cancer gene is inserted. Knock-out transgenic mice can be made by insertion of a marker gene or other heterologous gene into the endogenous lung cancer gene site in the mouse genome via homologous recombination. Such mice can also be made by substituting the endogenous lung cancer gene with a mutated
15 version of the lung cancer gene, or by mutating the endogenous lung cancer gene, e.g., by exposure to carcinogens.

A DNA construct is introduced into the nuclei of embryonic stem cells. Cells containing the newly engineered genetic lesion are injected into a host mouse embryo, which is re-implanted into a recipient female. Some of these embryos develop into chimeric mice
20 that possess germ cells partially derived from the mutant cell line. Therefore, by breeding the chimeric mice it is possible to obtain a new line of mice containing the introduced genetic lesion (see, e.g., Capecchi, et al. (1989) Science 244:1288). Chimeric targeted mice can be derived according to Hogan, et al. (1988) Manipulating the Mouse Embryo: A Laboratory Manual, Cold Spring Harbor Laboratory and Robertson (ed. 1987) Teratocarcinomas and
25 Embryonic Stem Cells: A Practical Approach, IRL Press, Washington, D.C.

Alternatively, various immune-suppressed or immune-deficient host animals can be used. For example, genetically athymic "nude" mouse (see, e.g., Giovanella, et al. (1974) J. Natl. Cancer Inst. 52:921), a SCID mouse, a thymectomized mouse, or an irradiated mouse (see, e.g., Bradley, et al. (1978) Br. J. Cancer 38:263; Selby, et al. (1980) Br. J. Cancer 41:52)
30 can be used as a host. Transplantable tumor cells (typically about 10^6 cells) injected into isogenic hosts will produce invasive tumors in a high proportions of cases, while normal cells of similar origin will not. In hosts which developed invasive tumors, cells expressing a lung cancer-associated sequences are injected subcutaneously. After a suitable length of time,

preferably 4-8 weeks, tumor growth is measured (e.g., by volume or by its two largest dimensions) and compared to the control. Tumors that have statistically significant reduction (using, e.g., Student's T test) are said to have inhibited growth.

5 Polynucleotide modulators of lung cancer

Antisense and RNAi Polynucleotides

In certain embodiments, the activity of a lung cancer-associated protein is downregulated, or entirely inhibited, by the use of antisense or an inhibitory polynucleotide, i.e., a nucleic acid complementary to, and which can preferably hybridize specifically to, a
10 coding mRNA nucleic acid sequence, e.g., a lung cancer protein mRNA, or a subsequence thereof. Binding of the antisense polynucleotide to the mRNA reduces the translation and/or stability of the mRNA.

In the context of this invention, antisense polynucleotides can comprise naturally-occurring nucleotides, or synthetic species formed from naturally-occurring subunits or their
15 close homologs. Antisense polynucleotides may also have altered sugar moieties or inter-sugar linkages. Exemplary among these are the phosphorothioate and other sulfur containing species which are known for use in the art. Analogs are comprehended by this invention so long as they function effectively to hybridize with the lung cancer protein mRNA. See, e.g., Isis Pharmaceuticals, Carlsbad, CA; Sequitor, Inc., Natick, MA.

20 Such antisense polynucleotides can readily be synthesized using recombinant means, or can be synthesized *in vitro*. Equipment for such synthesis is sold by several vendors, including Applied Biosystems. The preparation of other oligonucleotides such as phosphorothioates and alkylated derivatives is also well known to those of skill in the art.

Antisense molecules as used herein include antisense or sense oligonucleotides.
25 Sense oligonucleotides can, e.g., be employed to block transcription by binding to the antisense strand. The antisense and sense oligonucleotide comprise a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target mRNA (sense) or DNA (antisense) sequences for lung cancer molecules. A preferred antisense molecule is for a lung cancer sequence in the tables, or for a ligand or activator thereof. Antisense or sense
30 oligonucleotides, according to the present invention, comprise a fragment generally at least about 14 nucleotides, preferably from about 14 to 30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein

is described in, e.g., Stein and Cohen (1988) Cancer Res. 48:2659 and van der Krol, et al. (1988) BioTechniques 6:958).

RNA interference is a mechanism to suppress gene expression in a sequence specific manner. See, e.g., Brumelkamp, et al. (2002) Scienceexpress (21March2002); Sharp (1999) Genes Dev. 13:139-141; and Cathew (2001) Curr. Op. Cell Biol. 13:244-248. In mammalian cells, short, e.g., 21 nt, double stranded small interfering RNAs (siRNA) have been shown to be effective at inducing an RNAi response. See, e.g., Elbashir, et al. (2001) Nature 411:494-498. The mechanism may be used to downregulate expression levels of identified genes, e.g., treatment of or validation of relevance to disease.

Ribozymes

In addition to antisense polynucleotides, ribozymes can be used to target and inhibit transcription of lung cancer-associated nucleotide sequences. A ribozyme is an RNA molecule that catalytically cleaves other RNA molecules. Different kinds of ribozymes have been described, including group I ribozymes, hammerhead ribozymes, hairpin ribozymes, RNase P, and axhead ribozymes (see, e.g., Castanotto, et al. (1994) Adv. in Pharmacology 25: 289-317 for a general review of the properties of different ribozymes).

The general features of hairpin ribozymes are described, e.g., in Hampel, et al. (1990) Nucl. Acids Res. 18:299-304; European Patent Publication No. 0 360 257; U.S. Patent No. 5,254,678. Methods of preparing are well known to those of skill in the art (see, e.g., WO 94/26877; Ojwang, et al. (1993) Proc. Natl. Acad. Sci. USA 90:6340-6344; Yamada, et al. (1994) Human Gene Therapy 1:39-45; Leavitt, et al. (1995) Proc. Natl. Acad. Sci. USA 92:699-703; Leavitt, et al. (19994) Human Gene Therapy 5:1151-120; and Yamada, et al. (1994) Virology 205: 121-126).

Polynucleotide modulators of lung cancer may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell. Alternatively, a polynucleotide modulator of lung cancer may be introduced into a cell containing the target nucleic acid sequence, e.g., by

formation of an polynucleotide-lipid complex, as described in WO 90/10448. It is understood that the use of antisense molecules or knock out and knock in models may also be used in screening assays as discussed above, in addition to methods of treatment.

Thus, in one embodiment, methods of modulating lung cancer in cells or organisms are provided. In one embodiment, the methods comprise administering to a cell an anti-lung cancer antibody that reduces or eliminates the biological activity of an endogenous lung cancer protein. Alternatively, the methods comprise administering to a cell or organism a recombinant nucleic acid encoding a lung cancer protein. This may be accomplished in any number of ways. In a preferred embodiment, e.g., when the lung cancer sequence is down-regulated in lung cancer, such state may be reversed by increasing the amount of lung cancer gene product in the cell. This can be accomplished, e.g., by overexpressing the endogenous lung cancer gene or administering a gene encoding the lung cancer sequence, using known gene-therapy techniques. In a preferred embodiment, the gene therapy techniques include the incorporation of the exogenous gene using enhanced homologous recombination (EHR), e.g., as described in PCT/US93/03868, hereby incorporated by reference in its entirety. Alternatively, e.g., when the lung cancer sequence is up-regulated in lung cancer, the activity of the endogenous lung cancer gene is decreased, e.g., by the administration of a lung cancer antisense or RNAi nucleic acid.

In one embodiment, the lung cancer proteins of the present invention may be used to generate polyclonal and monoclonal antibodies to lung cancer proteins. Similarly, the lung cancer proteins can be coupled, using standard technology, to affinity chromatography columns. These columns may then be used to purify lung cancer antibodies useful for production, diagnostic, or therapeutic purposes. In a preferred embodiment, the antibodies are generated to epitopes unique to a lung cancer protein; that is, the antibodies show little or no cross-reactivity to other proteins. The lung cancer antibodies may be coupled to standard affinity chromatography columns and used to purify lung cancer proteins. The antibodies may also be used as blocking polypeptides, as outlined above, since they will specifically bind to the lung cancer protein.

Methods of identifying variant lung cancer-associated sequences

Without being bound by theory, expression of various lung cancer sequences is correlated with lung cancer. Accordingly, disorders based on mutant or variant lung cancer genes may be determined. In one embodiment, the invention provides methods for

identifying cells containing variant lung cancer genes, e.g., determining all or part of the sequence of at least one endogenous lung cancer genes in a cell. In a preferred embodiment, the invention provides methods of identifying the lung cancer genotype of an individual, e.g., determining all or part of the sequence of at least one lung cancer gene of the individual.

5 This is generally done in at least one tissue of the individual, and may include the evaluation of a number of tissues or different samples of the same tissue. The method may include comparing the sequence of the sequenced lung cancer gene to a known lung cancer gene, i.e., a wild-type gene.

10 The sequence of all or part of the lung cancer gene can then be compared to the sequence of a known lung cancer gene to determine if any differences exist. This can be done using known homology programs, such as Bestfit, etc. In a preferred embodiment, the presence of a difference in the sequence between the lung cancer gene of the patient and the known lung cancer gene correlates with a disease state or a propensity for a disease state, as outlined herein.

15 In a preferred embodiment, the lung cancer genes are used as probes to determine the number of copies of the lung cancer gene in the genome.

In another preferred embodiment, the lung cancer genes are used as probes to determine the chromosomal localization of the lung cancer genes. Information such as chromosomal localization finds use in providing a diagnosis or prognosis in particular when
20 chromosomal abnormalities such as translocations, and the like are identified in the lung cancer gene locus.

Administration of pharmaceutical and vaccine compositions

In one embodiment, a therapeutically effective dose of a lung cancer protein or
25 modulator thereof, is administered to a patient. By "therapeutically effective dose" herein is meant a dose that produces effects for which it is administered. The exact dose will depend on the purpose of the treatment, and will be ascertainable by one skilled in the art using known techniques (e.g., Ansel, et al. (1992) Pharmaceutical Dosage Forms and Drug Delivery; Lieberman, Pharmaceutical Dosage Forms (vols. 1-3), Dekker, ISBN 0824770846,
30 082476918X, 0824712692, 0824716981; Lloyd (1999) The Art, Science and Technology of Pharmaceutical Compounding; and Pickar (1999) Dosage Calculations). Adjustments for lung cancer degradation, systemic versus localized delivery, and rate of new protease synthesis, as well as the age, body weight, general health, sex, diet, time of administration,

drug interaction and the severity of the condition may be necessary, and will be ascertainable with routine experimentation by those skilled in the art.

A "patient" for the purposes of the present invention includes both humans and other animals, particularly mammals. Thus the methods are applicable to both human therapy and
5 veterinary applications. In the preferred embodiment the patient is a mammal, preferably a primate, and in the most preferred embodiment the patient is human.

The administration of the lung cancer proteins and modulators thereof of the present invention can be done in a variety of ways, including, but not limited to, orally, subcutaneously, intravenously, intranasally, transdermally, intraperitoneally, intramuscularly,
10 intrapulmonary, vaginally, rectally, or intraocularly. In some instances, e.g., in the treatment of wounds and inflammation, the lung cancer proteins and modulators may be directly applied as a solution or spray.

The pharmaceutical compositions of the present invention comprise a lung cancer protein in a form suitable for administration to a patient. In the preferred embodiment, the
15 pharmaceutical compositions are in a water soluble form, such as being present as pharmaceutically acceptable salts, which is meant to include both acid and base addition salts. "Pharmaceutically acceptable acid addition salt" refers to those salts that retain the biological effectiveness of the free bases and that are not biologically or otherwise undesirable, formed with inorganic acids such as hydrochloric acid, hydrobromic acid,
20 sulfuric acid, nitric acid, phosphoric acid and the like, and organic acids such as acetic acid, propionic acid, glycolic acid, pyruvic acid, oxalic acid, maleic acid, malonic acid, succinic acid, fumaric acid, tartaric acid, citric acid, benzoic acid, cinnamic acid, mandelic acid, methanesulfonic acid, ethanesulfonic acid, p-toluenesulfonic acid, salicylic acid and the like. "Pharmaceutically acceptable base addition salts" include those derived from inorganic bases
25 such as sodium, potassium, lithium, ammonium, calcium, magnesium, iron, zinc, copper, manganese, aluminum salts and the like. Particularly preferred are the ammonium, potassium, sodium, calcium, and magnesium salts. Salts derived from pharmaceutically acceptable organic non-toxic bases include salts of primary, secondary, and tertiary amines, substituted amines including naturally occurring substituted amines, cyclic amines and basic
30 ion exchange resins, such as isopropylamine, trimethylamine, diethylamine, triethylamine, tripropylamine, and ethanolamine.

The pharmaceutical compositions may also include one or more of the following: carrier proteins such as serum albumin; buffers; fillers such as microcrystalline cellulose,

lactose, corn and other starches; binding agents; sweeteners and other flavoring agents; coloring agents; and polyethylene glycol.

The pharmaceutical compositions can be administered in a variety of unit dosage forms depending upon the method of administration. For example, unit dosage forms
5 suitable for oral administration include, but are not limited to, powder, tablets, pills, capsules and lozenges. It is recognized that lung cancer protein modulators (e.g., antibodies, antisense constructs, ribozymes, small organic molecules, etc.) when administered orally, should be protected from digestion. This is typically accomplished either by complexing the
10 molecule(s) with a composition to render it resistant to acidic and enzymatic hydrolysis, or by packaging the molecule(s) in an appropriately resistant carrier, such as a liposome or a protection barrier. Means of protecting agents from digestion are well known in the art.

The compositions for administration will commonly comprise a lung cancer protein modulator dissolved in a pharmaceutically acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers can be used, e.g., buffered saline and the like. These solutions
15 are sterile and generally free of undesirable matter. These compositions may be sterilized by conventional, well known sterilization techniques. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions such as pH adjusting and buffering agents, toxicity adjusting agents and the like,
20 e.g., sodium acetate, sodium chloride, potassium chloride, calcium chloride, sodium lactate and the like. The concentration of active agent in these formulations can vary widely, and will be selected primarily based on fluid volumes, viscosities, body weight and the like in accordance with the particular mode of administration selected and the patient's needs (e.g., Remington's Pharmaceutical Science (15th ed., 1980) and Hardman, et al. (eds. 1996) Goodman and Gilman: The Pharmacological Basis of Therapeutics).

25 Thus, a typical pharmaceutical composition for intravenous administration would be about 0.1 to 10 mg per patient per day. Dosages from 0.1 up to about 100 mg per patient per day may be used, particularly when the drug is administered to a secluded site and not into the blood stream, such as into a body cavity or into a lumen of an organ. Substantially higher dosages are possible in topical administration. Actual methods for preparing parenterally
30 administrable compositions will be known or apparent to those skilled in the art, e.g., Remington's Pharmaceutical Science and Goodman and Gilman, The Pharmacological Basis of Therapeutics, *supra*.

The compositions containing modulators of lung cancer proteins can be administered for therapeutic or prophylactic treatments. In therapeutic applications, compositions are administered to a patient suffering from a disease (e.g., a cancer) in an amount sufficient to cure or at least partially arrest the disease and its complications. An amount adequate to accomplish this is defined as a "therapeutically effective dose." Amounts effective for this use will depend upon the severity of the disease and the general state of the patient's health. Single or multiple administrations of the compositions may be administered depending on the dosage and frequency as required and tolerated by the patient. In any event, the composition should provide a sufficient quantity of the agents of this invention to effectively treat the patient. An amount of modulator that is capable of preventing or slowing the development of cancer in a mammal is referred to as a "prophylactically effective dose." The particular dose required for a prophylactic treatment will depend upon the medical condition and history of the mammal, the particular cancer being prevented, as well as other factors such as age, weight, gender, administration route, efficiency, etc. Such prophylactic treatments may be used, e.g., in a mammal who has previously had cancer to prevent a recurrence of the cancer, or in a mammal who is suspected of having a significant likelihood of developing cancer based, at least in part, upon gene expression profiles. Vaccine strategies may be used, in either a DNA vaccine form, or protein vaccine.

It will be appreciated that the present lung cancer protein-modulating compounds can be administered alone or in combination with additional lung cancer modulating compounds or with other therapeutic agent, e.g., other anti-cancer agents or treatments.

In numerous embodiments, one or more nucleic acids, e.g., polynucleotides comprising nucleic acid sequences set forth in the tables, such as antisense or RNAi polynucleotides or ribozymes, will be introduced into cells, *in vitro* or *in vivo*. The present invention provides methods, reagents, vectors, and cells useful for expression of lung cancer-associated polypeptides and nucleic acids using *in vitro* (cell-free), *ex vivo*, or *in vivo* (cell or organism-based) recombinant expression systems.

The particular procedure used to introduce the nucleic acids into a host cell for expression of a protein or nucleic acid is application specific. Many procedures for introducing foreign nucleotide sequences into host cells may be used. These include the use of calcium phosphate transfection, spheroplasts, electroporation, liposomes, microinjection, plasma vectors, viral vectors and other well known methods for introducing cloned genomic DNA, cDNA, synthetic DNA or other foreign genetic material into a host cell (see, e.g.,

Berger and Kimmel, Guide to Molecular Cloning Techniques. Methods in Enzymology volume 152 (Berger), Ausubel, et al. (eds. 1999) Current Protocols (supplemented through 1999), and Sambrook, et al. (1989) Molecular Cloning - A Laboratory Manual (2nd ed., Vol. 1-3).

5 In a preferred embodiment, lung cancer proteins and modulators are administered as therapeutic agents, and can be formulated as outlined above. Similarly, lung cancer genes (including both the full-length sequence, partial sequences, or regulatory sequences of the lung cancer coding regions) can be administered in a gene therapy application. These lung cancer genes can include antisense or inhibitory applications, e.g., as inhibitory RNA or gene
10 therapy (e.g., for incorporation into the genome) or as antisense compositions.

Lung cancer polypeptides and polynucleotides can also be administered as vaccine compositions to stimulate HTL, CTL, and antibody responses.. Such vaccine compositions can include, e.g., lipidated peptides (see, e.g., Vitiello, et al. (1995) J. Clin. Invest. 95:341), peptide compositions encapsulated in poly(DL-lactide-co-glycolide) ("PLG") microspheres
15 (see, e.g., Eldridge, et al. (1991) Molec. Immunol. 28:287-294; Alonso, et al. (1994) Vaccine 12:299-306; Jones, et al. (1995) Vaccine 13:675-681), peptide compositions contained in immune stimulating complexes (ISCOMS) (see, e.g., Takahashi, et al. (1990) Nature 344:873-875; Hu, et al. (1998) Clin Exp Immunol. 113:235-243), multiple antigen peptide systems (MAPs) (see, e.g., Tam (1988) Proc. Natl. Acad. Sci. U.S.A. 85:5409-5413; Tam
20 (1996) J. Immunol. Methods 196:17-32), peptides formulated as multivalent peptides; peptides for use in ballistic delivery systems, typically crystallized peptides, viral delivery vectors (Perkus, et al., p. 379 In: Kaufmann (ed. 1996) Concepts in vaccine development; Chakrabarti, et al. (1986) Nature 320:535; Hu, et al. (1986) Nature 320:537; Kieny, et al. (1986) AIDS Bio/Technology 4:790; Top, et al. (1971) J. Infect. Dis. 124:148; Chanda, et al.
25 (1990) Virology 175:535), particles of viral or synthetic origin (see, e.g., Kofler, et al. (1996) J. Immunol. Methods 192:25; Eldridge, et al. (1993) Sem. Hematol. 30:16; Falo, et al. (1995) Nature Med. 7:649), adjuvants (Warren, et al. (1986) Annu. Rev. Immunol. 4:369; Gupta, et al. (1993) Vaccine 11:293), liposomes (Reddy, et al. (1992) J. Immunol. 148:1585; Rock (1996) Immunol. Today 17:131), or, naked or particle absorbed cDNA (Ulmer, et al. (1993)
30 Science 259:1745; Robinson, et al. (1993) Vaccine 11:957; Shiver, et al., p. 423 In: Kaufmann (ed. 1996) Concepts in vaccine development; Cease and Berzofsky (1994) Annu. Rev. Immunol. 12:923 and Eldridge, et al. (1993) Sem. Hematol. 30:16). Toxin-targeted

delivery technologies, also known as receptor mediated targeting, such as those of Avant Immunotherapeutics, Inc. (Needham, Massachusetts) may also be used.

Vaccine compositions often include adjuvants. Many adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, *Bordetella pertussis* or *Mycobacterium tuberculosis* derived proteins. Certain adjuvants are commercially available as, e.g., Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); AS-2 (SmithKline Beecham, Philadelphia, PA); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF, interleukin-2, -7, -12, and other like growth factors, may also be used as adjuvants.

Vaccines can be administered as nucleic acid compositions wherein DNA or RNA encoding one or more of the polypeptides, or a fragment thereof, is administered to a patient. This approach is described, for instance, in Wolff, et. al. (1990) Science 247:1465 as well as U.S. Patent Nos. 5,580,859; 5,589,466; 5,804,566; 5,739,118; 5,736,524; 5,679,647; WO 98/04720; and in more detail below. Examples of DNA-based delivery technologies include "naked DNA", facilitated (bupivacaine, polymers, peptide-mediated) delivery, cationic lipid complexes, and particle-mediated ("gene gun") or pressure-mediated delivery (see, e.g., U.S. Patent No. 5,922,687).

For therapeutic or prophylactic immunization purposes, the peptides of the invention can be expressed by viral or bacterial vectors. Examples of expression vectors include attenuated viral hosts, such as vaccinia or fowlpox. This approach involves the use of vaccinia virus, e.g., as a vector to express nucleotide sequences that encode lung cancer polypeptides or polypeptide fragments. Upon introduction into a host, the recombinant vaccinia virus expresses the immunogenic peptide, and thereby elicits an immune response. Vaccinia vectors and methods useful in immunization protocols are described in, e.g., U.S. Patent No. 4,722,848. Another vector is BCG (Bacille Calmette Guerin). BCG vectors are described in Stover, et al. (1991) Nature 351:456-460. A wide variety of other vectors useful for therapeutic administration or immunization e.g., adeno and adeno-associated virus vectors, retroviral vectors, *Salmonella typhi* vectors, detoxified anthrax toxin vectors, and the

like, will be apparent to those skilled in the art from the description herein (see, e.g., Shata, et al. (2000) Mol Med Today 6:66-71; Shedlock, et al. (2000) J. Leukoc. Biol. 68:793-806; Hipp, et al. (2000) In Vivo 14:571-85).

5 Methods for the use of genes as DNA vaccines are well known, and include placing a lung cancer gene or portion of a lung cancer gene under the control of a regulatable promoter or a tissue-specific promoter for expression in a lung cancer patient. The lung cancer gene used for DNA vaccines can encode full-length lung cancer proteins, but more preferably encodes portions of the lung cancer proteins including peptides derived from the lung cancer protein. In one embodiment, a patient is immunized with a DNA vaccine comprising a
10 plurality of nucleotide sequences derived from a lung cancer gene. For example, lung cancer-associated genes or sequence encoding subfragments of a lung cancer protein are introduced into expression vectors and tested for their immunogenicity in the context of Class I MHC and an ability to generate cytotoxic T cell responses. This procedure provides for production of cytotoxic T cell responses against cells which present antigen, including intracellular
15 epitopes.

 In a preferred embodiment, DNA vaccines include a gene encoding an adjuvant molecule with the DNA vaccine. Such adjuvant molecules include cytokines that increase the immunogenic response to the lung cancer polypeptide encoded by the DNA vaccine. Additional or alternative adjuvants are available.

20 In another preferred embodiment lung cancer genes find use in generating animal models of lung cancer. When the lung cancer gene identified is repressed or diminished in metastatic tissue, gene therapy technology, e.g., wherein antisense or inhibitory RNA directed to the lung cancer gene will also diminish or repress expression of the gene. Animal models of lung cancer find use in screening for modulators of a lung cancer-associated sequence or
25 modulators of lung cancer. Similarly, transgenic animal technology including gene knockout technology, e.g., as a result of homologous recombination with an appropriate gene targeting vector, will result in the absence or increased expression of the lung cancer protein. When desired, tissue-specific expression or knockout of the lung cancer protein may be necessary.

 It is also possible that the lung cancer protein is overexpressed in lung cancer. As
30 such, transgenic animals can be generated that overexpress the lung cancer protein. Depending on the desired expression level, promoters of various strengths can be employed to express the transgene. Also, the number of copies of the integrated transgene can be determined and compared for a determination of the expression level of the transgene.

Animals generated by such methods will find use as animal models of lung cancer and are additionally useful in screening for modulators to treat lung cancer.

Kits for Use in Diagnostic and/or Prognostic Applications

5 For use in diagnostic, research, and therapeutic applications suggested above, kits are also provided by the invention. In diagnostic and research applications such kits may include at least one of the following: assay reagents, buffers, lung cancer-specific nucleic acids or antibodies, hybridization probes and/or primers, antisense polynucleotides, ribozymes, RNAi, dominant negative lung cancer polypeptides or polynucleotides, small molecule inhibitors of
10 lung cancer-associated sequences, etc. A therapeutic product may include sterile saline or another pharmaceutically acceptable emulsion and suspension base.

 In addition, the kits may include instructional materials containing instructions (e.g., protocols) for the practice of the methods of this invention. While the instructional materials typically comprise written or printed materials they are not limited to such. A medium
15 capable of storing such instructions and communicating them to an end user is contemplated by this invention. Such media include, but are not limited to electronic storage media (e.g., magnetic discs, tapes, cartridges, chips), optical media (e.g., CD ROM), and the like. Such media may include addresses to internet sites that provide such instructional materials.

 The present invention also provides for kits for screening for modulators of lung
20 cancer-associated sequences. Such kits can be prepared from readily available materials and reagents. For example, such kits can comprise one or more of the following materials: a lung cancer-associated polypeptide or polynucleotide, reaction tubes, and instructions for testing lung cancer-associated activity. Optionally, the kit contains biologically active lung cancer protein. A wide variety of kits and components can be prepared according to the present
25 invention, depending upon the intended user of the kit and the particular needs of the user. Diagnosis would typically involve evaluation of a plurality of genes or products. The genes typically will be selected based on correlations with important parameters in disease which may be identified in historical or outcome data.

EXAMPLES

Example 1: Gene Chip Analysis

5 Molecular profiles of various normal and cancerous tissues were determined and analyzed using gene chips. RNA was isolated and gene chip analysis was performed as described (Glynne, et al. (2000) Nature 403:672-676; Zhao, et al. (2000) Genes Dev. 14:981-993).

Tables 1A and 1B were previously filed on April 18, 2001 in USSN 60/284,770 (18501-001500US) and on November 29, 2001 in USSN 60/334,370 (18501-001520US)

5	Table 1A					
	Pkey	ExAccn	UnigenID	Unigene Title	70% chron/90% NL	70% SQAD/90% NL
	100134	D13264	Hs.49	macrophage scavenger receptor 1	1.61	0.74
	100780	HG3731-HT4001		***Immunoglobulin Heavy Chain, VdJc Reg	2.68	3.28
10	100971	J02874	Hs.83213	fatty acid binding protein 4; adipocyte	1.96	0.14
	101088	L05568	Hs.553	solute carrier family 6 (neurotransmitter)	0.79	0.07
	101102	L07594	Hs.79059	transforming growth factor; beta receptor	2.55	1
	101168	L15388	Hs.211569	G protein-coupled receptor kinase 5	0.88	0.27
	101277	L38486	Hs.118223	microfibrillar-associated protein 4	0.89	0.26
15	101330	L43821	Hs.80261	enhancer of filamentation 1 (cas-like do	0.59	0.29
	101336	L49169	Hs.75678	FBJ murine osteosarcoma viral oncogene h	1.15	0.41
	101345	L76380	Hs.152175	calcitonin receptor-like	0.81	0.31
	101678	M62505	Hs.2161	complement component 5 receptor 1 (C5a I	1.31	0.77
	101764	M80563	Hs.81256	S100 calcium-binding protein A4 (calcium	1.44	0.82
20	101771	M81750	Hs.153837	myeloid cell nuclear differentiation ant	0.96	0.45
	101842	M93221	Hs.75182	mannose receptor; C type 1	1.27	0.37
	102283	U31384	Hs.83381	guanine nucleotide binding protein 11	1.04	0.3
	102363	U39447	Hs.198241	amine oxidase; copper containing 3 (vasc	0.96	0.26
	102507	U52154	Hs.193044	potassium inwardly-rectifying channel; s	2.81	3.45
25	102698	U75272	Hs.1867	progastricsin (pepsinogen C)	0.95	0.23
	103025	X54131	Hs.123641	protein tyrosine phosphatase; receptor t	1.62	0.21
	103280	X79981	Hs.76206	cadherin 5; VE-cadherin (vascular epithe	0.9	0.41
	103496	Y09267	Hs.132821	flavin containing monooxygenase 2	1.27	0.49
	103541	Z11697	Hs.79197	CD83 antigen (activated B lymphocytes; I	1.86	1
30	103554	Z18951	Hs.74034	caveolin 1; caveolae protein; 22kD	1.27	0.47
	104212	AB002298	Hs.173035	KIAA0300 protein	1.17	0.16
	104691	AA011176	Hs.37744	ESTs	1.08	0.35
	104825	AA035613	Hs.141883	ESTs	0.75	0.27
	104857	AA043219	Hs.19058	ESTs	2.6	3.3
35	104865	AA045136	Hs.22575	ESTs	1.23	0.49
	104989	AA102098	Hs.118615	ESTs	0.63	0.32
	105729	AA292694	Hs.3807	ESTs; Weakly similar to PHOSPHOLEMMAN PR	0.86	0.34
	105847	AA398606	Hs.32241	ESTs	1.32	0.4
	105894	AA400979	Hs.25691	calcitonin receptor-like receptor activi	0.78	0.28
	106490	AA451861	Hs.115537	ESTs; Weakly similar to dipeptidase prec	1.2	0.47
40	106536	AA453997	Hs.23804	ESTs	0.82	0.15
	106605	AA457718	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076 (fr	0.99	0.07
	106667	AA461086	Hs.16578	ESTs	1.17	0.4
	106773	AA478109	Hs.188833	ESTs	1.46	0.43
45	106797	AA478962	Hs.169943	ESTs	1.18	0.32
	106844	AA485055	Hs.158213	sperm associated antigen 6	0.98	0.51
	106870	AA487576	Hs.26530	serum deprivation response (phosphatidyl	1.05	0.14
	106954	AA496980	Hs.204038	ESTs	1.25	0.33
	107054	AA600150	Hs.14366	ESTs	1.11	0.4
50	107292	T30407	Hs.4789	ESTs; Weakly similar to oxidative-stress	1.07	2.58
	107994	AA036811	Hs.165030	ESTs	0.7	0.21
	107997	AA037388	Hs.82223	Human DNA sequence from clone 141H5 on c	1.02	0.48
	108041	AA041552	Hs.61957	ESTs	1.44	0.51
	108087	AA045709	Hs.40545	ESTs	1.98	1
55	108382	AA074885	Hs.67726	macrophage receptor with collagenous str	1.52	0.72
	108435	AA078787	Hs.194101	ESTs	2.53	1.53
	108480	AA081093	Hs.68055	ESTs	1.56	0.48
	109252	AA194830	Hs.85944	ESTs	2.69	3.18
	109550	F01534	Hs.26981	ESTs	1.19	0.65
60	109613	F03031	Hs.27519	ESTs	1.01	0.29
	109837	H00656	Hs.29792	ESTs	0.81	0.15
	109893	H04768	Hs.30484	ESTs	1.44	0.32
	109984	H09594	Hs.10299	ESTs	0.62	0.14
	110099	H16568	Hs.23748	ESTs	1.01	0.28
65	110837	N30796	Hs.17424	ESTs; Weakly similar to semaphorin F [H.	1.1	0.22
	111247	N59825	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	1.26	0.26
	111341	N80935	Hs.22483	ESTs	1.57	0.52
	111510	R07856	Hs.16355	ESTs	3.96	1
	111737	R25410	Hs.9218	ESTs	0.97	0.24
70	113195	T57112		***yc20g11.s1 Stralagene lung (#937210)	1.22	0.35
	113238	T62979	Hs.189813	ESTs	2.27	0.45
	113540	T90496	Hs.16757	ESTs	1.06	0.22
	113552	T90889	Hs.16026	ESTs	1.16	0.42
	113606	T93093	Hs.17125	ESTs	1.48	0.7
75	113695	T96965	Hs.17948	ESTs	1.54	0.28
	113946	W84753	Hs.37896	ESTs	1.79	0.72
	114261	Z39898	Hs.21948	ESTs	1.95	0.25
	114359	Z41589	Hs.153483	ESTs; Moderately similar to H1 chloride	1.42	0.13
	115230	AA278300	Hs.182980	ESTs	2.62	0.42
80	115279	AA279760	Hs.63671	ESTs	1.79	0.91
	115566	AA398083	Hs.43977	ESTs	0.86	0.2
	115965	AA446661	Hs.173233	ESTs	0.79	0.04
	116166	AA461556	Hs.202949	KIAA1102 protein	2.29	0.68
	116279	AA486073	Hs.57362	ESTs	2.27	0.78
	117023	H88167	Hs.41105	ESTs	1.36	0.16

	117209	H99959	Hs.42768	ESTs	1.46	0.48
	118901	N90719	Hs.94445	ESTs	1.51	1
	118981	N93839	Hs.39288	ESTs	1.34	0.48
5	118073	R32894	Hs.45514	v-ets avian erythroblastosis virus E26 o	1.14	0.27
	119221	R98105		***yr30g11.s1 Soares fetal liver spleen	1.32	0.53
	119824	W74536	Hs.184	advanced glycosylation end product-speci	1	0.19
	119861	W80715		ESTs; Moderately similar to IIII ALU SUB	1.83	0.45
	120041	W92775	Hs.59368	ESTs	1.23	0.55
10	120132	Z38839	Hs.125019	ESTs; Highly similar to KIAA0886 protein	0.91	0.37
	120467	AA251579	Hs.187628	ESTs	1.87	1.91
	121314	AA402799	Hs.182538	ESTs	1.3	0.31
	121643	AA417078	Hs.193767	ESTs	2.31	0.68
	121690	AA418074	Hs.110286	ESTs	1.47	0.51
	122633	AA454080	Hs.34853	inhibitor of DNA binding 4; dominant neg	1.31	0.63
15	123978	C20653	Hs.170278	ESTs	1.52	0.32
	124214	H58608	Hs.151323	ESTs	0.93	0.35
	124357	N22401		***yw37g07.s1 Morton Fetal Cochlea Homo	1.29	1
	124438	N40188	Hs.102550	ESTs	1.36	0.7
	125167	W45560	Hs.102541	ESTs	1.46	0.69
20	125174	W51835	Hs.231082	EST	3.07	3.76
	125422	AA903229	Hs.153717	ESTs	1.34	0.3
	125561	AI417667	Hs.22978	ESTs	1.89	0.63
	125831	D60988		***HUM145B08B Clontech human fetal brain	0.94	0.36
	127002	R35380	Hs.24979	ESTs	3.02	4.06
25	127307	AA369367	Hs.126712	ESTs; Weakly similar to pL2 hypotheticala	1.01	0.69
	127609	AA622559	Hs.150318	ESTs	1.21	0.32
	127959	AI302471	Hs.124292	ESTs	2.5	1
	128468	D52183	Hs.56340	ESTs	1.13	0.33
30	128624	AA479209	Hs.102647	ESTs	1.45	0.58
	128789	AA486567	Hs.105895	ESTs	1.1	0.34
	128798	AF014958	Hs.105938	chemokine (C-C motif) receptor-like 2	1.16	0.55
	128952	R51076	Hs.107361	ESTs; Highly similar to Rap2 interacting	2.04	2.4
	129057	X62466	Hs.214742	CDW52 antigen (CAMPATH-1 antigen)	1.77	0.73
	129210	AA401654	Hs.202949	KIAA1102 protein	1.11	0.36
35	129240	W24360	Hs.237868	interleukin 7 receptor	0.91	0.41
	129402	T63781		***yc21g01.s1 Stratagene lung (#937210)	1.36	0.43
	129565	X77777	Hs.198726	vasoactive intestinal peptide receptor 1	0.67	0.08
	129593	AA487015	Hs.98314	Homo sapiens mRNA; cDNA DKFZp586L0120 (f	1.3	0.42
40	129626	AA447410	Hs.11712	ESTs; Weakly similar to IIII ALU SUBFAM1	1.28	0.46
	129699	AA458578	Hs.12017	KIAA0439 protein; homolog of yeast ublqu	1.58	1
	129898	N48595	Hs.13256	ESTs	1.13	0.53
	129958	L20591	Hs.1378	annexin A3	0.81	0.31
	130273	U59914	Hs.153863	MAD (mothers against decapentaplegic; Dr	0.59	0.22
45	130655	N92934	Hs.17409	cysteine-rich protein 1 (intestinal)	1.44	0.76
	130657	T94452	Hs.201591	ESTs	0.96	0.42
	131061	N64328	Hs.22567	ESTs; Moderately similar to HYPOTHETICAL	1.51	0.45
	131066	F09006	Hs.22588	ESTs	0.97	0.37
	131263	R38334	Hs.24950	regulator of G-protein signalling 5	2.34	2.82
50	131589	U52100	Hs.29191	epithelial membrane protein 2	1.2	0.62
	131686	AA157428	Hs.30687	Grb2-associated binder 2	0.95	0.38
	131751	H18335	Hs.31562	ESTs	1.47	0.52
	132430	T23830	Hs.258875	EST	1.86	2.09
	132476	N67192	Hs.49476	Homo sapiens clone TUA8 Cri-du-chat regi	1.73	0.58
55	132836	F09557	Hs.57929	silt (Drosophila) homolog 3	0.91	0.29
	133120	X64559	Hs.65424	tetranectin (plasminogen-binding protein	0.82	0.2
	133488	D45370	Hs.74120	adipose specific 2	1.29	0.48
	133565	H57058	Hs.204831	ESTs	2.25	0.57
	133651	U97105	Hs.173381	dihydropyrimidinase-like 2	1.65	0.62
60	133835	AA059489	Hs.76640	ESTs; Highly similar to RGC-32 [R.norveg	1.16	0.34
	133978	W73859	Hs.78061	transcription factor 21	0.79	0.27
	133985	L34657	Hs.78146	platelet/endothelial cell adhesion molec	0.99	0.28
	134299	AA487558	Hs.8135	ESTs	1.02	0.46
	134300	U81984	Hs.166082	endothelial PAS domain protein 1	0.86	0.42
65	134323	AA028976	Hs.8175	Homo sapiens mRNA; cDNA DKFZp564M0763 (f	1.19	0.27
	134343	D50683	Hs.82028	transforming growth factor; beta recepto	1.21	0.67
	134417	D87969	Hs.82921	solute carrier family 35 (CMP-sialic aci	1.28	1
	134561	U76421	Hs.85302	adenosine deaminase; RNA-specific; B1 (h	2.12	0.55
	134624	W67147	Hs.8700	deleted in liver cancer 1	2.35	2.74
70	134696	H88354	Hs.8881	ESTs	1.35	0.33
	134749	L10956	Hs.89485	carbonic anhydrase IV	0.89	0.2
	134786	L06139	Hs.89640	TEK tyrosine kinase; endothelial (venous	0.48	0.21
	134869	T35288	Hs.90421	ESTs; Moderately similar to IIII ALU SUB	2.14	2.64
	135346	M21056	Hs.992	phospholipase A2; group 1B (pancreas)	0.63	0.13
75	100113	D00591	Hs.84746	Chromosome condensation 1	1	2.15
	100147	D13666	Hs.136348	Homo sapiens mRNA for osteoblast specifi	0.5	2
	100280	D42085	Hs.155314	KIAA0095 gene product	1.02	1.39
	100335	D63391	Hs.6793	platelet-activating factor acetylhydrola	1	5.58
	100360	D78335	Hs.75939	Uridine monophosphate kinase	0.91	2.04
80	100372	D79997	Hs.184339	KIAA0175 gene product	0.75	2.03
	100486	HG1112-HT1112		TIGR: ras-like protein TC4	1.09	1.93
	100559	HG2197-HT2267		*collagen, type VII, alpha 1*	0.97	3.6
	100576	HG2290-HT2386		*calitonin/alpha-CGRP, alt. transcript	1	1
	100668	HG2981-HT3938		*TIGR: CD44 (epican, alt. transcript 12	0.85	1.9
85	100906	HG4716-HT5158		Guanosine 5'-Monophosphate Synthase	1.18	2.29
	100930	HG721-HT4827		*TIGR: placental protein 14, endometrial	1	1.45

5	100960	J00124	Hs.117729	keratin 14 (epidermolysis bullosa simple	0.84	2.6
	101031	J05070	Hs.151738	*Matrix metalloproteinase 9 (gelatinase	0.77	1.52
	101111	L08424	Hs.1619	Achaete-scute complex (Drosophila) homol	1	1
	101124	L10343	Hs.112341	*Protease inhibitor 3, skn-derived (SKA	0.62	2.67
	101175	L18920	Hs.36980	*Melanoma antigen, family A, 2"	1	1
10	101204	L24203	Hs.82237	Ataxia-telangiectasia group D-associated	0.74	4.1
	101431	M19888	Hs.1076	Small proline-rich protein 1B (cornifin)	0.85	2.51
	101448	M21389	Hs.195850	keratin 5 (epidermolysis bullosa simplex	0.61	8.83
	101511	M27826	Hs.267319	Endogenous retroviral protease	1.03	1.13
	101526	M29540	Hs.220529	Carcinoembryonic antigen-related cell ad	1.07	4.61
15	101548	M31328	Hs.71642	*Guanine nucleotide binding protein (G p	0.97	1.13
	101625	M57293		*Human parathyroid hormone-related pepti	1	1
	101649	M60047	Hs.1690	Heparin-binding growth factor binding pr	1	2.7
	101724	M69225	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	1	8.98
	101748	M76482	Hs.1925	Desmoglein 3 (pemphigus vulgaris antigen	1	2.78
20	101759	M80244	Hs.184601	*Solute carrier family 7 (cationic amino	1.07	2.45
	101804	M86699	Hs.169840	TTK protein kinase	1	1
	101806	M86757	Hs.112408	S100 calcium-binding protein A7 (psorias	0.74	1.76
	101809	M86849		*Homo sapiens connexin 26 (GJB2) mRNA, c	1	7
	101845	M93426	Hs.78867	*Protein tyrosine phosphatase, receptor-	1	1
25	101851	M94250	Hs.82045	Midkine (neurite growth-promoting factor	1.13	2.6
	102083	U10323	Hs.75117	*Interleukin enhancer binding factor 2,	1.03	1.61
	102154	U17760	Hs.75517	*Laminin, beta 3 (nlcein (125kD), kalin	0.94	3.62
	102193	U20758	Hs.313	secreted phosphoprotein 1 (osteopontin;	0.34	4.59
	102305	U33286	Hs.90073	chromosome segregation 1 (yeast homolog)	1.45	2.97
30	102348	U37519	Hs.87539	Aldehyde dehydrogenase 8	0.52	2.25
	102581	U61145	Hs.77258	Enhancer of zeste (Drosophila) homolog 2	0.91	2.46
	102610	U65011	Hs.30743	Preferentially expressed antigen in mela	1	3.88
	102623	U66083	Hs.37110	*Melanoma antigen, family A, 9 (MAGE-9)*	1	1
	102669	U71207	Hs.29279	Eyes absent (Drosophila) homolog 2	1	1
35	102696	U74612	Hs.239	Forkhead box M1	1.06	2.77
	102829	U91618	Hs.80962	Neurotensin	1	1
	102888	X04741	Hs.76118	Ubiquitin carboxyl-terminal esterase L1	1.13	2.59
	102913	X07696	Hs.80342	keratin 15	0.7	4.72
	102915	X07820	Hs.2258	Matrix Metalloproteinase 10 (Stromolysin	1.15	3.35
40	102963	X15943	Hs.37058	*Calcitonin/calcitonin-related polypepti	1	1
	103021	X53587	Hs.85266	*Integrin, beta 4"	1.38	2.34
	103036	X54925	Hs.83169	Matrix metalloprotease 1 (interstitial c	1	14.93
	103058	X57348	Hs.184510	Stratiferin	1.25	4.17
	103060	X57766	Hs.155324	matrix metalloproteinase 11 (stromelysin	1	1.72
45	103119	X63629	Hs.2877	*Cadherin 3, P-cadherin (placental)"	1.16	7.38
	103206	X72755	Hs.77367	monokine induced by gamma interferon	0.71	1.48
	103242	X76342	Hs.389	*Alcohol dehydrogenase 7 (class IV), mu	1	1
	103312	X82693	Hs.3185	*Lymphocyte antigen 6 complex, locus D;	0.92	1.28
	103478	Y07755	Hs.38991	S100 calcium-binding protein A2	1.05	5.81
50	103558	Z19574	Hs.2785	keratin 17	0.65	6.68
	103576	Z26317	Hs.2631	Desmoglein 2	0.79	1.73
	103587	Z29083	Hs.82128	ST4 Oncofetal antigen	1	3.93
	103594	Z31560	Hs.816	*SRY (sex determining region Y)-box 2, p	0.71	7.23
	103768	AA089997		*ESTs, Highly similar to integral membra	0.99	1.8
55	104168	AA454908	Hs.8127	KIAA0144 gene product	0.96	1.29
	104558	R56678	Hs.88959	Human DNA sequence from clone 967N21 on	1.23	7.23
	104689	AA010665		ESTs	0.96	2.11
	104733	AA018498	Hs.23071	ESTs	1.18	1.88
	104906	AA065809	Hs.26802	Protein kinase domains containing protei	1.11	3.15
60	104978	AA088458	Hs.19322	ESTs; Weakly similar to !!!! ALU SUBFAMI	1.64	2.89
	105012	AA116036	Hs.9329	*Homo sapiens mRNA for fls353, complete	1.19	3.91
	105175	AA186804	Hs.25740	ESTs; Weakly similar to unknown [S.cerev	0.9	4.63
	105263	AA227926	Hs.6682	ESTs	0.95	2.87
	105298	AA233459	Hs.26369	ESTs	1	1.13
65	105312	AA233854	Hs.23348	S-phase kinase-associated protein 2 (p45	1.32	3.01
	105719	AA291644	Hs.36793	Hypothetical protein FLJ23188	1.28	2.31
	105743	AA293300	Hs.9598	ESTs	1	1
	106012	AA411621	Hs.8895	ESTs; same as 8FH67	0.94	2.04
	106231	AA429571	Hs.36002	KIAA1355 protein	1.04	1.5
70	106540	AA454607	Hs.38114	Hypothetical protein FLJ11100	1.26	2.26
	106575	AA456039	Hs.105421	ESTs	1	2
	106632	AA459897	Hs.11950	GPI-anchored metastasis-associated prote	0.87	1.32
	106727	AA465342	Hs.34045	Hypothetical protein FLJ20764	0.87	1.59
	106908	AA490237	Hs.222024	Transcription factor BMAL2 (cycle-like f	0.61	1.6
75	107059	AA608545	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	0.48	2.67
	107104	AA609788	Hs.15243	Nucleolar protein 1 (120kD)	1.01	1.44
	107151	AA621169	Hs.8687	ESTs; procollagen I-N proteinase	0.97	2.89
	107284	S74039	Hs.291904	Accessory proteins BAP31/BAP29	1.15	3.65
	107901	AA026418	Hs.91539	ESTs	0.72	3.44
80	107922	AA028028	Hs.61480	Ig superfamily receptor LNIR precursor	1	2.48
	107932	AA029317	Hs.18878	Hypothetical protein FLJ21620	1	1
	108695	AA121315	Hs.70823	KIAA1077 protein	0.91	3.53
	108857	AA133250	Hs.62180	ESTs	1	1
	108860	AA133334	Hs.129911	ESTs	0.73	7.3
85	108990	AA152296	Hs.72045	ESTs	1	1
	109166	AA179845	Hs.73625	*RAB6 Interacting, kinesin-like (rabkine	1	4.55
	109424	AA227919	Hs.85962	Hyaluronan synthase 3	1	1.28
	109565	F05012	Hs.27027	Hypothetical protein DKFZp762H1311	1.42	2
	109970	H09281	Hs.13234	ESTs	1.13	2.16

5	110015	H10998	Hs.7164	A disintegrin and metalloproteinase doma	0.84	1.95
	110156	H18957	Hs.4213	ESTs	0.94	1.41
	110561	H59617	Hs.5199	HSPC150 protein similar to ubiquitin-con	0.91	3.18
	111223	N68921	Hs.34806	ESTs; Weakly similar to neogenin [H.sapi	0.91	3.13
	111345	N89820	Hs.14559	Hypothetical protein FLJ10540	1	1.25
10	111876	R38239	Hs.293246	*ESTs, Weakly similar to putative p150 [0.83	1.27
	111902	R39191	Hs.109445	KIAA1020 protein	0.91	0.91
	112244	R51309	Hs.70823	KIAA1077 protein	0.77	3.01
	112973	T17271		*cDNA FLJ13308 fis, clone OVARC1001436,	1	1
	112989	T23482	Hs.89981	*Diacylglycerol kinase, zeta (104kD)*	0.55	1.03
15	113047	T25867	Hs.7549	ESTs	0.87	2
	113095	T40920	Hs.126733	ESTs	1	1
	113531	T90345	Hs.16740	Hypothetical protein FLJ11036	0.42	1.44
	113970	W86748	Hs.8109	ESTs	1.17	1.73
	114346	Z41450	Hs.130489	*ATPase, aminophospholipid transporter-I	0.86	0.82
20	114407	AA010188	Hs.103305	ESTs	0.8	1.88
	114471	AA026074	Hs.104613	RP42 homolog	1.06	1.34
	114509	AA043551	Hs.101799	KIAA1350 protein	1.82	2.32
	115060	AA253214	Hs.198249	*Gap junction protein, beta 5 (connexin	0.79	1.49
	115091	AA255900	Hs.184523	KIAA0965 protein	0.72	1.92
25	115123	AA256642	Hs.236894	*ESTs, High sim to LRP1_hu low density l	0.59	1.97
	115291	AA279943	Hs.122579	ESTs	1	1.25
	115506	AA292537	Hs.45207	Hypothetical protein KIAA1335	1.15	1.48
	115522	AA331393	Hs.47378	ESTs	0.5	3.29
	115536	AA347193	Hs.62180	ESTs	1	1
30	115697	AA411502	Hs.63325	Homo sapiens type II membrane serine pro	1	6.53
	115909	AA436666	Hs.59761	ESTs	1	6.98
	115978	AA447522	Hs.69517	Differentially expressed in Fanconi anem	1	2.31
	116028	AA452112	Hs.42644	thioredoxin-like	0.99	1.68
	116107	AA456968	Hs.92030	ESTs	1.14	1.8
35	116134	AA460246	Hs.50441	CGI-04 protein	1.11	1.86
	116157	AA461063	Hs.44298	Hypothetical protein	0.99	1.9
	116158	AA461187	Hs.61762	Hypoxia-inducible protein 2	0.44	0.86
	116335	AA495830	Hs.87013	*Homo sapiens cDNA FLJ10238 fis, clone H	0.62	3.89
	116483	C14092	Hs.76118	Ubiquitin carboxyl-terminal esterase L1	1.04	2.36
40	117320	N23239	Hs.211092	LUNX protein; PLUNC(palate lung & nasal	0.51	0.64
	117557	N33920	Hs.44532	Diubiquitin	1.11	2.63
	117693	N40939	Hs.112110	PTD007 protein	0.98	1.79
	117881	N50073	Hs.260622	Butyrate-induced transcript 1	1	1.43
	118368	N64339	Hs.48956	ESTs	0.67	2.86
45	118566	N68558	Hs.42824	Hypothetical protein FLJ10718	1.21	0.83
	118695	N71781	Hs.50081	KIAA1199 see CVA7.doc	0.88	1.63
	119780	W72967	Hs.181381	ESTs; Weakly similar to hypothetical pro	1	1
	119845	W79920	Hs.58561	G protein-coupled receptor 87	1	1
	120102	W95428	Hs.132927	*ESTs, Moderately similar to p53 regulat	1	1
50	120104	W95477	Hs.180479	ESTs	0.69	3.07
	120486	AA253400	Hs.137569	Tumor protein 63 kDa with strong homolog	1.08	12.05
	120859	AA350158	Hs.1619	Achaete-scute complex (Drosophila) homol	1	1
	120880	AA360240	Hs.97019	EST	1	1
	120948	AA397822	Hs.104650	Hypothetical protein FLJ10292	1.04	2.15
55	120983	AA398209	Hs.97687	EST	1	1
	121362	AA405500	Hs.97932	Chondromodulin I precursor	1	1
	121369	AA405657	Hs.128791	CGI-09 protein	1	1.8
	121791	AA423978	Hs.293317	*ESTs, Weakly similar to JM27 [H.sapiens	1	1
	123005	AA479726	Hs.105577	ESTs	1	1
60	123044	AA481549	Hs.130881	B-cell CLL/lymphoma 11A (zinc finger pro	0.95	1.88
	123160	AA488687	Hs.284235	ESTs	1.59	4.98
	123479	AA599469	Hs.135056	clone RP5-850E9 on chromosome 20	1.19	1.64
	123571	AA608956	Hs.112619	*ESTs, Weakly similar to PQ0109 Purkinje	1.03	1.14
	123829	AA620697	Hs.112208	XAGE-1 protein	1.39	2.2
65	124006	D60302	Hs.108977	ESTs	1	4.85
	124059	F13673	Hs.99769	ESTs	1.49	8.62
	124960	T15386	Hs.194766	Seizure related gene 6 (mouse)-like	0.76	0.77
	125218	W73561	Hs.110024	NADH:ubiquinone oxidoreductase MLRQ subu	1.33	1.77
	125453	R06041	Hs.18048	*Melanoma antigen, family A, 10*	0.8	1.42
70	125759	AA425587	Hs.82226	Glycoprotein (transmembrane) nmb	1.52	2.26
	125972	AA434562	Hs.35406	*ESTs, Highly similar to unnamed protein	1.05	2.48
	125994	H55782	Hs.270799	EST	1	1.95
	126395	N70192	Hs.278956	Hypothetical protein FLJ12929	1	1.35
	126645	A167942	Hs.61635	STEAP1 (Homo sapiens BAC clone RG041D11	1	2.23
75	127221	A1354332	Hs.72365	ESTs	0.73	3.27
	127479	AA513722	Hs.179729	collagen; type X; alpha 1 (Schmid metaph	0.51	1.94
	128192	A1204246		KIAA1085 protein	1.8	3.16
	128610	L38608	Hs.10247	activated leucocyte cell adhesion molecu	0.89	0.97
	128777	U46006	Hs.10526	Cysteine and glycine-rich protein 2	1	1
80	128924	AA234962	Hs.26557	Plakophilin 3	1.3	2.97
	129041	H58873	Hs.169902	*Solute carrier family 2 (facilitated gl	0.84	2.04
	129099	H50398	Hs.108660	*ATP-binding cassette, sub-family C (CFT	0.87	1.04
	129404	AA172056	Hs.111128	ESTs	1	1
	129466	L42583		*Genbank Homo sapiens keratin 6 isoform	0.72	12.67
85	129605	S72493	Hs.115947	Keratin 16 (focal non-epidermolytic palm	0.92	1.5
	129628	U26727	Hs.1174	*Cyclin-dependent kinase inhibitor 2A (m	0.85	1.93
	130023	X13461	Hs.239600	Calmodulin-like 3	0.84	1.22
	130080	X14850	Hs.147097	*H2A histone family, member X*	0.98	1.96
	130385	AA126474	Hs.155223	stannocalcin 2	1	1

	130410	V01514	Hs.155421	Alpha-fetoprotein	0.63	0.63
	130441	U35835	Hs.301387	*Human DNA-PK mRNA, partial cds*	1.15	3.65
	130482	L32866	Hs.1578	Baculoviral IAP repeat-containing 5 (sur	1	1.88
5	130553	AA430032	Hs.252587	Pituitary tumor-transforming 1	0.92	1.96
	130577	M35410	Hs.162	Insulin-like growth factor binding prote	1.17	4.7
	130627	L23808	Hs.1695	Matrix metalloproteinase 12 (macrophage	0.69	4.05
	130800	AA223386	Hs.19574	ESTs; Weakly similar to katanin p80 subu	1.13	2.41
	130939	AA598689	Hs.21400	ESTs	0.8	0.89
10	131046	X02530	Hs.2248	INTERFERON-GAMMA INDUCED PROTEIN PRECURS	0.8	1.15
	131244	D38076	Hs.24763	RAN binding protein 1	1.13	1.85
	131877	J04088	Hs.156346	Topoisomerase (DNA) II alpha (170kD)	1	1
	131927	AA461549	Hs.34780	*Doublecortin; lissencephaly, X-linked (0.81	0.62
	131965	W90146	Hs.35962	ESTs	0.74	3.27
	131978	D80008	Hs.36232	KIAA0186 gene product	1	1
15	132354	L05187	Hs.211913	Small proline-rich protein 1A	0.69	1.43
	132543	AA417152	Hs.5101	ESTs; Highly similar to protein regulati	0.79	4.27
	132632	N59764	Hs.5398	guanine-monophosphate synthetase	1	1.08
	132653	U31201	Hs.54451	*laminin gamma2 chain gene (LAMC2), exon	1	1
20	132659	Z75190	Hs.54481	*Low density lipoprotein receptor-relate	0.89	0.89
	132710	W93726	Hs.55279	*Serine (or cysteine) proteinase inhibit	0.64	4.41
	132758	W52432	Hs.56105	*ESTs, Weakly similar to WDNM RAT WDNM1	1.55	2.08
	132767	L05188	Hs.231622	Small proline-rich protein 2B	0.83	1.66
	132816	M74542	Hs.575	Aldehyde dehydrogenase 3	0.55	0.55
25	132990	AA458761	Hs.18387	transcription factor AP-2 alpha (activat	1	3.53
	133070	U69611	Hs.64311	*A disintegrin and metalloproteinase dom	1.16	2
	133282	U52960	Hs.286145	*SRB7 (suppressor of RNA polymerase B, y	1	2.7
	133317	AA215299	Hs.70830	U6 snRNA-associated Sm-like protein LSM7	0.95	1.42
	133370	AA156897	Hs.72157	Homo sapiens mRNA; cDNA DKFZp564H1922	1.12	2.55
30	133391	X57579	Hs.727	H.sapiens activin beta-A subunit (exon 2	1.65	1.76
	133832	H03387	Hs.241305	estrogen-responsive B box protein (EBBP)	1.02	1.39
	134032	Z81326	Hs.78589	*Serine (or cysteine) proteinase inhibit	1	1
	134168	AA398908	Hs.181634	*Homo sapiens cDNA: FLJ23602 fis, clone	0.95	1.53
	134218	AA227480	Hs.80205	Pim-2 oncogene	1.38	2.48
35	134405	R67275	Hs.82772	***collagen, type XI, alpha 1***	0.76	2.86
	134453	X70683	Hs.83484	SRX (sex determining region Y)-box 4	1.89	3.78
	134470	X54942	Hs.83758	CDC28 protein kinase 2	1.82	4.11
	134645	U87459	Hs.167379	*Cancer/testis antigen (NY-ESO-1, CTAG1,	0.82	0.83
	134781	M17183	Hs.89626	Parathyroid hormone-like hormone	1	1
40	135002	U19147	Hs.272484	G antigen 6	1	1
	100040	M97935		AFFX control: STAT1	0.92	1.25
	101201	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin;	2.92	8.5
	101664	M60752	Hs.121017	H2A histone family; member A	1	1
	102025	U03911	Hs.78934	mutS (E. coli) homolog 2 (colon cancer;	0.8	1.61
45	102031	U04898	Hs.2156	RAR-related orphan receptor A	1	1
	102221	U24576		LIM domain only 4	1	1
	102270	U30255	Hs.75888	phosphogluconate dehydrogenase	1.08	1.43
	102339	U37022	Hs.95577	cyclin-dependent kinase 4	0.88	1.32
	102391	U41668	Hs.77494	deoxyguanosine kinase	1.07	1.58
50	103000	X51956	Hs.146580	enolase 2; (gamma; neuronal)	0.91	1.49
	103395	X94754	Hs.119503	methionine-tRNA synthetase	0.89	1.32
	105638	AA281599	Hs.20418	Homo sapiens mRNA for for histone H2B; c	0.91	1.25
	105726	AA292328	Hs.9754	activating transcription factor 5	0.94	1.48
	114841	AA234722	Hs.55408	ESTs; Moderately similar to CALCIUM-DEPE	0.78	1.56
55	115206	AA262491	Hs.186572	ESTs	1	1
	115906	AA436616	Hs.82302	ESTs	0.74	2.52
	119132	R49046	Hs.107911	ATP-binding cassette; sub-family B (MDR/	1.1	1.51
	124163	H30539	Hs.189838	ESTs	1	1
	126487	AA482505	Hs.184601	solute carrier family 7 (cationic amino	1.01	1.46
60	127141	AA307960	Hs.75478	KIAA0956 protein	0.85	1.4
	128034	AA905754	Hs.75103	tyrosine 3-monooxygenase/tryptophan 5-mo	1	1.18
	128609	AA234365	Hs.102458	survival of motor neuron protein Interac	1	1.5
	128895	R37753	Hs.106985	ESTs	1.7	2
	130199	Z48579	Hs.172028	a disintegrin and metalloprotease domain	1	1
65	130524	U89995	Hs.159234	forkhead box E1	1	1
	133000	U24152	Hs.62402	p21/Cdc42/Rac1-activated kinase 1 (yeast	1	1
	133658	M25756	Hs.75426	secretogranin II (chromogranin C)	1	1
	135047	AA460466	Hs.93597	ESTs	1	1
	100053	M27830		AFFX control: 28S ribosomal RNA	0.88	1.53
70	100114	D00596	Hs.82962	thymidylate synthetase	0.68	1.86
	100128	D11094	Hs.61153	proteasome (prosome; macropain) 26S subu	1.29	2.03
	100154	D14657	Hs.81892	KIAA0101 gene product	0.71	4.26
	100161	D14694	Hs.77329	phosphatidylserine synthase 1	1.02	1.56
	100168	D14874	Hs.394	adrenomedullin	0.46	1.17
75	100187	D17793	Hs.78183	aldo-keto reductase family 1; member C3	1	1
	100188	D21063	Hs.57101	minichromosome maintenance deficient (S.	0.97	1.4
	100217	D26600	Hs.89545	proteasome (prosome; macropain) subunit;	1.13	1.9
	100220	D28364		***Human mRNA for annexin II, 5'UTR (seq	1.11	1.53
	100287	D43950	Hs.1600	chaperonin containing TCP1; subunit 5 (e	1.13	2.09
80	100297	D49489	Hs.182429	protein disulfide isomerase-related prot	0.92	1.78
	100330	D55716	Hs.77152	minichromosome maintenance deficient (S.	1.07	1.61
	100355	D78129		***Homo sapiens mRNA for squalene epoxid	0.96	1.87
	100364	D78586	Hs.154868	carbamoyl-phosphate synthetase 2; aspart	1.49	2.46
	100368	D79987	Hs.153479	extra spindle poles; S. cerevisiae; homo	0.59	1.32
	100398	D84557	Hs.155462	minichromosome maintenance deficient (ml	1.08	1.9
85	100438	D87448	Hs.91417	topoisomerase (DNA) II binding protein	1	2.15

	100455	D87953	Hs.75789	N-myc downstream regulated	0.91	1.48
	100491	HG1153-HT1153		Nucleoside Diphosphate Kinase Nm23-H2s	0.99	1.41
	100518	HG174-HT174		Desmoplakin I	1.28	3.17
5	100528	HG1828-HT1857		***Nexin, Glia-Derived***	0.68	1.9
	100661	HG2874-HT3018		Ribosomal Protein L39 Homolog	1.1	5.44
	100667	HG2981-HT3127		***Epicar, Alt. Splice 11***	0.8	1.97
	100830	HG4074-HT4344		Rad2	1.01	2.12
	101081	K03515	Hs.944	glucose phosphate isomerase	0.91	1.79
10	101131	L10838	Hs.167460	splicing factor; arginine/serine-rich 3	1.23	1.87
	101162	L14595	Hs.174203	solute carrier family 1 (glutamate/neutr	1.35	2.73
	101181	L19686	Hs.73798	macrophage migration inhibitory factor (1.03	1.78
	101183	L19779	Hs.795	H2A histone family; member O	0.57	1.3
	101216	L25876	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	0.7	2.2
15	101228	L27706	Hs.82916	chaperonin containing TCP1; subunit 6A (0.99	1.99
	101233	L29008	Hs.878	sorbitol dehydrogenase	0.82	2.11
	101247	L33801	Hs.78802	glycogen synthase kinase 3 beta	1.2	1.91
	101332	L47276		***Homo sapiens (cell line HL-6) alpha 1	0.69	2.78
	101342	L76191	Hs.182018	Interleukin-1 receptor-associated kinase	1.04	1.84
20	101396	M15796	Hs.78996	proliferating cell nuclear antigen	0.95	3.55
	101423	M18391	Hs.89839	EphA1	1	1.5
	101445	M21259	Hs.1065	small nuclear ribonucleoprotein polypept	1.21	1.96
	101505	M27396	Hs.75692	asparagine synthetase	0.93	1.6
	101525	M29536	Hs.12163	eukaryotic translation initiation factor	1.19	1.93
25	101535	M30448	Hs.251669	casein kinase 2; beta polypeptide	0.96	1.42
	101607	M38690	Hs.1244	CD9 antigen (p24)	1.11	1.25
	101624	M55998		***Human alpha-1 collagen type I gene, 3	1.17	1.98
	101758	M77836	Hs.79217	pyrroline-5-carboxylate reductase 1	1.77	3.45
	101839	M93036	Hs.692	membrane component; chromosomal 4; surfa	0.71	1.45
30	101853	M94362	Hs.76084	lamin B2	0.84	1.19
	101977	S83364		***putative Rab5-interacting protein (cl	0.89	1.9
	101992	U01038	Hs.77597	polo (Drosophila)-like kinase	0.65	1.46
	102009	U02680	Hs.82643	protein tyrosine kinase 9	1.23	3.35
	102012	U03057	Hs.118400	singed (Drosophila)-like (sea urchin fas	0.85	1.88
35	102039	U05861	Hs.201967	aldo-keto reductase family 1; member C1	0.93	2.32
	102123	U14518	Hs.1594	centromere protein A (17kD)	1	4.28
	102130	U15009	Hs.1575	small nuclear ribonucleoprotein D3 polyp	0.89	1.42
	102148	U16954	Hs.75823	ALL1-fused gene from chromosome 1q	0.8	2.95
	102210	U23028	Hs.2437	eukaryotic translation initiation factor	1.01	1.34
40	102220	U24389	Hs.65436	lysyl oxidase-like 1	1.15	2.34
	102260	U28386	Hs.159557	karyopherin alpha 2 (RAG cohort 1; impor	1.14	2.69
	102330	U35451	Hs.77254	chromobox homolog 1 (Drosophila HP1 beta	1.05	1.7
	102423	U44754	Hs.179312	small nuclear RNA activating complex; po	1.14	2.99
	102455	U48705	Hs.75562	discoidin domain receptor family; member	1.05	2.01
45	102499	U51478	Hs.76941	ATPase; Na+/K+ transporting; beta 3 poly	1.27	1.92
	102522	U53347	Hs.183556	solute carrier family 1 (neutral amino a	0.84	1.31
	102590	U62136		***Homo sapiens enterocyte differentiall	1.11	1.6
	102676	U72514	Hs.12045	putative protein	1.04	2.17
	102687	U73379	Hs.93002	ubiquitin carrier protein E2-C	0.86	2.28
50	102704	U76638	Hs.54089	BRCA1 associated RING domain 1	1.12	1.63
	102781	U83843		***Human HIV-1 Nef interacting protein (0.9	1.39
	102784	U85658	Hs.61796	transcription factor AP-2 gamma (activat	0.98	2.16
	102827	U91327	Hs.6456	chaperonin containing TCP1; subunit 2 (b	0.96	1.62
	102935	X13482	Hs.80506	small nuclear ribonucleoprotein polypept	1.21	4.2
55	102972	X16662	Hs.87268	annexin A8	1.25	2.32
	102983	X17620	Hs.118638	non-metastatic cells 1; protein (NM23A)	1.03	1.83
	103023	X53793	Hs.117950	multifunctional polypeptide similar to S	1.58	5.44
	103038	X54941	Hs.77550	CDC28 protein kinase 1	1.32	3.79
	103075	X59543	Hs.2934	ribonucleotide reductase M1 polypeptide	1.11	2.58
60	103168	X68314	Hs.2704	glutathione peroxidase 2 (gastrointestin	0.75	3.05
	103185	X69910	Hs.74368	transmembrane protein (63kD); endoplasm	1.01	1.97
	103212	X73874	Hs.2393	phosphorylase kinase; alpha 1 (muscle)	0.95	1.72
	103223	X74801	Hs.1708	chaperonin containing TCP1; subunit 3 (g	0.97	1.77
	103260	X78416	Hs.3155	casein; alpha	1	1
65	103262	X78555	Hs.204133	hexabrachion (tenascin C; cytotoxicin)	1.23	3.09
	103330	X85373	Hs.77496	small nuclear ribonucleoprotein polypept	1.12	2.25
	103364	X90872	Hs.75854	SULT1C1 sulfotransferase	2.85	4.62
	103375	X91868	Hs.54416	sine oculis homeobox (Drosophila) homolo	1	2.48
	103391	X94453	Hs.114366	pyrroline-5-carboxylate synthetase (glut	1	1.53
70	103404	X95586	Hs.78596	proteasome (prosome; macropain) subunit;	0.92	1.53
	103437	X98260	Hs.82254	M-phase phosphoprotein 11	0.92	1.54
	103448	X99133	Hs.204238	lipocalin 2 (oncogene 24p3)	0.55	0.96
	103805	Z35402	Hs.194657	cadherin 1; E-cadherin (epithelial)	1.32	2.51
	103646	Z68228	Hs.2340	junction plakoglobin	0.88	1.28
75	103658	Z74615	Hs.172928	collagen; type I; alpha 1	1.06	2.98
	103774	AA092898	Hs.92918	ESTs; Weakly similar to R07G3.8 [C.elega	1.88	4.66
	104261	AF008442	Hs.5409	RNA polymerase I subunit	0.87	2.17
	104276	C02193	Hs.85222	ESTs; Weakly similar to R27090_2 [H.sapi	1.4	2.49
	104289	C16281	Hs.75478	KIAA0956 protein	1.15	1.68
80	104434	L02870	Hs.1640	collagen; type VII; alpha 1 (epidermolys	1.04	1.49
	104453	M19169	Hs.123114	cystatin SN	0.38	0.76
	104611	R98280	Hs.125845	ribulose-5-phosphate-3-epimerase	1.08	2.25
	104758	AA024661	Hs.7010	ESTs; Weakly similar to ACYL-COA DEHYDRO	1.14	1.65
	105114	AA156532	Hs.11801	adenosine A2b receptor pseudogene	0.91	1.38
85	105132	AA159501	Hs.247280	HBV associated factor	1.08	1.7
	105174	AA186613	Hs.34744	ESTs	0.95	2.05

	105280	AA232215	Hs.14600	ESTs	1	1.4
	105344	AA235303	Hs.8645	ESTs	0.72	2.02
	105516	AA257971	Hs.21214	ESTs	1.35	3.56
5	105621	AA280865	Hs.6375	Homo sapiens mRNA; cDNA DKFZp564K0222 (f	1.23	1.82
	105698	AA287393	Hs.15202	ESTs; Weakly similar to oligodendrocyte-	0.98	1.28
	105705	AA290767	Hs.101282	Homo sapiens mRNA; cDNA DKFZp434B102 (fr	0.92	1.32
	105724	AA292098	Hs.22934	ESTs; Weakly similar to ZINC FINGER PROT	0.99	1.41
	105782	AA350215	Hs.21580	ESTs	1	1
10	105799	AA372018	Hs.24743	ESTs	1.08	1.78
	105807	AA393803	Hs.16869	ESTs; Moderately similar to COLLAGEN ALP	0.95	1.34
	105891	AA400768	Hs.26662	ESTs; Weakly similar to tumor necrosis f	0.87	2.25
	105936	AA404338		ESTs	1.14	1.46
	106069	AA417741	Hs.29899	ESTs; Weakly similar to ZINC FINGER PROT	1	1
	106103	AA421104	Hs.12094	ESTs	1.04	1.44
15	106140	AA424524	Hs.14912	KIAA0286 protein	1.23	2.11
	106149	AA424881	Hs.256301	ESTs	0.83	1.48
	106154	AA425304	Hs.6994	ESTs	0.77	2.05
	106182	AA426609	Hs.10862	ESTs	0.74	2.23
20	106220	AA428582	Hs.32196	ESTs; Moderately similar to metargidin p	0.97	1.99
	106228	AA429290	Hs.17719	ESTs	0.99	1.54
	106318	AA436570	Hs.9605	pre-mRNA cleavage factor Im (25kD)	0.95	2.09
	106341	AA441798	Hs.5243	ESTs; Moderately similar to p11.2 hypothe	0.98	2.66
	106432	AA448850	Hs.17138	ESTs	0.95	1.93
25	106474	AA450212	Hs.42484	Homo sapiens mRNA; cDNA DKFZp564C053 (fr	1	1
	106483	AA451676	Hs.30299	IGF-II mRNA-binding protein 2	1.4	2.29
	106599	AA457235	Hs.12842	ESTs; Moderately similar to non-function	1	1.82
	106611	AA458904	Hs.26267	ESTs; Weakly similar to torsinA [H.sapie	1.49	2.78
	106654	AA460449	Hs.3784	ESTs; Highly similar to phosphoserine am	1	1.4
30	107076	AA609145	Hs.21143	ESTs; Weakly similar to fos39554_1 [H.s	1.11	1.49
	107115	AA610108	Hs.27693	ESTs; Highly similar to CGI-124 protein	1	1.03
	107129	AA620553	Hs.4756	flap structure-specific endonuclease 1	1.13	3.63
	107159	AA621340	Hs.10600	ESTs; Weakly similar to ORF YKR081c [S.c	1.05	2.09
	107444	W28391	Hs.5181	proliferation-associated 2G4; 38kD	1.18	1.9
35	107481	W58247	Hs.27437	Homo sapiens kinesin superfamily motor K	0.99	2.74
	107516	X56597	Hs.99853	fibrillarin	0.94	1.77
	107529	Y12065	Hs.5092	nuclear protein (KKE/D repeat)	1.05	2.29
	107531	Y13936	Hs.17883	protein phosphatase 1G (formerly 2C); ma	1.06	1.62
	107801	AA019433	Hs.173100	ESTs	1.03	1.4
40	107957	AA031948	Hs.57548	ESTs	0.95	1.46
	108565	AA085342	Hs.1526	ATPase; Ca++ transporting; cardiac muscl	0.69	1.35
	108780	AA128561	Hs.117938	collagen; type XVII; alpha 1	1	7.63
	108828	AA131584	Hs.71435	DKFZP564O0463 protein	1.33	2.56
	109060	AA160879	Hs.241551	chloride channel; calcium activated; fam	0.67	1.42
45	109112	AA169379	Hs.72865	ESTs	1.03	2.31
	109344	AA213696	Hs.86559	poly(A)-binding protein-like 1	0.97	1.55
	109412	AA227145	Hs.209473	ESTs; Weakly similar to REGULATOR OF MIT	0.76	1.87
	107800	N23174	Hs.22891	solute carrier family 7 (cationic amino	0.9	0.95
	110958	N50550	Hs.24587	signal transduction protein (SH3 contain	1.17	2.26
50	111018	N54067	Hs.3628	mitogen-activated protein kinase kinase	1.21	1.85
	111337	N78612	Hs.16607	ESTs; Highly similar to Myosin heavy cha	1	1.45
	112305	R54822	Hs.26244	ESTs	1	1
	112401	R61279	Hs.237536	ESTs; Weakly similar to F25B5.3 [C.elega	1.24	1.64
	112853	T02843	Hs.4351	EST	1.56	1.96
55	112869	T03313	Hs.4747	dyskeratosis congenita 1; dyskerin	1.03	1.57
	112992	T23513	Hs.7147	ESTs	1	1
	113048	T25895	Hs.184008	ESTs; Weakly similar to RNA-binding prot	1.37	2.26
	113063	T32438	Hs.5027	ESTs	1	1
	113179	T55182	Hs.152571	ESTs; Highly similar to IGF-II mRNA-bind	1.33	2.7
60	113573	T91168	Hs.15990	ESTs	0.76	1.47
	113811	W44928	Hs.4878	ESTs	0.79	1.51
	114086	Z38266	Hs.12770	Homo sapiens PAC clone DJ0777023 from 7p	0.9	1.34
	114587	AA070827	Hs.180320	ESTs; Weakly similar to GOLGI 4-TRANSMEM	1.02	1.76
	114846	AA234929	Hs.44343	ESTs	1.32	2.36
65	114964	AA243873	Hs.82184	ring finger protein 3	1.1	1.84
	115047	AA252627	Hs.22554	homeo box B5	1.01	2.38
	115166	AA258409	Hs.198907	myelin protein zero-like 1	1.05	2.31
	115167	AA258421	Hs.43728	hypothetical protein	1.52	2.52
	115239	AA278650	Hs.73291	ESTs; Weakly similar to similar to the b	0.7	2.67
70	115278	AA279757	Hs.67466	ESTs; Weakly similar to BACN32G11.d [D.m	1.14	2.12
	115652	AA405098	Hs.38178	ESTs	0.82	4.67
	115875	AA433943	Hs.43946	ESTs; Weakly similar to Weak similarity	1.2	1.98
	116004	AA449122	Hs.76086	ESTs; Highly similar to small zinc finge	0.98	1.31
	116121	AA459254	Hs.48855	ESTs	0.97	1.55
75	116129	AA459956	Hs.49163	ESTs; Highly similar to putative ribonuc	1.08	2.73
	116190	AA464963	Hs.67776	ESTs	0.8	1.57
	116312	AA490494	Hs.65403	ESTs	1.37	2.65
	116732	F13779	Hs.165909	ESTs	0.92	1.8
	117602	N35020	Hs.44685	ESTs; Weakly similar to GOLIATH PROTEIN	1.15	1.84
80	117950	N51394	Hs.75478	KIAA0956 protein	1.04	2.36
	117992	N52000	Hs.172089	Homo sapiens mRNA; cDNA DKFZp586B0222 (f	0.62	1.29
	118785	N75386	Hs.111867	GLI-Kruppel family member GLI2	1	1
	119717	W69134	Hs.57987	ESTs	1	1.4
	119814	W74069	Hs.58350	ESTs	0.78	1.77
85	120128	Z38499	Hs.91448	MKP-1 like protein tyrosine phosphatase	0.86	1.46
	120242	Z98443	Hs.85366	ESTs	0.83	2.01

	120483	AA252994	Hs.1578	apoptosis inhibitor 4 (survivin)	0.74	1.64
	121054	AA398604	Hs.97387	ESTs	1.05	1.93
	121326	AA404246	Hs.97031	ESTs; Weakly similar to Similar to phyto	0.98	1.3
5	121376	AA405699	Hs.166232	ESTs; Moderately similar to SODIUM- AND	0.91	1.83
	121457	AA411448	Hs.208985	ESTs	0.91	1.59
	121780	AA422086	Hs.124660	ESTs	0.46	0.55
	121781	AA422150	Hs.98370	cytochrome P540 family member predicted	1.07	1.54
	121844	AA425732	Hs.98485	gap junction protein; beta 2; 26kD (conn	0.94	1.4
10	122059	AA431737	Hs.98749	EST	1.93	2.33
	122338	AA443311	Hs.98998	ESTs	1	1
	122354	AA443772	Hs.186692	ESTs	0.88	1.39
	122591	AA453265	Hs.99311	ESTs; Weakly similar to MRJ (H.sapiens)	2.28	2.93
	122790	AA460156	Hs.99556	ESTs	0.88	1.3
15	123398	AA521265	Hs.105514	ESTs	1	1.93
	123518	AA608531	Hs.170313	ESTs	1	1
	123673	AA609471	Hs.112712	ESTs	1	1.15
	124000	D57317	Hs.74861	activated RNA polymerase II transcriptio	0.74	1.12
	124367	N24006	Hs.99348	distal-less homeo box 5	0.67	1.1
20	124447	NA8000	Hs.140945	Homo sapiens mRNA; cDNA DKFZp586L141 (fr	1.19	1.7
	125756	W25498	Hs.81634	ATP synthase; H+ transporting; mitochond	0.93	1.59
	125769	AI382972	Hs.82128	5T4 oncofetal trophoblast glycoprotein	1.65	6.76
	125852	H09290	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (f	0.72	2.26
	125924	AA526849	Hs.82109	syndecan 1	1.22	2.25
25	126037	M85772	Hs.6066	KIAA1112 protein	1.36	1.63
	126214	N29455	Hs.74316	desmoplakin (DPI; DPLI)	1.93	3.55
	126414	N78770	Hs.223439	ESTs	1.21	1.66
	126737	AA488132	Hs.62741	ESTs	1	1
	126743	AA179253	Hs.172182	poly(A)-binding protein; cytoplasmic 1	1.3	2.16
30	126928	AA179546	Hs.832	ESTs; Highly similar to INTEGRIN BETA-8	2.53	2.8
	127432	AA501734	Hs.170311	heterogeneous nuclear ribonucleoprotein	1.57	2.12
	128218	H02682	Hs.99189	ESTs; Moderately similar to recombinatio	1.24	2.09
	128527	M31523	Hs.101047	transcription factor 3 (E2A immunoglobul	1.08	1.78
	128568	X60673	Hs.247568	adenylate kinase 3	1.23	3.48
35	128584	M11433	Hs.101850	retinol-binding protein 1; cellular	0.87	2.42
	128628	C14037	Hs.251978	EST	1.22	1.9
	128691	W27939	Hs.103834	ESTs	1.1	1.73
	128714	V00599	Hs.179661	Homo sapiens clone 24703 beta-tubulin mR	0.92	1.17
	128733	AA328993	Hs.104558	ESTs	1.34	1.94
40	128781	X85372	Hs.105465	small nuclear ribonucleoprotein polypept	0.9	1.34
	129052	AA496297	Hs.182740	ribosomal protein S11	2.59	3.19
	129095	L12350	Hs.108623	thrombospondin 2	1.04	3.2
	129241	AA435665	Hs.109706	ESTs; Moderately similar to HN1 (M.muscu	0.95	1.61
	129665	M88458	Hs.118778	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	1.28	2.63
45	129703	AA401348	Hs.179999	ESTs	0.97	1.63
	129720	AA476582	Hs.12152	ESTs; Moderately similar to SIGNAL RECOG	1.09	1.79
	129850	N20593	Hs.56845	GDP dissociation inhibitor 2	0.74	1.68
	129896	AA043021	Hs.13225	UDP-Gal:betaGlcNAc beta 1;4- galactosyl	1.43	4.19
	130069	AA055896	Hs.146428	collagen; type V; alpha 1	1.17	1.98
50	130405	H88359	Hs.155396	nuclear factor (erythroid-derived 2)-lik	1.26	1.79
	130541	X05608	Hs.211584	neurofilament; light polypeptide (68kD)	1	1
	130599	M91670	Hs.174070	ubiquitin carrier protein	1.07	1.66
	130867	J04093	Hs.2056	UDP glycosyltransferase 1	1	4.8
	131009	AA063596	Hs.22142	ESTs; Weakly similar to NADH-CYTOCHROME	0.93	1.05
55	131028	U20240	Hs.2227	CCAAT/enhancer binding protein (C/EBP);	1	1.23
	131083	U66661	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	1.1	1.8
	131091	T35341	Hs.22880	ESTs; Highly similar to dipeptidyl pept	1.28	1.98
	131144	C14412	Hs.23528	ESTs; Highly similar to HSPC038 protein	1.43	2.06
	131148	C00038	Hs.23579	ESTs	0.88	3.38
60	131164	Y00503	Hs.182265	keralin 19	1.19	2.77
	131185	M25753	Hs.23960	cyclin B1	0.86	3.84
	131219	C00476	Hs.24395	small Inducible cytokine subfamily B (Cy	0.66	2.96
	131454	AA455896	Hs.2699	glypican 1	0.99	1.54
	131687	L11066	Hs.3069	heat shock 70kD protein 9B (mortalin-2)	1	1.18
65	131689	AA599653	Hs.30696	transcription factor-like 5 (basic helix	1	1.95
	131692	D50914	Hs.30736	KIAA0124 protein	1.55	2.39
	131786	AA135554	Hs.32125	ESTs	1	1.33
	131843	AA195893	Hs.184062	ESTs; Moderately similar to putative Rab	0.83	1.63
	131860	U02082	Hs.334	Oncogene TIM	1.08	2.2
70	131884	H90124	Hs.3463	ribosomal protein S23	1.23	1.24
	131903	AA481723	Hs.3436	deleted in oral cancer (mouse; homolog)	0.91	1.18
	131945	M87339	Hs.35120	replication factor C (activator 1) 4 (37	1	2.8
	131958	AA093998	Hs.3566	ESTs; Highly similar to phosphorylation	0.87	1.36
	131964	W42508	Hs.3583	ESTs	1	1.25
75	132001	J00277	Hs.37003	v-Ha-ras Harvey rat sarcoma viral oncoge	1.12	1.43
	132040	AA146843	Hs.172894	BH3 interacting domain death agonist	1	1.55
	132065	D82226	Hs.211594	proteasome (prosome; macropain) 26S subu	0.89	1.27
	132109	AA599801	Hs.40098	ESTs	1	1.05
	132112	AA150661	Hs.40154	jumonji (mouse) homolog	0.99	1.44
80	132123	AA447123	Hs.250705	ESTs	1.06	2.46
	132162	H89551	Hs.41241	ESTs	1.08	2.46
	132180	AA405569	Hs.418	fibroblast activation protein; alpha; se	1.02	4.56
	132309	AA460917	Hs.2780	jun D proto-oncogene	1.16	1.8
	132371	AA235448	Hs.46677	ESTs	0.8	1.26
85	132618	AA253330	Hs.5344	adaptor-related protein complex 1; gamma	0.5	1.49
	132738	U68019	Hs.211578	MAD (mothers against decapentaplegic; Dr	1.21	1.81

132771	AA488432	Hs.56407	phosphoserine phosphatase	1	1.3
132833	U78525	Hs.57783	eukaryotic translation initiation factor	0.91	1.43
132922	T23641	Hs.6066	KIAA1112 protein	1.16	1.53
132959	AA028103	Hs.61472	ESTs; Weakly similar to unknown [S.cerev	1.02	1.88
132994	AA505133	Hs.7594	solute carrier family 2 (facilitated glu	0.72	2.97
133005	C21400	Hs.103329	KIAA0970 protein	0.88	1.34
133065	X62535	Hs.172690	diacylglycerol kinase; alpha (80kD)	0.93	1.23
133083	N70633	Hs.6456	chaperonin containing TCP1; subunit 2 (b	1.14	1.76
133086	L17131	Hs.139800	high-mobility group (nonhistone chromoso	0.97	1.43
133134	T89703	Hs.65648	RNA binding motif protein 8	1.1	1.8
133195	AA350744	Hs.181409	KIAA1007 protein	2.29	2.69
133313	AA249427	Hs.70704	ESTs	1.07	1.68
133331	T62039	Hs.158675	ribosomal protein L14	0.85	1.18
133438	D13370	Hs.73722	APEX nuclease (multifunctional DNA repa	0.91	1.45
133445	T99303	Hs.73797	guanine nucleotide binding protein (G pr	0.94	1.68
133483	X52426	Hs.74070	keratin 13	0.85	1.14
133492	L40397	Hs.74137	transmembrane trafficking protein	1.1	1.69
133504	W95070	Hs.74316	desmoplakin (DP1; DP1)	0.7	6.21
133517	X52947	Hs.74471	gap junction protein; alpha 1; 43kD (con	0.95	1.3
133540	D78151	Hs.74619	proteasome (prosome; macropain) 26S subu	0.91	1.25
133594	L07758	Hs.172589	nuclear phosphoprotein similar to S. cer	0.84	1.29
133627	U09587	Hs.75280	glycyl-tRNA synthetase	1.09	1.99
133671	T25747	Hs.75471	zinc finger protein 146	1.02	1.5
133859	U86782	Hs.178761	26S proteasome-associated pad1 homolog	1.11	3.33
133865	F09315	Hs.170290	disca; large (Drosophila) homolog 5	1.84	6.7
133913	W84712	Hs.7753	calumenin	1.15	1.86
133963	L34587	Hs.184693	transcription elongation factor B (SIII)	1.3	1.91
133982	U47621	Hs.207251	nucleolar autoantigen (55kD) similar to	1.3	1.99
134100	L07540	Hs.171075	replication factor C (activator 1) 5 (36	0.72	1.65
134110	U41060	Hs.79136	LIV-1 protein; estrogen regulated	1.04	1.62
134158	U15174	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	1	1.55
134161	U97188	Hs.79440	IGF-II mRNA-binding protein 3	0.82	1.95
134193	F09570	Hs.7980	ESTs	0.98	1.48
134367	X54199	Hs.82285	phosphoribosylglycinamide formyltransfer	1	2.8
134402	U25165	Hs.82712	fragile X mental retardation; autosomal	1.26	2
134457	D86963	Hs.174044	dishevelled 3 (homologous to Drosophila	1	1.47
134469	X17567	Hs.83753	small nuclear ribonucleoprotein polypept	0.94	1.57
134498	M63180	Hs.84131	threonyl-tRNA synthetase	1.2	2.64
134501	W84870	Hs.211568	eukaryotic translation initiation factor	0.84	1.36
134507	M63488	Hs.84318	replication protein A1 (70kD)	1.7	2.93
134548	U41515	Hs.85215	Deleted in split-hand/split-foot 1 regio	1.46	2.73
134599	X99226	Hs.86297	Fanconi anemia; complementation group A	1.36	2.22
134692	R73567	Hs.8850	a disintegrin and metalloproteinase doma	0.77	1.64
134693	N70361	Hs.8854	ESTs	1.09	1.82
134806	Z49099	Hs.89718	spermine synthase	0.98	1.35
134821	Z34974	Hs.198382	plakophilin 1 (ectodermal dysplasia/skin	0.99	1.4
134864	Y08999	Hs.90370	actin related protein 2/3 complex; subun	0.95	1.42
134914	U29615	Hs.91093	chitinase 1 (chitinobiosidase)	1.16	1.29
134953	L10678	Hs.91747	profilin 2	0.95	1.76
134993	AA282343	Hs.9242	purine-rich element binding protein B	0.98	1.73
135051	C15324	Hs.93668	ESTs	1.35	2.11
135158	U51711		Human desmocollin-2 mRNA; 3' UTR	0.86	1.16

Table 1B shows the accession numbers for those pkays in Table 1A lacking unigenal IDs. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the Accession column.

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT	Accessions
100661	23182_1	BE623001 L05096 AA383604 AW966416 N53295 AA460213 AW571519 AA603655
100667	26401_3	L05424 X56794 S66400 X55150 W60071 AW351820 X55938 M83326 BE005289 BE070059 M83324 BE005248 BE069717 BE181648 BE069700 AW606203 BE069721 AW382138 AW803776 BE463954 BE005334 BE005274 T27386 AA932714 AA972695 AW377728 A1632506 T29066 A1783934 AW377727 BE163715 AL047291 AA279047 AA523003 BE008048 BE440141 W23614 BE090519 BE092193 N29181 N20358 N44153 BE546944 T69231 AW377441 AA907406 H50799 AW051416 A1420712 BE620922 A1279161 AA992549 W47198 BE005241 A1342698 H50700 A1969974 A1863855 AA374490 AW130675 A1950633 AA146687 H99482 X55150 BE005414 BE005339 N28294 A1673068 A1887890 AW804171 A1675961 AW804172 AA778841 AL048050 A1127757 A1095568 AW204965 AW468978 W31898 A1052595 A1278771 BE464018 A1081503 A1824196 AA513211 AA411062 AW084376 N48752 AA703209 N35580 AW059918 AA054563 A1280942 T27619 BE621435 N66010 AW589527 A1160414 AA283090 AA962536 H82726 W52115 W45432 W60433 AA577548 AA146714 BE150994 AA054615 AW796025 AW382768 BE565671 C00444 AA054555
100668	26401_3	L05424 X56794 S66400 X55150 W60071 AW351820 X55938 M83326 BE005289 BE070059 M83324 BE005248 BE069717 BE181648 BE069700 AW606203 BE069721 AW382138 AW803776 BE463954 BE005334 BE005274 T27386 AA932714 AA972695 AW377728 A1632506 T29066 A1783934 AW377727 BE163715 AL047291 AA279047 AA523003 BE008048 BE440141 W23614 BE090519 BE092193 N29181 N20358 N44153 BE546944 T69231 AW377441 AA907406 H50799 AW051416 A1420712 BE620922 A1279161 AA992549 W47198 BE005241 A1342698 H50700 A1969974 A1863855 AA374490 AW130675 A1950633 AA146687 H99482 X55150 BE005414 BE005339 N28294 A1673068 A1887890 AW804171 A1675961 AW804172 AA778841 AL048050 A1127757 A1095568 AW204965 AW468978 W31898 A1052595 A1278771 BE464018 A1081503 A1824196 AA513211 AA411062 AW084376 N48752 AA703209 N35580 AW059918 AA054563 A1280942 T27619 BE621435 N66010 AW589527 A1160414 AA283090 AA962536 H82726 W52115 W45432 W60433 AA577548 AA146714 BE150994 AA054615 AW796025 AW382768 BE565671 C00444 AA054555
101332	25130_1	J04088 NM_001067 AF071747 AJ011741 N85424 AL042407 AA218572 BE296748 BE083981 AL040877 AW499918 AW675045 H17813 BE081283 AA670403 AW504327 BE094229 AA104024 A1471482 A1970337 AA737616 A1827444 AW003286 A1742333 A1344044 A1765634

5

10

15

20

25

30

35

40

45

50

55

60

65

70

75

80

85

100780 458_127

100830 4002_1

100906 4312_1

100930 16865_1

102221 3861_1

101809 32963_1

102590 15932_1

101977 29073_1

102781 20812_1

A1948838 AW235336 AW172827 AA095289 BE046383 A1734240 W16699 A1660329 A1289433 AA933778 AW469242 AA468838 AA806983
 AA625873 W78031 BE206307 AA550803 A1743147 A1990075 AA948274 AA129533 A1635399 AA605313 A1624669 AW584319 A1221834 A1337434
 A10307706 BE550282 A1760467 A1630836 A1221521 AW674314 AW078889 A1933732 A1686969 A1186928 AW074595 A1127486 A1079644
 A1910815 H17814 AA310903 AW137854 T19279 AA026682 AA306035 AW383390 AW383389 AW383422 AW383427 AW383395 H09977
 AA306247 AA352501 AW403639 F05421 AA224473 AA305321 H93904 AA089612 AW391543 AW402915 AW173382 AW402701 AW403113
 R94438 N73126 H93466 AA090928 AA095051 T29025 AW951071 L47277 L47276 A1375913 BE384156 W24652 AA746288 AA568223 BE090591
 H93033 N57027 AA504348 AA327653 AW959913 N53767 AA843715 A1453437 AW263710 A1076594 AA583483 AW873194 AW575166 A1128799
 A1803319 AL042776 AW074313 A1887722 A1032284 AA447521 A1123885 N29334 A1354911 AW090687 AA236763 AA435535 AA236910
 AA047124 AA236734 AW514610 H93467 AA952007 A1446783 AA127259 A1613495 A1686720 A1587374 AA936731 AA702453 A1859757
 AA216786 A1251819 A1469227 AA806022 A1092324 N71868 AA968782 AA236919 AA809450 AA227220 AA765284 A1192007 AA768810
 AA805794 AA729280 AA806238 AW768817 N71879 A1050686 AA505822 AA668974 A1688160 BE045915 AW466315 AA731314 AA649568
 AA834316 AW591901 AW063876 AW294770 A1300266 A1336094 A1560380 AA721755 H09978 D20305 D29165 AW821790 BE150864 F01876
 A1457474 AW466316 AA550969 AA530788
 BE561958 BE561728 BE397612 BE514391 BE269037 BE514207 BE562381 BE514256 BE514403 BE514250 BE397832 BE269598 BE559865
 BE396881 BE560031 BE514199 BE560037 BE560454
 AC004770 W05005 AA356068 AA094281 H29358 T56781 AW875313 L37374 BE312466 BE311755 BE207106 BE293320 BE018115 AW239090
 BE548830 AW247547 AA776062 BE397382 AA486713 T10111 T09340 AW498981 BE547280 AA356003 AW581520 AW875331 AA580720
 AW875336 BE276873 BE408229 AW188148 BE255166 BE253761 AW793727 AW373141 AW581548 AA471223 AA305950 BE263976 AA626820
 BE257409 AW360962 AA090655 C00312 BE312741 BE407213 AA209352 AW298199 AW248553 AW297794 AW371322 BE300586 AW731972
 AW615446 BE301599 AW615520 AA486714 AW440257 AA196516 AA564630 AA618079 AW192592 AW474985 AA604580 A1027461 AA765440
 A1680394 AL135548 A1683224 A1581126 AW245096 AW194154 H29274 N70363 AA629758 AA580602 AA862006 A1683841 A1097667 A1629583
 A1358774 BE243487 AA620553 AA653297 AA292690 T10110 Z38906 AA908544 AA340930 A1185438 T03328 T28844 A1687010 A1864965
 A1872575 BE388740 T56780 AW373138 BE258717 AA998971
 AU076916 BE298110 AW239395 AW672700 NM_003875 U10860 AW651755 BE297958 C03806 A195876 AA644165 T36030 AW392852
 AA446421 AW881866 A1469428 BE548103 T96204 R94457 N78225 A1564549 AW004984 AW780423 AW675448 AW087890 AA971454 AA305698
 AW879433 AA535069 A1394371 AA928053 A1378367 N59764 A1364000 A1431285 T81090 AW674657 AW674987 AA897396 AW673412 BE063175
 AW674408 A1020211 R00723 A1753769 A1460161 AW079585 AW275744 A1873729 D25791 BE537646 T81139 R00722
 J04129 NM_002571 AA293088 AA477016 AA404631 T28299 AA476904 AA433965 AA430486 AA495907 A151391 AA291495 AA402723 W25651
 W076816 A1826712 AW296294 AA293479 A1276581 AW044154 A1080180 A1477985 A1274168 A1474212 AA495908 AA635664 A1092114
 A1804952 AA479874 A1597661 A1420511 AA479738 AA421417 AA421247 AA436220 AL047797 M34046 NA2277 AA228076 W02698 A1420297
 AA434011 A1369971 AA479731 A1865541 A1418020 AA421246 AA452764 AL048051
 NM_006769 U24576 AW161961 AW160473 AW160465 AW160472 AW161069 A1824831 AW162635 A1990356 AW162477 AW162571 A1520836
 AW162352 AW162351 AW162752 A1962216 A1537346 AA853902 H17667 BE045346 BE559802 BE255391 AA985217 AA235051 A129757
 AW368451 T34489 D56106 D56351 A1936579 AW023219 AW889335 AW889120 AW889232 AW889175 BE093702 AW889349 AA147646
 A1952998 AA912579 A143358 AW902211 R64717 AW157236 A1815242 D45274 AW263991 AA442920 AA129965 AL035713 A1923255 A1949082
 A142826 A1684160 A1701987 A1678954 A1827349 BE463635 AW628092 AW302281 AA493203 BE348856 BE536419 AW183969 AW673561
 AW592609 A1224044 H43943 AA091912 R49632 R48353 A1568409 R48256 A1198046 H27986 H43899 A1687559 A1680310 A1624220 H17052
 A1156410 N56082 A1699430 AA664529 T09406 T10459 AA627608 A1379584 N88331 N88633 AW022651 AA971281 AA248036 A1039197
 A1914689 AA973825 AL047305 AA129966 A1798369 AW264348 A1445879 A1658759 N67924 A1933507 A1216121 A1333174 T10972 A1376028
 A186756 A1273778 AA610487 A1797946 AA853903 AA903939 A1338587 A1278494 AW627595 AA904019
 M86849 AA315280 NM_004004 AA315269 BE142653 AA461400 AW020422 BE152893 AW383155 AA430688 AW117930 AW384563 AW384544
 AW384566 AW378307 AW378323 AW839085 AA257102 AW378317 AW276080 AW271245 AW378298 AW384497 A1598114 AW264544 A1018136
 AW021810 AA961504 AW086214 AW771489 AW192483 A1290266 AW192488 AW384490 AW007451 AW890895 AA554460 AA613715
 AW020068 A1783695 A1589498 A1917637 AW264471 AW384491 A1816732 AW368530 AW368521 AW368543 AA461087 A1341438 A1970613
 A1040737 A1418400 AA947181 AA962716 A1280695 AW769275 AW023591 A1160977 AA055400 N71882 AA490466 AW243772 AW316636
 A1076554 AW511702 N69323 H88912 AA257017 A1952506 H88913 A1912481 AA600714 BE465701 N64149 C00523 N64240 AA677120
 R61573 BE005029 X98091 AA297307 BE537267 BE566138 BE568139 F11561 BE564795 BE568776 AW064005 BE586479 BE380035 BE567012
 BE568634 BE566568 AA298068 BE566043 BE566881 BE566818 AA283070 BE565414 BE566738 BE568585 BE566567 BE566116 BE566433
 U62136 AF049140 BE567057 BE567297 BE567403 BE564316 BE567400 BE568854 BE566588 AA448772 AA071363 AW732642 BE564996
 AA297763 AA278550 AA421083 AA298184 AA091007 AA984577 AA205916 N28759 AL031291 C15767 C15761 H02728 BE566410 AA129335
 AA419499 N87741 BE379689 BE004824 BE379611 D25874 AA148454 AA323654 AW950311 AA448795 AW749423 AA773386 AA773843
 AW020327 BE348580 BE504258 BE549990 BE220200 A1673334 A1202679 AA975515 D61421 A1168688 AA102843 AW246821 A1276203
 A1074054 A1633824 A1962927 A1148926 N50969 A1308911 AA410994 AW373025 AA148455 H02620 AA688293 A1246318 N22220 A1917777
 A1050943 A1097286 AA663794 AW368662 AW627826 AW078734 A1253060 AA749154 AA832236 A1192358 AW024676 AA448676 AA764891
 BE439467 AA661534 AA258061 A1090546 AA995157 A1051011 AA584421 A1026032 AW591338 AW589563 AA776914 AW024684 AA421002
 F09219 BE464500 A1383595 AA954244 AA601583 AA737304 AA195549 AA805778 A1055876 AA169492 AW013961 A1672608 AW514211 D59441
 AW582574 AA160935 BE566501 BE564612 BE565353 BE568195 BE565447 BE568302 BE566097 BE565470 BE564270 AL036217 AW749424
 BE567494 AA102842 AA414761 AV661237 C14211 AA651866 AW798997 AA470605
 AF112213 AL050318 T24804 AW248136 BE386341 BE283177 W16677 BE250224 BE563669 BE267405 BE546577 AV651354 AV651292
 A1346903 A1539128 A1189171 S83364 AW073849 A1816760 AW073309 A1422690 AA296692 A1860301 A1805446 N77735 A1340328 BE092530
 AW028742 BE088442 AA657742 AA742438 AW170086 A1038920 A1432379 N36073 A1936194 AA868655 AA983612 A1077505 BE080433
 A1375014 A1126547 A1348244 A1346077 A1748952 N26915 A1753574 A1093341 A1278762 BE092517 N74204 H08158 T58149 A1129303 N58366
 AA524456 BE122661 AA542925 A1246120 A1735203 AA706829 AA877544 A1082289 AA926687 N92840 AW249798 AA934763 AW998363
 A1128632 N25202 A1240209 AW118892 N80744 R35655 A1342321 A1340141 AW878792 A1857321 H09610 W04601 AW006650 AA126006
 AA553675 A1052791 AW059835 A1041906 AA814658 AW002059 AA729483 A1609301 AA994633 AA903651 A1459183 T95072 AW088630
 AA126112 A1800091 A1581215 H17502 AW475072 A1819003 A1683272 A1262701 AW793140 T81787 R99586 A1275160 A1310420 A1698929
 AA159174 A1827968 F30305 F30309 AA806662 A1091923 AW878722 AA583430 AW571913 A1674584 AA292533 A1079471 AA642325 AA719050
 AW793172 AA305476 AW103745 T23459 N79525 A1784438 AA534551 AW193751 A1074360 BE281214 T32229 W25066 W01205 T63086
 AW795348 A1361287 AW795353 AW795349 AA594759 A1400295 D11489 A1370689 AA482356 AA485295 W40151 AA564661 AW300745
 A1346938 A1374975 A1423782 AW193899 AA612604 A1183409 AA996156 AW366963 AW366977 A1284860 AA846503 A1985064 AA844576
 AA737921 AA873274 BE241546 BE241540 AA484058 AW468970 AA127876 AA159120 AW001568 AW795213 AW795258 AW795330 BE250589
 BE387572 AA910895 AA161217 BE250380 W31500 T95167 A1719306 A1359224
 BE258778 BE281230 BE410044 T33723 AW672694 AW410439 NM_006429 AF026292 T35505 BE542333 T08940 AU076737 AW247471
 BE393215 AW328640 BE542408 T32170 BE302544 T31855 BE206898 BE275738 T32570 BE386426 BE298746 BE389937 BE293991 BE315289
 BE389578 R34739 R15312 BE279365 BE277756 AL036019 T33725 BE277779 BE302962 AL047294 BE276505 T09070 T33673 BE312580
 AW387774 BE257175 AW674367 BE253331 BE270344 BE299831 BE273576 T32062 A1751831 BE618381 AA304899 BE252268 U46364
 BE256790 BE207199 BE256209 BE251941 BE250791 BE313955 BE269806 BE543623 BE279212 BE252220 T31669
 AA315781 A1192212 N84547 BE292737 BE259631 AA232179 A1133144 T31292 AA315945 BE407301 BE251184 BE409006 A1880158 A1904003
 A1904114 AW651768 AW651763 R58247 BE271897 U83843 C05298 BE261609 BE255973 AA351650 N84631 BE263537 AA455233 AA328465
 AA324549 AW575525 BE252296 BE257551 AL048332 BE208630 AA359336 AW372787 AA151742 AA305816 BE076852 BE076796 BE263161
 AA323785 AA676588 AA626565 AW078917 W87657 R09002 R94021 AA312032 BE276665 AA295608 AW407162 AA329374 AW877912 N27885
 AA369256 AA360968 BE250476 N85427 BE265569 A1278639 A1816576 A1691037 AW328683 A1567949 A1983455 A1277332 A1811297 A1571508
 AW073674 BE286039 BE487326 A1828796 A1816578 AW511604 A1921213 AW152427 A1795787 A1801618 AW168866 A1628144 A1890339
 AW173890 AW511540 BE535620 AA383014 BE301164 A1866596 AW514909 AA658050 AW575243 AA074631 A1093488 AW575408 AW675443
 AW615836 AW732027 AW377638 AA321784 AA641629 AA633105 AA527640 AW129146 AW615672 BE394607 AA483902 AW475032 BE378532

5

10

15

20

25

30

35

40

45

50

55

60

65

70

75

80

85

AA872808 AI469388 AW105268 BE047301 AW591843 AW410066 AW517153 AI950495 AA746641 AI914878 AA873185 AI696911 AA548625
AA911505 AA148762 AW674535 AI587329 BE238328 AW270348 AA158225 AW117705 AW474997 AW519193 AA614757 AW664383 AI082647
AW590973 AI476711 AA192213 N88741 BE464552 AW072679 AI453708 AA152166 AA805924 AI581078 AI125768 AW173484 AI961980
BE300766 AI199698 AI636792 AW247333 AW272861 AA078818 AA150012 AA551232 AA678821 AW873869 AW768266 AI660315 AA319210
AA814551 AA157994 AA318886 AI582862 AW089224 AI356098 AI343694 AW072598 N12054 AI301249 AA742924 H17917 AW328584
AW248898 AI751830 AA907816 R08898 AW087989 AI828300 AA148596 AI269577 T33426 AA213571 AI973201 AA666279 R49612 AI573183
AW799762 AW410068 AW789666 AI962097 AI475204 D57490 AW517631 BE245270 AW470008 T33427 AW005731 AI795795 T23753 AW272981
T15747 AA552875 T23644 AW361289 AI758558 BE207435 AA876958 T03361 AA833569 F37533 AA582321 AW082524 R42212 AA973847
T18900 AA086202 AI559867 AI302418 AA948667 AA745670 T08939 T33724 T33722 BE621568 D57489 D25906 BE621151 F16510 C05966
T35127 AA630427 AI933481 AA309426 AI918440 BE661854 BE618866 BE394675 BE296173 AW951687 BE383739 BE616141 BE312730
BE535351 AW080576 BE313330 BE618664 AI354390 AA847315 BE544509 BE515212 BE297833 BE278808 BE544844 AW090178 AI890664
BE546708 AW189943 BE274412 BE382399 BE266392 BE264949 BE280696 BE383237 BE261756 BE257721 BE312683 BE275476 BE514880
BE545314 BE313587 BE384537 BE386691 BE264813 AW592575 AI336332 AI278641 AI795791 BE222662 AW249316 AA314361 AL036012
AW402923 BE266845 AA075945 AA314436 BE384640 AW731769 AW957077 AA552234 AA573560 AW367038 AA313399 AI983873 BE410159
BE263803 BE514339 BE409073 BE281296 BE543396 BE395387 BE088360 BE546946 BE546570 BE390628 AA074638 AA301821 AW845230
AW582379 AI949222 AW029572 AA515843 AW272394 BE250234
C14322 W74050 AI074232 AA595624 BE048955 AI148417 AI583145 AI473460 AI801688 AW573593 AI950741 AI628140 AW467921 R98105
AI149258 AI247584 AI078378 AI139850 AA489411 W24744 R98104 AI033826 AA699589 AI033120 N55544 W88984 AW970771 AA703362
AA099138 AA706792 AA046150 H98981 AI916874 AA953018 AI972749 AI921343 AA909044 AA094751 AI203124 AA582143 AI446654
AW235415 R70377 AA099236 F20703 AA524436 R69484
H04043 D60988 D60337
AI204246 AI204250 AI194050
H83266 T63524 AA304359 AW960551 AI672874 AI749427 AA227777 AW027055 AA971834 T49644 T54122 AI983239 AI808233 T91264 T96544
AI50945 AI709114 R72382 T48788 R47826 AW385418 AI095484 T49645 AA928653 AA570082 AW007545 T57178 AA516413 AA913118 T57112
AA564433 AA774503 AA367671 T59757
W78816 AI720806 AI633854 AI632086 AI668663 N70894 AW571809 AI383592 AI201348 W80715 N91880 AW963101 AA339011
AB033023 BE391906 BE275965 BE277872 BE003882 AA313774 BE019159 BE298024 BE299727 BE300011 BE390277 BE394764 N87550
BE409419 BE408652 BE408197 AL119332 AA622427 AI816265 AA610118 T07318 AA019839 AA634430 BE205794 BE049461 AI042322
AI652711 AI917645 AA630045 AW191969 AI817882 T12771 AI803663 AI095533 H46019 AW592438 AI675552 D61149 AW132058
AA639614 AI925762 AW088153 T17455 AA018640 AW751475 BE300241 AI816255 BE391981 AW408671 AA353910 AW875446 AW875703
AW875926 AW875645 AW875647 AW938037 AL138042 AW892619 BE243018 AW995454 BE246381 BE009082 BE278921 AW967842 AA262454
H30121
W72062 AF088057 W76255 AI827219 AI631461 AW449295 AI354957 AI913803 T82772 AI222040 T62921 T63781
AI678765 H12175 R14664 AI914049 AA995383 H08009 H19418 AW953728 AI358021 AA587361 AI269377 AA369905 AW957113 H27693
AI300474 H73776 W74397 AA579604 AI131018 W72331 AI719085 AA568348 AI859045 AI814819 AI888714 BE467470 AW131268 H19419
T27694 AI342165 AI914155 AA534872 BE018176 R60208 H11647 R45641 AI860466 BE301656 AI125453 AI498120 AA593735 AA879110
AI018404 T35018 AA588397 AW449767 AA470365 BE501139 AA588354 AI337500 AW078532 Z41279 AI125449 AA935725 AA404338
L42583 NM_005554 L42601 BE183076 AI641221 BE140567 L42610 V01516 J00269 AW275792 AW383052 AW380143 AI541102 BE612846
AI541344 AW238368 BE613405 BE615705 BE615530 BE615301 AW379823 AW794706 AA194806 AA194806 AA586721 AI609242 AA431973 AA232959
AI246504 AI540333 AW238681 AA640939 AI540863 AI608860 AW662564 AW366725 AW368983 AW366870 AA596020 AW794721 AW794511
AI591181 BE182523 AW794644 AW794620 AI935234 AI608903 AI608623 AW797080 AW084935 BE182517 BE182319 AI890082 AW238346
AW797012 BE182522 AW794838 AI608794 AW304289 AA147193 AA559595 AW381128 AW366720 AA583718 AI828416 BE122864 AW368343
AA431080 AW082039 AW380976 AA587144 AA443636 AW872937 AW794448 AW378382 AW085761 AW794718 AW263895 AA583587
AA583991 AA583994 AA586886 AA586880 AW368365 AI814460 AA586991 AI282829 AW378406 AA586721 AI609242 AA431973 AA232959
AI831095 AW263854 AW378391 AW378415 AW378381 AA036990 AW238395 AI285446 BE208219 BE049526 AA583605 AA583918 AW366711
AI285580 AW082642 AI285712 AA582875 AW591216 AW368719 AW378408 BE122835 AA582976 BE350422 AA418328 AA51454 AI565930
AA583700 AA150575 AW238427 AI287474 AA912658 AA584223 AW238528 C17918 AW136169 AA159847 AI923797 AI609009 BE182479
AI915198 AW378114 AA147179 AA584239 AA150632 AW168862 AW085999 AW082480 AA659742 AW079703 AI872793 AA583981 AI824571
BE182316 BE182507 AA23331 AI824572 AI540586 D29492 BE182931 AA036948 BE551821 D29401 AW378365 C00141 D29587
AW103359 W95238 AI991663 AA587298 BE184608 AA099833 W95121 W95150 D29584 AI934111 D29456 D29533 AW265380 D29290
AW238463 AA121041 D29204 AA595925 D29441 AW081840 AA587018 D29323 AA582891 BE182433 BE182437 BE158295 BE182434
AW016534 AA314369 AA290715 BE586863 AW629494 D28364 AW995678
AI907114 AA580734 AL041945 AA101515 AA121344 D78130 NM_003129 AA341650 T84166 AF098866 AI130976 BE089553
T661122 AW175590 F05344 AI114790 R12900 AA194871 AA132298 D78129 AA132213 AW948930 AW948919 AA263053 AW946593 AW948840
AA278558 R50895 N26940 N40818 AW021255 AA054851 AA663379 AW948795 AW948893 AA400356 AW948911 N85024 W78844 AI341546
AI760182 AA286783 BE617763 BE617263 AW263690 BE049454 BE617928 AW515038 AW950584 AA601009 AI079194 AA147204 AW083163
AA130981 AI218369 AA604784 AI806267 AI559556 AA232318 AA258065 AI471982 AA687949 AI143944 AI439441 AI679049 AI084342
AI212830 AA948469 AI802469 H05720 AA113270 AA158138 AA076231 AI521024 AI810962 AI133616 AA805106 AA101516 R40052 R50778
R43280 T65036 AW131924 AA114251 AI152331 F09650 AA580614 AA558927 C75491 Z38352 AA954595 F5606 W78472
D56165 M36981 X58965 NM_002512 BE379177 AA314838 BE256445 BE252016 AW248343 AI720933 AW085701 BE386050 BE619742
AA482961 AI003658 H43261 AA657978 AI735072 R83138 AA722002 AA628271 AW273877 BE464626 AA071483 AA429973 AA494342
AA620436 AA775597 AA775601 AA826847 AI192585 AA826359 AA411159 AI193419 AI204013 AA705323 AA716255 AI784611 AI081144
AI128227 AA828464 AI148911 AI493446 AI626084 AI189180 AI721196 AI190618 AA284987 AI128543 AA632054 AI333073 AI278470 AI313688
AI491768 AA937581 AA630065 AA834257 AW249841 AA583742 AI309756 AA961676 AI760860 AA557818 AA954238 H43655 AI302564
AA127545 AI609219 H20426 AI042292 AI056466 AA581836 W47002 AA422057 AA937673 F29757 AA829208 AW327462 AA372098 W02144
AA036805 AA487365 AA961037 AI139946 AA487250 AA737118 AI952504 AI242293 AA650552 AI708401 AI633133 AA630848 AA654317 F24128
AI434165 W46252 AW043879 AI033763 F37228 AA687809 N49087 AA876981 AA506947 AI914572 AI833284 F22253 AA026222 R50166
AI219267 N27095 AA496512 AI784222 AI289904 AA513146 AA528547 AA418700 F36721 AI880700 AI601170 AI862851 AA524499
AA642220 AA496628 AI718709 W80579 AI720547 F20718 AA649943 AA588229 N40503 H46029 BE262669 BE391069 BE537538 AI510751
AI906968 AI318611 H46099 AI472604 T60667 AA373087 W32479 AA514034 BE619183 AA134672 AA127544 H26942 BE536689 AW327461
AA422139 AW262357 AW327348 F33510 AI630382 AW827126 F27133 AI335189 AW517599 W80471 AA885814 N89881 BE393173 AA617760
AA584268 AA460537 AA446261 H20425 N64040 AW276801 AA316367 AA071232 BE545409 AA308292 BE274447 AA308861 AA340038
AA341808 AA865579 AI018634 AI766314 AI919302 AA872367 AA991404 AI906961 AA888375 BE621012 AA505388 AA935192 AA290828
R50220 H50814 H44721 AW951723 AA514796 AA418708 AW673377 AA379622 AA977995 AA708224 AA708216 AI318249 AI318233 AA411160
AA026221 AA316774 AA486908 AI500094 AA096362 AW583742 BE536422 BE618653 R70203 AA131732 AA345048 BE562720 T28342
NM_004415 AL031058 M77830 BE149760 AW752599 AW848723 AW376697 AW376817 AW376699 AW848377 AW376782 AW848789
AW361413 AW849074 AW997139 AW799304 AW799309 BE077020 BE077017 BE185187 AW997196 BE156621 BE179915 BE006561 BE143155
AW890985 BE002107 AW103521 AA857313 BE011378 AW170253 BE185750 AW886475 BE160433 J05211 BE082576 BE082584
BE004047 AW607238 AW377700 AW377699 BE082526 BE082505 BE082507 BE082514 AW178000 AW177933 AI905935 AW747877 AW748114
BE148518 AW265328 AW847678 AW847688 AW365151 AW365148 AW365153 AW365156 AW365157 AW365154 AW068940
BE005272 AW365145 BE001925 BE182166 BE144243 BE001923 AI951766 AI434518 BE184920 BE184933 AI284090 BE184941 AW804674
BE184924 C04715 W39488 AW995615 BE184948 BE159646 AW066653 AA099891 AA131128 AA337270 AA340777 AA384371 AA852212
R58704 AW366566 AW364859 AA025851 AA025852 AA455100 AA719958 AW352220 AW996245 BE165351 BE073467 AA377127 AW890264
AW609750 AW391912 AW849690 T87267 AW853812 AA852213 W74149 BE009090 AA056401 H91011 AW368529 AW390272 C18467

5

10

15

20

25

AW674920 N57176 AA026480 AW576767 H93284 AA026863 AW177787 AA026654 AW177786 BE092134 BE092136 AW177784
AI022862 BE091653 AW376811 AW848592 AA040018 BE185331 BE182164 AA368554 AW951576 T29918 AA131077 W95048 W25458
AW205789 H90899 N29754 W32490 R20904 BE167181 BE167165 N84767 H27408 H30146 AI190590 C03378 AI554403 AI205263 AA128470
AI392926 AF139065 AW370813 AW370827 AW798417 AW798780 AW798883 AW798569 R33557 AA149190 C03029 AW177783 AA088866
AW370829 AA247685 BE002273 AI760816 AI439101 AW879451 AI700963 AA451923 AI340326 AI590975 T48793 AI568096 AI142882 AA039975
AI470146 AA946936 BE067737 BE067786 W19287 AA644381 AA702424 AI417612 AI306554 AI686869 AI568892 AW190555 AI571075 AI220573
AA056527 AI471874 AI304772 AW517828 AI915596 AI627383 AI270345 AW021347 AW166807 AW105614 AI346078 AA552300 W95070
AI494069 AI911702 AA149191 AA026864 AI830049 AI887258 AW780435 AI910434 AI819984 AI858282 AI078449 AI025932 AI860584 AI635878
AA026047 AA703232 D12062 AW192085 AA658154 AW514597 AW591892 T87181 AA782066 AW243815 AW150038 AW268383 AW004633
AI927207 AA782109 AW473233 AI804485 AW169216 AI572669 AA602182 AW015480 AW771865 AI270027 AA961816 AA283207 AI076962
AM98487 AI348053 AI783914 H44405 AW799118 AA128330 AA515500 AA918281 W02156 AI905927 AA022701 W38382 R20795 T77861
AW860878
100528 45979_1 BE386801 AU077299 AA143755 BE302747 AA853375 U30162 BE274163 BE277479 BE408180 BE274874 C15000 AA047476 N27099 AI359165
AI636794 AI151283 AI863925 AW444977 AI207392 AA931263 AA443112 R40138 AW068538 AA351008 AA676972 R62503 AA916492 AW001865
H42334 H38280 AA121497 AA114137 AI750938 M17783 AA383786 BE274462 AI753182 C05975 AA347404 AW069298 AI754351 AI754044
AA188808 AA186879 AA565243 AL040655 AA456177 AI750722 AA045756 AA213580 C16936 AW578747 AW753731 AI41632 N44761 R58560
R61260 AA039902 N59721 AW992543 R68380 AA149686 T29017 H03739 BE383822 BE387105 BE408251 BE410425 H41660 AA247591
BE389677 AI752233 AI566195 AA868004 AI424523 AW753720 AA852159 BE386803
100559 2260_1 NM_000094 L02870 D13694 S51236 M96984 AW946290 M65158 AI285422 D29523 AL119886 AW630655 L06862 AI884355 AW168737 T29085
AW797005 AW801340 AI355504 AW079048 AW801337 AI690455 AI972063 AW268565 W68588 AA587326 AA883498 AI033523 AW510356
AW591998 H98463 AL043852 AI150055 AI566239 AI624803 AA844717 H40670 AA922334 AI864424 AW615094 AW451233 AI302203 F31221
AI872170 W68589 AA904478 AI917631 AW014208 AW450759 AA847625 AI284033 AA848176 AA598507
100576 9986_1 X00356 NM_001741 M26095 X03662 M12667 X02330 X02330 AA716058 AW296074 X04861 AI695720 AA719597
124357 genbank_N22401 N22401
101624 entrez_M55998 M55998
101625 entrez_M57293 M57293
135158 57963_1 AL037551 AI804716 AW439811 AI569470 AA075299 AI738572 AI270388 AI816783 AW263026 AI633951 AI655285 AI990572 AI950425
AW241533 AA916883 AA576693 AA160156 AA613783 AW078884 AI888282 AI275241 AI133467 AA164921

Tables 2A-8C were previously filed on November 9, 2001 in USSN 60/339,245 (18501-004100US)

Table 2A shows 504 genes down-regulated in lung tumors relative to normal lung and chronically diseased lung. Chronically diseased lung samples represent chronic non-malignant lung diseases such as fibrosis, emphysema, and bronchitis. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: 90th percentile of AI for normal lung samples divided by the 80th percentile of AI for adenocarcinoma and squamous cell carcinoma lung tumor samples.
 R2: median of AI for normal lung samples divided by 90th percentile of AI for adenocarcinoma and squamous cell carcinoma lung tumor samples.
 R3: median of AI for normal lung samples minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples divided by the 90th percentile of AI for adenocarcinoma and squamous cell carcinoma lung tumor samples minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples.
 R4: average of AI for normal lung samples divided by average AI for squamous cell carcinoma and adenocarcinoma lung tumors.
 R5: median of AI for normal lung samples divided by the 90th percentile of AI for adenocarcinomas.
 R6: median of AI for normal lung samples minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples divided by the 90th percentile of AI for adenocarcinomas minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples.
 R7: average of AI for normal lung samples divided by the 90th percentile of AI for squamous cell carcinomas.
 R8: median of AI for normal lung samples minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples divided by the 90th percentile of AI for squamous cell carcinomas minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples.

Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2	R3	R4	R5	R6	R7	R8
100096	Z97171	Hs.78454	myocilin; trabecular meshwork inducible	40.20							
100115	NM_002084	Hs.336920	glutathione peroxidase 3 (plasma)								3.46
100138	U83508	Hs.2463	angiopoietin 1			2.30					
100299	D49493	Hs.2171	growth differentiation factor 10		11.00						
100305	U86749	Hs.80598	transcription elongation factor A (SII);						3.06		
100447	NM_014767	Hs.74583	KIAA0275 gene product								3.16
100458	S74019	Hs.247979	Vpre-B	42.40							
100862	AA005247	Hs.285754	Hepatocyte Growth Factor Receptor						4.13		
100959	AA359129	Hs.118127	actin; alpha; cardiac muscle				125.60				
101032	BE206854	Hs.46039	phosphoglycerate mutase 2 (muscle)	36.40							
101081	AF047347	Hs.4680	amyloid beta (A4) precursor protein-bind				34.60				
101088	X70697	Hs.553	solute carrier family 6 (neurotransmitte				193.20				
101125	AJ250562	Hs.82749	transmembrane 4 superfamily member 2						3.10		
101180	U11874	Hs.846	Interleukin 8 receptor; beta				54.86				
101308	L41390		*Homo sapiens core 2 beta-1,6-N-acetylgl	33.20							
101330	L43821	Hs.80261	enhancer of filamentation 1 (cas-like do				36.40				
101345	NM_005795	Hs.152175	Calcitonin receptor-like			2.29					
101346	AJ738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N				70.55				
101397	M26380	Hs.180878	lipoprotein lipase								3.54
101414	NM_000066	Hs.38069	complement component 8; beta polypeptide							3.81	
101435	NM_001100	Hs.1288	actin; alpha 1; skeletal muscle				34.60				
101507	X16896	Hs.82112	interleukin 1 receptor; type I				37.60				
101530	M29874	Hs.1360	cytochrome P450; subfamily IIB (phenobar								4.25
101537	AJ469059	Hs.184915	zinc finger protein; Y-linked			2.54					
101542	NM_000102	Hs.1363	cytochrome P450; subfamily XVII (steroid		5.50						
101545	BE246154	Hs.154210	EDG1; endothelial differentiation, sphin	39.40							
101554	BE207611	Hs.123078	thyroid stimulating hormone receptor		13.00						
101560	AW858272	Hs.83733	intercellular adhesion molecule 2, exon								3.38
101574	M34182	Hs.158029	protein kinase; cAMP-dependent; catalyti						4.37		
101605	M37984	Hs.118845	troponin C; slow								3.80
101621	BE391804	Hs.62661	guanylate binding protein 1; Interferon-	30.20							
101680	AA299330	Hs.1042	Sjogren syndrome antigen A1 (52kD; ribon						3.37	2.75	
101829	AW452398	Hs.129763	solute carrier family 8 (sodium/calcium								
101842	M93221	Hs.75182	mannose receptor; C type 1				38.20				
101961	AW004056	Hs.168357	*Hs-TBX2=T-box gene (T-box region) [huma			2.32					
101994	T92248	Hs.2240	uteroglobin								6.85
102020	AU077315	Hs.154970	transcription factor CP2			2.45					
102091	BE280901	Hs.83155	aldehyde dehydrogenase 7								6.75
102112	AW025430	Hs.155591	forkhead box F1	54.60							
102190	AA723157	Hs.73769	folate receptor 1 (adult)								3.98
102202	NM_000507	Hs.574	fructose-bisphosphatase 1								3.62
102241	NM_007351	Hs.268107	Multimerin			2.32					
102310	U33839		Accession not listed in Genbank		7.00						
102397	U41898		*Human sodium cotransporter RKST1 mRNA,	29.40							
102571	U60115	Hs.239069	*Homo sapiens skeletal muscle LIM-protein								3.75
102620	AA976427	Hs.121513	Human clone W2-6 mRNA from chromosome X						3.07		
102636	U67092		*Human ataxia-telangiectasia locus prote			2.40					
102667	U70867	Hs.83974	solute carrier family 21 (prostaglandin			3.15					
102675	U72512	Hs.7771	*Human B-cell receptor associated protei						3.56		
102698	M18667	Hs.1867	progastricin (pepsinogen C)								4.51
102727	U79251	Hs.99902	opioid-binding protein/cell adhesion mol					12.00			
102852	V00571	Hs.75294	corticotropin releasing hormone	37.40							
103026	X54162	Hs.79386	thyroid and eye muscle autoantigen D1 (6					13.00			
103028	X54380	Hs.74094	pregnancy-zone protein	28.80							
103098	M86361		Human mRNA for T cell receptor; clone IG					10.00			
103117	X63578	Hs.295449	parvalbumin		6.00						
103241	X76223		H.sapiens MAL gene exon 4			2.47					
103280	U84722	Hs.76206	Cadherin 5, VE-cadherin (vascular epithe			2.69					
103360	Y16791	Hs.73082	keratin; hair; acidic; 5							2.16	

WO 02/086443

PCT/US02/12476

5.97

	103496	Y09267	Hs.132821	flavin containing monooxygenase 2						
	103508	Y10141		"H.sapiens DAT1 gene, partial, VNTR"				3.27		
	103561	NM_001843	Hs.143434	contactin 1	2.40					
5	103569	NM_005512	Hs.151641	glycoprotein A repetitions predominant	2.99					
	103575	Z26256		"H.sapiens isoform 1 gene for L-type cal				4.18		
	103627	Z48513		H.sapiens XG mRNA (clone PEP6)				3.44		
	103767	BE244667	Hs.296155	CGI-100 protein					2.25	
	103850	AA187101	Hs.213194	Hypothetical protein MGC10895; sim to SR		46.55				
10	104078	AA402801	Hs.303276	ESTs				3.05		
	104326	AW732858	Hs.143067	ESTs				3.54		
	104352	BE219898	Hs.173135	dual-specificity tyrosine-(Y)-phosphoryl				3.16		
	104398	AI423930	Hs.36790	ESTs; Weakly similar to putative p150 [H	64.80					
	104473	AI904823	Hs.31297	ESTs						3.38
	104493	AW860427	Hs.79059	ESTs; Moderately similar to TGF-BETA REC		2.47				
15	104495	AW975687	Hs.292979	ESTs	28.60					
	104595	AI799603	Hs.271568	ESTs				3.42		
	104597	AI364504	Hs.93967	ESTs; Weakly similar to Slit-1 protein [6.00				
	104659	AW969769	Hs.105201	ESTs	34.00					
20	104686	AA010539	Hs.18912	ESTs		11.00				
	104691	U29690	Hs.37744	ESTs; Beta-1-adrenergic receptor	56.80					
	104764	AI039243	Hs.278585	ESTs		60.40				
	104776	AA026349		ESTs	34.20					
	104825	AA035613	Hs.141883	ESTs		3.03				
	104865	T79340	Hs.22575	Homo sapiens cDNA: FLJ21042 fls, clone C	41.20					
25	104942	NM_016348	Hs.10235	ESTs						3.27
	104989	R65998	Hs.285243	ESTs			40.00			
	105062	AW954355	Hs.36529	ESTs						3.20
	105101	H63202	Hs.38163	ESTs	34.20					
30	105173	U54617	Hs.8364	ESTs						4.17
	105194	R06780	Hs.19800	ESTs		16.00				
	105226	R58958	Hs.26808	ESTs			2.34			
	105256	AA430650	Hs.16529	transmembrane 4 superfamily member (tet			2.72			
	105394	BE245812	Hs.8941	ESTs			2.61			
35	105647	Y09306	Hs.30148	homeodomain-interacting protein kinase 3	33.60					3.59
	105789	AF106941	Hs.18142	arrestin; beta 2						
	105817	AA397825		synaptopodin				4.46		
	105847	AW964490	Hs.32241	ESTs		35.40				
40	105894	AI904740	Hs.25691	calcitonin receptor-like receptor activi		3.43				
	105999	BE268786	Hs.21543	ESTs	7.00					
	106075	AA045290	Hs.25930	ESTs			42.60			
	106178	AL049935	Hs.301763	KIAA0554 protein	34.80					
	106381	AB040916	Hs.24106	ESTs			12.00			
	106467	AA450040	Hs.154162	ADP-ribosylation factor-like 2				3.69		
45	106536	AA329648	Hs.23604	ESTs			96.40			
	106569	R20909	Hs.300741	sorcin			47.20			
	106605	AW772298	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076 (fr			220.40			
	106842	AF124251	Hs.26054	novel SH2-containing protein 3		2.55				
	106844	AA485055	Hs.158213	sperm associated antigen 6	39.20					
50	106870	AI983730	Hs.26530	sperm deprivation response (phosphatidyl		2.28				
	106943	AW888222	Hs.9973	ESTs						4.28
	106954	AF128847	Hs.204038	ESTs						4.32
	107106	AA862496	Hs.28482	ESTs			10.45			
	107163	AF233588	Hs.27018	ESTs		2.57				
55	107201	D20378	Hs.30731	EST				3.84		
	107238	D59362	Hs.330777	EST		8.00				
	107376	U90545	Hs.327179	solute carrier family 17 (sodium phospho		10.67				
	107530	Y13822	Hs.85087	latent transforming growth factor beta b		2.32				
	107688	AW082221	Hs.60536	ESTs			34.60			
60	107706	AA015579	Hs.29276	ESTs	28.40					
	107723	AA015967		EST				3.29		
	107727	AA149707	Hs.173091	DKFZP434K151 protein			80.80			
	107750	AA017291	Hs.60781	ESTs			51.40			
	107751	AA017301	Hs.235390	ESTs				3.14		
65	107873	AK000520	Hs.143811	ESTs		9.00				
	107899	BE019261	Hs.83869	ESTs; Weakly similar to IIII ALU SUBFAM1				3.65		
	107994	AA036811	Hs.48469	ESTs			44.60			
	107997	AL049176	Hs.82223	Human DNA sequence from clone 141H5 on c			32.00			
	108041	AW204712	Hs.61957	ESTs			30.80			
70	108048	AI797341	Hs.165195	ESTs				4.75		
	108338	AA070773		*zm53g11.s1 Stratagene fibroblast (#9372		2.33				
	108434	AA078899		*zm94b1.s1 Stratagene colon HT29 (#93722				2.92		
	108447	AA079126		*zm92a11.s1 Stratagene ovarian cancer (#				3.06		
	108480	AL133092	Hs.68055	ESTs			34.00			
75	108499	AA083103		*zn1b12.s1 Stratagene hNT neuron (#93723						3.36
	108535	R13949	Hs.226440	Homo sapiens clone 24881 mRNA sequence			19.00			
	108550	AA084867		*zn11f6.s1 Stratagene hNT neuron (#93723			12.00			
	108604	AA934589	Hs.49696	ESTs		2.33				
	108625	AW972330	Hs.283022	ESTs						5.82
80	108629	AA102425		*zn24c6.s1 Stratagene neuroepithelium NT				3.42		
	108655	AA099960		*zm65c6.s1 Stratagene fibroblast (#93721		7.00				
	108756	AA127221	Hs.117037	Homo sapiens mRNA; cDNA DKFZp564N1164 (f		6.05				
	108864	AI733852	Hs.199957	ESTs	28.80					
	108895	AL138272	Hs.62713	ESTs	32.80					
85	108921	AI568801	Hs.71721	ESTs			57.80			
	108967	AA142989	Hs.71730	ESTs	28.80					

WO 02/086443

PCT/US02/12476

5	109001	AI056548	Hs.72116	ESTs, Moderately similar to hedgehog-int	2.57				
	109003	AA147497	Hs.71825	ESTs				2.11	
	109004	AA156235	Hs.139077	EST	5.60				
	109065	AA161125	Hs.252739	EST			10.00		
	109250	H83784	Hs.62113	ESTs; Weakly similar to PHOSPHATIDYLETHA					3.44
10	109490	AA233416	Hs.139202	ESTs					2.92
	109510	AI798863	Hs.87191	ESTs		2.40			
	109578	F02208	Hs.27214	ESTs	10.00				
	109601	F02695	Hs.311662	EST			40.80		
	109613	H47315	Hs.27519	ESTs			54.40		
15	109560	R31770	Hs.23540	ESTs	31.20				
	109682	H18017	Hs.22869	ESTs	8.40				
	109724	D59899	Hs.127842	ESTs			29.40		
	109782	AB020644	Hs.14945	long fatty acyl-CoA synthetase 2 gene			8.00		
	109833	R79864	Hs.29889	ESTs	10.00				
20	109837	H00656	Hs.29792	ESTs		6.49			
	109977	T64183	Hs.282982	ESTs					2.75
	109984	AI796320	Hs.10299	ESTs			107.00		
	110146	H41324	Hs.31581	ESTs; Moderately similar to SYNTAXIN 1B					2.22
	110271	H28985	Hs.31330	ESTs				3.48	
25	110280	AW874263	Hs.32468	ESTs	44.20				
	110420	R93141	Hs.184261	ESTs			32.00		
	110578	T62507	Hs.11038	ESTs	28.40				
	110634	R98905	Hs.35592	ESTs			20.00		
	110726	AW961818	Hs.24379	potassium voltage-gated channel; shaker-					4.15
30	110837	H03109	Hs.108920	ESTs; Weakly similar to semaphorin F [H.			56.80		
	110875	N35070	Hs.26401	tumor necrosis factor (ligand) superfamily		3.13			
	110894	R92356	Hs.66881	ESTs; Moderately similar to cytoplasmic	5.33		44.60		
	110971	AI760098	Hs.21411	ESTs					
	111023	AV655386	Hs.7645	ESTs	32.40				
35	111057	T79639	Hs.14629	ESTs			17.14		
	111247	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f				4.58	
	111330	BE247767	Hs.18166	KIAA0870 protein					3.42
	111374	BE250726	Hs.283724	ESTs; Moderately similar to HYA22 [H.sap					3.91
	111442	AW449573	Hs.181003	ESTs			33.20		
40	111737	H04607	Hs.9218	ESTs			53.00		
	111747	AI741471	Hs.23666	ESTs	46.20				
	111807	R33508	Hs.18827	ESTs	16.00				
	111862	R37472	Hs.21559	EST				3.91	
	112045	AI372588	Hs.8022	TU3A protein					2.74
45	112057	R43713	Hs.22945	EST					4.92
	112214	AW148652	Hs.167398	ESTs			13.00		
	112263	R52393	Hs.25917	ESTs		2.43			
	112314	AW206093	Hs.748	ESTs	9.00				
	112324	R55965	Hs.26479	limbic system-associated membrane protein			14.00		
50	112362	AW300887	Hs.26638	ESTs; Weakly similar to CD20 receptor [H					
	112380	H63010	Hs.5740	ESTs		2.49			
	112425	AA324998	Hs.321677	ESTs; Weakly similar to IIII ALU SUBFAMI	8.00				
	112473	R65993	Hs.279798	pregnancy specific beta-1-glycoprotein 9				4.53	
	112492	N51620	Hs.28694	ESTs			29.80		
55	112541	AF038392	Hs.116674	ESTs				3.62	
	112620	R80652	Hs.29040	ESTs		2.37			
	112623	AW373104	Hs.25094	ESTs		2.26			
	112867	T03264	Hs.167393	ESTs			12.00		
	112894	T08188	Hs.3770	ESTs	6.50				
60	112954	AA928953	Hs.6655	ESTs	7.00				
	113029	AW081710	Hs.7369	ESTs; Weakly similar to IIII ALU SUBFAMI					4.39
	113086	AA346839	Hs.209100	DKFZP434C171 protein					4.47
	113140	T50405	Hs.175967	ESTs			10.00		
	113252	NM_004469	Hs.11392	c-fos induced growth factor (vascular en	14.00				
65	113257	AI821378	Hs.159367	ESTs				3.72	
	113394	T81473	Hs.177894	ESTs				3.60	
	113437	T85349	Hs.15923	EST	35.00				
	113454	AI022166	Hs.16188	ESTs	6.00				
	113502	T89130		ESTs	39.60				
70	113552	AI654223	Hs.16026	ESTs					3.88
	113645	T95358	Hs.333181	ESTs				2.58	
	113691	T96935	Hs.17932	EST			38.20		
	113706	AA004693	Hs.269192	ESTs				3.09	
	113863	U89281	Hs.11958	oxidative 3 alpha hydroxysteroid dehydro		2.31			
75	113924	BE178285	Hs.170056	Homo sapiens mRNA; cDNA DKFZp586B0220 (f	30.40				
	114035	W92798	Hs.269181	ESTs			13.00		
	114058	AK002016	Hs.114727	ESTs					5.00
	114084	AA708035	Hs.12248	ESTs			40.60		
	114121	H05785	Hs.25425	ESTs		2.31			
80	114124	W57554	Hs.125019	Human lymphoid nuclear protein (LAF-4)	7.00				
	114275	AW515443	Hs.306117	Interleukin 13 receptor; alpha 1	6.00				
	114297	AA149707	Hs.173091	DKFZP434K151 protein			48.80		
	114427	AA017176	Hs.33532	ESTs; Highly similar to Miz-1 protein [H				3.45	
	114449	AA020736		*ze63b11.s1 Soares retina N2b4HR Homo sa			10.00		
85	114452	AI369275	Hs.243010	ESTs, Moderately similar to RTC0_HUMAN G	14.00				
	114609	AA079505		*zm97a5.s1 Stratagene colon HT29 (#93722				3.13	
	114648	AA101056		*zn25b3.s1 Stratagene neuroepithelium NT			35.40		
	114731	BE094291	Hs.155651	Homo sapiens HNF-3beta mRNA for hepatocy					3.42
	114762	AA146979	Hs.288464	ESTs	33.00				

WO 02/086443

PCT/US02/12476

	114776	AA151719	Hs.95834	ESTs	34.40				
	115009	AA251561	Hs.48689	ESTs	30.20				
	115272	AW015947		ESTs; Weakly similar to hypothetical L1	32.60				
5	115279	AW964897	Hs.290825	ESTs		6.00		12.00	
	115302	AL109719	Hs.47578	ESTs					3.32
	115365	AW976252	Hs.268391	ESTs					
	115559	AL079707	Hs.207443	ESTs				48.00	
	115566	AI142336	Hs.43977	ESTs				56.20	
10	115683	AF255910	Hs.54650	ESTs; Weakly similar to (define not ava	31.40				
	115744	AA418538	Hs.43945	ESTs; Highly similar to dJ1178H5.3 [H.s.a				33.60	
	115819	AA486620	Hs.41135	Endomucin 2				74.40	
	115949	AI478427	Hs.43125	ESTs		3.18			
	115965	AA001732	Hs.173233	ESTs				388.80	
15	116035	AA621405	Hs.184664	ESTs				33.20	
	116049	AA454033	Hs.41644	ESTs				45.80	
	116081	AI190071	Hs.55278	ESTs					3.57
	116082	AB029498	Hs.59729	ESTs		3.06			
	116213	AA292105	Hs.326740	leucine rich repeat (in FLII) Interactin	50.80				
20	116228	AI767947	Hs.50841	ESTs; Weakly similar to tuftelin [M.musc		3.85			
	116250	N76712	Hs.44829	ESTs		6.00			
	116419	AI613480	Hs.47152	ESTs; Weakly similar to testicular tekti				30.00	
	116617	D80761	Hs.45220	EST		2.27			
	116784	AB007979	Hs.301281	tenascin R (restriclin; janusin)	47.20				
25	116835	N39230	Hs.38218	ESTs				41.20	
	116970	AB023179	Hs.9059	KIAA0962 protein				91.00	11.00
	117023	AW070211	Hs.102415	ESTs					
	117027	AW085208	Hs.130093	ESTs	49.40				
	117036	H88908	Hs.41192	EST				32.60	
30	117110	AA160079	Hs.172932	ESTs		8.67			
	117209	W03011	Hs.306881	ESTs				30.60	
	117325	N23599	Hs.43396	ESTs					9.29
	117454	N29569	Hs.44055	ESTs					3.19
	117475	N30205	Hs.93740	ESTs	44.00				
35	117543	BE219453	Hs.42722	ESTs		16.00			
	117567	AW444761	Hs.44565	ESTs				12.00	
	117570	N48649	Hs.44583	ESTs				11.00	
	117600	N34963	Hs.44676	EST					3.74
	117730	N45513	Hs.46608	ESTs		6.00			
40	117791	N48325	Hs.93956	EST		9.00			
	117929	N51075	Hs.47191	ESTs				29.20	
	117990	AA446167	Hs.47385	ESTs		8.00			
	118224	N62275	Hs.48503	EST	31.40				
	118244	N62516	Hs.48556	ESTs	32.80				
45	118357	AL109687	Hs.124154	Homo sapiens mRNA full length insert cDN			2.40		
	118446	N66361	Hs.269121	ESTs			2.28		
	118447	N66399	Hs.49193	EST	30.80				
	118530	N67900	Hs.118446	ESTs					3.10
	118549	N68163	Hs.322954	EST					3.41
50	118823	W03754	Hs.50813	ESTs; Weakly similar to long chain fatty		3.94			
	118862	W17065	Hs.54522	ESTs					3.58
	118935	AI979247	Hs.247043	KIAA0525 protein				33.00	
	118944	AI734233	Hs.226142	ESTs; Weakly similar to !!!! ALU SUBFAM					11.43
	118995	N94591	Hs.323056	ESTs		14.00			
55	119073	BE246360	Hs.279477	ERG-2/ERG-1; V-ets avian erythroblastosi				52.60	
	119268	T16335	Hs.65325	EST	31.40				
	119514	W37937		Accession not listed in Genbank					3.50
	119824	W74536	Hs.184	advanced glycosylation end product-spec		2.75			
	119831	AL117664	Hs.58419	DKFZP586L2024 protein					3.21
60	119861	W78816	Hs.49943	ESTs; Moderately similar to !!!! ALU SUB				33.80	
	119889	W84346	Hs.58671	ESTs				30.03	
	119921	W86192	Hs.58815	ESTs	29.00				
	120082	H80286	Hs.40111	ESTs					3.80
	120094	AA811339	Hs.124049	ESTs		6.00			
65	120132	W57554	Hs.125019	Human lymphoid nuclear protein (LAF-4)				36.60	
	120378	AA223249	Hs.285728	ESTs		12.00			
	120404	AB023230	Hs.96427	KIAA1013 protein	39.40				
	120504	AA256837		ESTs				8.00	
70	120512	N55761	Hs.194718	ESTs	33.00				
	120667	AA287740	Hs.78335	microtubule-associated protein; RP/EB fa					4.18
	120777	AA287702	Hs.10031	KIAA0955 protein				46.60	
	121082	AA398722		ESTs				39.00	
	121191	AA400205	Hs.104447	ESTs	41.60				
	121248	AA400914	Hs.97827	EST					5.08
75	121363	AI287280	Hs.97933	ESTs				12.00	
	121366	AI743515		ESTs				20.00	
	121483	AI660332	Hs.25274	ESTs; Moderately similar to putative sev					3.32
	121518	AA412155		ESTs				30.20	
	121545	AA412442	Hs.98132	ESTs		2.29			
80	121622	AA416931	Hs.126065	ESTs		9.00			
	121665	AA416556	Hs.98234	ESTs				34.80	
	121709	AI338247	Hs.98314	Homo sapiens mRNA; cDNA DKFZp586L0120 (f	34.80				
	121730	AI140683	Hs.98328	ESTs	38.80				
	121740	AA421138	Hs.98334	EST		7.00			
85	121772	AI590770	Hs.110347	Homo sapiens mRNA for alpha integrin bin	36.20				
	121821	AL040235	Hs.3346	ESTs					3.61

WO 02/086443

PCT/US02/12476

	121835	AB033030	Hs.300670	ESTs	2.34				
	121841	AA427794	Hs.104864	ESTs	2.61				
	121885	AA934883	Hs.98467	ESTs				2.25	
	121888	AA426429	Hs.98463	ESTs				2.92	
5	121938	AA428659	Hs.98610	ESTs			46.80		
	121950	AA429515		EST			31.40		
	122030	AA431310	Hs.98724	ESTs	34.40				
	122054	AA431725	Hs.98746	EST					3.58
10	122211	AA300900	Hs.98849	ESTs; Moderately similar to bithoraxoid-	49.40				
	122233	AA436455	Hs.98872	EST	29.80				
	122247	AA436675	Hs.98890	EST			39.80		
	122253	AA436703	Hs.104938	ESTs; Weakly similar to hypothetical pro	9.00				
	122266	AA436840	Hs.98907	EST				3.60	
	122285	AA436981	Hs.121602	EST				3.14	
15	122409	AA446830	Hs.99081	ESTs	30.80				
	122485	AA524547	Hs.160318	phospholemman		2.65			
	122697	AA420683	Hs.98321	Homo sapiens cDNA FLJ14103 fis, clone MA	15.00				
	122772	AW117452	Hs.99489	ESTs	6.67				
	122831	AI857570	Hs.5120	ESTs				3.37	
20	122913	AI638774	Hs.105328	ESTs			32.20		
	123049	BE047680	Hs.211869	ESTs			41.80		
	123076	AI345569	Hs.190046	ESTs	35.80				
	123136	AW451999	Hs.194024	ESTs					2.58
	123309	N52937	Hs.102679	ESTs			19.00		
25	123455	AA353113	Hs.112497	ESTs			82.80		
	123691	AA609579	Hs.112724	ESTs				3.95	
	123756	AA609971	Hs.112795	EST	35.40				
	123802	AA620448		Homo sapiens clone 24760 mRNA sequence	58.00				
30	123837	AI807243	Hs.112893	ESTs			32.40		
	123844	AA938905	Hs.120017	olfactory receptor; family 7; subfamily	2.63				
	123936	NM_004673	Hs.241519	ESTs	29.00				
	123987	C21171	Hs.95497	ESTs; Weakly similar to GLUCOSE TRANSPOR			70.60		
	124013	AI521936	Hs.107149	ESTs; Weakly similar to PTB-ASSOCIATED S	28.40				
35	124160	R40290	Hs.124685	ESTs			13.00		
	124205	H77570	Hs.108135	ESTs				4.74	
	124226	AA618527	Hs.190266	ESTs		2.35			
	124246	H67680	Hs.270962	ESTs			29.40		
	124348	AI796320	Hs.10299	ESTs	17.00				
40	124358	AW070211	Hs.102415	*yw35g11.s1 Morton Fetal Cochlea Homo sa		3.07			
	124409	AI814166	Hs.107197	ESTs				3.14	
	124442	AW663632	Hs.285625	TATA box binding protein (TBP)-associate	2.48				
	124468	N51413	Hs.109284	ESTs			30.80		
	124479	AB011130	Hs.127436	calcium channel; voltage-dependent; alph					6.03
45	124519	AI870056	Hs.137274	ESTs; Weakly similar to SPLICEOSOME ASSO	2.50				
	124711	NM_004657	Hs.26530	serum deprivation response (phosphatidyl	59.20				
	124866	AI768289	Hs.304389	ESTs	8.00				
	124874	BE550182	Hs.127826	ESTs			37.60		
	125097	AW576389	Hs.335774	ESTs			10.00		
50	125179	AW206468	Hs.103118	ESTs				3.12	
	125200	AW836591	Hs.103156	ESTs					2.79
	125299	T32982	Hs.102720	ESTs			34.20		
	125400	AL110151	Hs.128797	DKFZP586D0824 protein	29.00				
	125810	H00083		aryl hydrocarbon receptor-interacting pr	32.20				
55	126176	BE242256	Hs.2441	KIAA0022 gene product	12.00				
	126303	D78841		HUM525A05B Human placenta polyA+ (TFu)			33.60		
	126403	AW629054	Hs.125976	ESTs; Weakly similar to metalloprotease/	35.80				
	126507	AL040137	Hs.23964	ESTs; Weakly similar to HC1 ORF [M.muscu			29.80		
	126773	AA648284	Hs.187584	ESTs	39.60				
60	127307	AW962712	Hs.126712	ESTs; Weakly similar to pIL2 hypothetica	28.80				
	127462	AA760776	Hs.293977	aa59b04.s1 NCLCGAP_GCB1 Homo sapiens c			34.40		
	127486	AW002846	Hs.105468	ESTs	9.00				
	127572	AA594027	Hs.191788	ESTs	2.36				
	127609	X80031	Hs.530	ESTs			29.40		
65	127832	AW976035	Hs.292396	ESTs			37.20		
	127898	AA774725	Hs.128970	ESTs				4.42	
	128073	AW340720	Hs.125983	ESTs			38.40		
	128101	AA905730	Hs.128254	ESTs	7.33				
	128149	NM_012214	Hs.177576	mannosyl (alpha-1,3)-glycoprotein beta-					2.58
70	128212	W27411	Hs.336920	glutathione peroxidase 3 (plasma)	3.09				
	128333	W68800	Hs.12125	ESTs; Weakly similar to LR8 [H.sapiens]			34.40		
	128364	N76462	Hs.269152	ESTs; Weakly similar to ZINC FINGER PROT	10.00				
	128426	AI265784	Hs.145197	ESTs				4.31	
	128598	AA305407	Hs.102308	potassium inwardly-rectifying channel; s	31.20				
75	128634	AA464918		ESTs; Moderately similar to IIII ALU SUB			41.60		
	128687	AW271273	Hs.23767	ESTs			87.00		
	128726	AI311238	Hs.104476	ESTs					4.02
	128773	NM_004131	Hs.1051	granzyme B (granzyme 2; cytotoxic T-lymp			9.00		
	128833	W26667	Hs.184581	ESTs					3.76
80	128870	H39537	Hs.75309	eukaryotic translation elongation factor	2.66				
	128878	R25513	Hs.10583	ESTs				3.10	
	128885	AF134803	Hs.180141	cofilin 2 (muscle)			11.00		
	128998	W04245	Hs.107761	ESTs; Weakly similar to PUTATIVE RHO/RAC				3.21	
	129000	AA744902	Hs.107767	ESTs; Moderately similar to CaM-KII inh					3.68
	129038	AW156903	Hs.108124	ribosomal protein L41				3.17	
85	129098	AW580945	Hs.330466	ESTs	34.60				

	129210	AL039940	Hs.202949	KIAA1102 protein					4.09
	129240	AA361258	Hs.237868	interleukin 7 receptor	2.29				
	129262	BE222198	Hs.109843	ESTs			3.30		
5	129301	AF182277	Hs.330780	Human cytochrome P450-11B (h11B3) mRNA;					4.05
	129331	AW167668	Hs.279772	ESTs; Highly similar to CGI-38 protein [4.09
	129381	AW245805	Hs.110903	claudin 5 (transmembrane protein deleted	2.93				
	129565	X77777	Hs.198726	vasoactive intestinal peptide receptor 1		160.80			
	129595	U09550	Hs.1154	oviductal glycoprotein 1; 120kD			10.00		
10	129613	AW978517	Hs.172847	ESTs; Weakly similar to collagen alpha 1				3.40	
	129782	AW016932	Hs.104105	EST	9.00				
	129950	F07783	Hs.1369	decay accelerating factor for complement					
	129958	R27496	Hs.1378	annexin A3		87.80			
	129959	AL036554	Hs.274463	defensin; alpha 1; myeloid-related seque		44.60			
15	130160	AA305688	Hs.267695	UDP-Gal:betaGlcNAc beta 1;3-galactosyltr	2.72				
	130259	NM_000328	Hs.153614	retinitis pigmentosa GTPase regulator	2.54				
	130273	AW972422	Hs.153863	MAD (mothers against decapentaplegic; Dr		51.60			
	130312	AF056195	Hs.15430	DKFZP586G1219 protein				3.16	
	130436	NM_001928	Hs.155597	D component of complement (adipsin)					4.11
20	130523	AA999702	Hs.214507	ESTs				4.77	
	130799	AB028945	Hs.12696	ESTs	6.00				
	130865	NM_005883	Hs.20912	adenomatous polyposis coli like				3.54	
	131002	AL050295	Hs.22039	KIAA0768 protein					3.50
	131012	AL039940	Hs.202949	KIAA1102 protein	20.00				
25	131031	NM_001650	Hs.288650	aquaporin 4	41.20				
	131061	N64328	Hs.268744	ESTs; Moderately similar to KIAA0273 [H.		31.40			
	131066	AW169287	Hs.22588	ESTs		29.60			
	131082	AI091121	Hs.246218	ESTs; Weakly similar to zinc finger prot			9.00		
	131087	AF147709	Hs.22824	ESTs; Weakly similar to p160 myb-binding					3.86
30	131161	AF033382	Hs.23735	potassium voltage-gated channel; subfami				3.14	
	131179	AA171388	Hs.184482	DKFZP586D0624 protein				3.80	
	131182	AI824144	Hs.23912	ESTs					3.67
	131205	NM_003102	Hs.2420	superoxide dismutase 3; extracellular	2.98				
	131277	AA131466	Hs.23767	ESTs	3.15				
35	131281	AA251716	Hs.25227	ESTs		32.20			
	131282	X03350	Hs.4	alcohol dehydrogenase 3 (class I); gamma					3.44
	131285	AI567943	Hs.25274	ESTs; Moderately similar to putative sev				6.40	
	131355	R52804	Hs.25956	DKFZP564D206 protein	8.00				
	131391	AW085781	Hs.26270	ESTs	10.00				
40	131461	AA992841	Hs.27263	butyrate response factor 2 (EGF-response	28.80				
	131487	F13036	Hs.27373	Homo sapiens mRNA; cDNA DKFZP564O1763 (f					4.03
	131517	AB037789	Hs.263395	ESTs; Highly similar to semaphorin 11a [39.00				
	131545	AL137432	Hs.28564	ESTs			11.00		
	131583	AK000383	Hs.323092	ESTs; Weakly similar to dual specificity			10.00		
45	131647	AA359615	Hs.30089	ESTs	2.47				
	131675	HI5205	Hs.30509	ESTs				3.06	
	131676	AI126821	Hs.30514	ESTs					
	131708	S60415	Hs.30941	calcium channel; voltage-dependent; beta	45.80				
	131717	X94630	Hs.3107	CD97 antigen	2.28				3.78
50	131756	AA443966	Hs.31595	ESTs		40.60			
	131762	AA744902	Hs.107767	ESTs; Moderately similar to CaM-KII inh1					3.67
	131821	AA017247	Hs.164577	ESTs	2.87				
	131839	AB014533	Hs.33010	KIAA0633 protein					3.48
	131861	AL095858	Hs.184245	KIAA0929 protein Mx2 interacting nuclea	54.00				
55	132015	AI418006	Hs.3731	ESTs		49.20			
	132070	BE622641	Hs.38489	ESTs		34.80			
	132242	AA332697	Hs.42721	ESTs	2.68				
	132334	AW080704	Hs.45033	lacrimal proline rich protein	4.66				
	132476	AL119844	Hs.49476	Homo sapiens clone TUA8 Cri-du-chat regi	34.20				
60	132490	NM_001290	Hs.4980	LIM binding domain 2					
	132533	AI922988	Hs.172510	ESTs	13.00				
	132598	X80031	Hs.530	collagen; type IV; alpha 3 (Goodpasture		30.60			
	132619	H28855	Hs.53447	ESTs; Moderately similar to kinesin IIg				4.02	
	132652	N41739	Hs.61260	ESTs				3.18	
65	132726	N52298	Hs.55608	ESTs; Weakly similar to cDNA EST yk484g1			11.43		
	133028	R51604	Hs.300842	ESTs	2.37				
	133071	BE384932	Hs.64313	ESTs	2.27				
	133120	NM_003278	Hs.65424	tetranectin (plasminogen-binding protein	2.63				
	133129	AA428580	Hs.65551	ESTs					5.49
70	133147	AA026533	Hs.66	Interleukin 1 receptor-like 1	6.20				
	133151	NM_014051	Hs.94896	ESTs				3.69	
	133213	AA903424	Hs.6786	ESTs		31.40			
	133276	AW978439	Hs.69504	ESTs			9.00		
	133377	AJ131245	Hs.7239	SEC24 (S. cerevisiae) related gene famil	41.20				
75	133407	AF017987	Hs.7306	secreted frizzled-related protein 1	50.20				
	133535	AL134030	Hs.284180	protocadherin 2 (cadherin-like 2)				3.72	
	133537	U41518	Hs.74602	aquaporin 1 (channel-forming integral pr					3.35
	133656	BE149455	Hs.75415	Accession not listed in Genbank	2.65				
	133689	NM_001872	Hs.75572	carboxypeptidase B2 (plasma)		90.80			
80	133779	T58486	Hs.222566	ESTs				3.05	
	133978	AF035718	Hs.78051	transcription factor 21	2.92				
	133985	L34657	Hs.78146	platelet/endothelial cell adhesion molec					3.45
	134000	AW175787	Hs.334841	selenium binding protein 1					4.05
	134111	AI372588	Hs.8022	TU3A protein	4.49				
85	134185	AA285136	Hs.301914	Homo sapiens mRNA; cDNA DKFZP586K1220 (f					3.27
	134204	AI873257	Hs.7994	ESTs; Weakly similar to CGI-69 protein {		40.80			

PCT/US02/12476

25 TABLE 2B shows the accession numbers for those primekeys lacking unigenal D's for Table 2A. For each probe set we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

30

101

Table 3A shows 452 genes up-regulated in chronically diseased lung relative to normal lung. Chronically diseased lung samples represent chronic non-malignant lung diseases such as fibrosis, emphysema, and bronchitis. These genes were selected from 59680 probesets on the Eos/Affymatrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

5	Pkey:	Unique Eos probeset identifier number				
	ExAccn:	Exemplar Accession number, Genbank accession number				
	UnigeneID:	Unigene number				
	Unigene Title:	Unigene gene title				
10	R1:	80th percentile of AI for chronically diseased lung samples divided by the 90th percentile of AI for normal lung samples.				
	R2:	80th percentile of AI for chronically diseased lung samples divided by the 90th percentile of normal lung samples, squamous cell carcinomas and adenocarcinomas				
15	R3:	70th percentile of AI for chronically diseased lung samples minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples divided by the 90th percentile of normal lung samples, squamous cell carcinomas and adenocarcinomas minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples				
	Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2
20	135423	U50531	Hs.138751	Human BRCA2 region, mRNA sequence CG030	12.40	
	135378	AW961818	Hs.24379	MUM2 protein		2.13
	135348	NM_000928	Hs.992	phospholipase A2, group IB (pancreas)		
	135235	AW298244	Hs.293507	ESTs	12.40	
	135057	U90268	Hs.93810	cerebral cavernous malformations 1	11.67	
25	134951	BE305081	Hs.169358	hypothetical protein		8.00
	134799	M36821	Hs.89690	GRO3 oncogene		8.20
	134786	T29618	Hs.89640	TEK tyrosine kinase, endothelial (venous		
	134772	NM_000829	Hs.163697	glutamate receptor, ionotropic, AMPA 4	29.80	
	134752	BE246762	Hs.89499	arachidonate 5-lipoxygenase		1.93
	134749	T28499	Hs.89485	carbonic anhydrase IV		2.07
30	134698	BE326276	Hs.8861	ESTs		
	134636	NM_005582	Hs.87205	lymphocyte antigen 64 (mouse) homolog, r	13.60	
	134627	AI018768	Hs.12482	glyceronephosphate O-acyltransferase		1.92
	134622	AW975159	Hs.293097	ESTs, Weakly similar to A55380 faciojeni		1.92
	134570	U66615	Hs.172280	SWI/SNF related, matrix associated, acti	13.20	
35	134561	U76421	Hs.85302	adenosine deaminase, RNA-specific, B1 (h		1.78
	134468	NM_001772	Hs.83731	CD33 antigen (gp67)		
	134417	NM_006416	Hs.82921	solute carrier family 35 (CMP-sialic aci		6.20
	134343	D50683	Hs.82028	transforming growth factor, beta recepto		
40	134323	BE170651	Hs.8700	deleted in liver cancer 1		
	134300	NM_001430	Hs.8136	endothelial PAS domain protein 1		
	134299	AW580939	Hs.97199	complement component C1q receptor		
	134253	X52075	Hs.80738	sialophorin (gpL115, leukosialin, CD43)	20.60	
	134182	D52059	Hs.7972	KIAA0871 protein	12.20	
45	133985	L34657	Hs.78146	platelet/endothelial cell adhesion molec		
	133978	AF035718	Hs.78061	transcription factor 21		
	133835	AI677897	Hs.76640	RGC32 protein		
	133651	AI301740	Hs.173381	dihydropyrimidinase-like 2	15.20	
	133633	D21262	Hs.75337	nucleolar and colled-body phosphoprotein		
50	133565	AW955776	Hs.313500	ESTs, Moderately similar to ALU7_HUMAN A		
	133548	AW946384	Hs.178112	DNA segment, single copy probe LNS-CAIL		1.77
	133488	AA335295	Hs.74120	adipose specific 2		
	133478	X83703	Hs.31432	cardiac ankyrin repeat protein		2.08
	133337	AF085983	Hs.293676	ESTs		9.60
	133200	AB037715	Hs.183639	hypothetical protein FLJ10210		1.77
55	133153	AF070592	Hs.66170	HSKM-B protein	30.60	
	133130	AI128606	Hs.6557	zinc finger protein 161	22.60	
	133120	NM_003278	Hs.65424	tetranectin (plasminogen-binding protein		
	132928	AW168082	Hs.169449	protein kinase C, alpha	13.80	
60	132836	AB023177	Hs.29900	KIAA0960 protein		
	132799	W73311	Hs.169407	SAC2 (suppressor of actin mutations 2,	41.60	
	132742	AA025480	Hs.292812	ESTs, Weakly similar to T33468 hypotheti	40.40	
	132548	X12830	Hs.193400	interleukin 6 receptor		7.20
	132476	AL119844	Hs.49476	Homo sapiens clone TUA8 Cri-du-chat regi		4.76
	132439	AK001942	Hs.4863	hypothetical protein DKFZp566A1524		1.88
65	132240	AB018324	Hs.42676	KIAA0781 protein	21.20	
	132210	NM_007203	Hs.42322	A kinase (PRKA) anchor protein 2		1.99
	132199	AL041299	Hs.165084	ESTs	15.20	
	131751	T96555	Hs.31562	ESTs		1.76
70	131745	AI828559	Hs.31447	ESTs, Moderately similar to A46010 X-li	27.80	
	131694	NM_000246	Hs.3076	MHC class II transactivator		4.00
	131686	NM_012296	Hs.30687	GRB2-associated binding protein 2		
	131676	AI126821	Hs.30514	ESTs		6.20
	131629	Z45794	Hs.238809	ESTs	21.40	
75	131589	C18825	Hs.29191	epithelial membrane protein 2		
	131536	AA019201	Hs.269210	ESTs		9.40
	131517	AB037789	Hs.263395	sema domain, transmembrane domain (TM),		3.59
	131355	R52804	Hs.25956	DKFZP564D206 protein		4.48
	131253	R71802	Hs.24853	ESTs	15.00	
80	131207	AF104266	Hs.24212	latrophilin		1.75
	131156	AI472209	Hs.323117	ESTs		1.84
	131066	AW169287	Hs.22588	ESTs		
	131061	N64328	Hs.268744	KIAA1796 protein		
	131053	AA348541	Hs.296261	guanine nucleotide binding protein (G pr		1.93
85	130895	AA641767	Hs.21015	hypothetical protein DKFZp564L0864 simil	16.60	
	130762	D84371	Hs.1898	paraoxonase 1	12.00	

	130657	AW337575	Hs.201591	ESTs		
	130655	AI831962	Hs.17409	cysteine-rich protein 1 (intestinal)		2.08
	130589	AL110226	Hs.16441	DKFZP434H204 protein		1.91
5	130562	D50402	Hs.182611	solute carrier family 11 (proton-coupled)		
	130555	R69743	Hs.116774	Integrin, alpha 1	9.60	
	130365	W56119	Hs.155103	eukaryotic translation initiation factor	11.60	
	130273	AW972422	Hs.153863	MAD (mothers against decapentaplegic, Dr	6.60	
	130259	NM_000328	Hs.153614	retinitis pigmentosa GTPase regulator		1.91
10	130090	H97878	Hs.132390	zinc finger protein 36 (KOX 18)	21.20	
	129958	R27496	Hs.1378	annexin A3	5.05	
	129898	AI672731	Hs.13256	ESTs		
	129875	AA181018	Hs.13056	hypothetical protein FLJ13920	18.60	
	129699	AB007899	Hs.12017	homolog of yeast ubiquitin-protein ligas		
15	129626	F13272	Hs.111334	fertilin, light polypeptide		
	129598	N30436	Hs.11556	Homo sapiens cDNA FLJ12566 fis, clone NT	22.63	
	129593	AI338247	Hs.98314	Homo sapiens mRNA; cDNA DKFZp586L0120 (f		2.53
	129565	X77777	Hs.198726	vasoactive intestinal peptide receptor 1		
	129527	AA769221	Hs.270847	delta-tubulin	39.20	
20	129402	W72062	Hs.11112	ESTs		2.11
	129385	AA172106	Hs.110950	Rag C protein	15.20	
	129315	NM_014563	Hs.174038	spondyloepiphyseal dysplasia, late	12.40	
	129312	T97579	Hs.110334	ESTs, Weakly similar to I78885 serine/th	20.83	
	129240	AA361258	Hs.237868	interleukin 7 receptor		1.95
	129210	AL039940	Hs.202949	KIAA1102 protein		
25	129122	AW958473	Hs.301957	nudix (nucleoside diphosphate linked moi	4.20	
	129057	N90866	Hs.276770	CDW52 antigen (CAMPATH-1 antigen)		
	128946	Y13153	Hs.107318	kynurenine 3-monooxygenase (kynurenine 3	5.20	
	128798	AF015525	Hs.302043	chemokine (C-C motif) receptor-like 2		
30	128789	AW368576	Hs.139851	caveolin 2		2.24
	128778	AA504776	Hs.186709	ESTs, Weakly similar to I38022 hypothet	12.20	
	128766	AW160432	Hs.296460	craniofacial development protein 1	26.40	
	128631	R44238	Hs.155546	KIAA1080 protein; Golgi-associated, gamm		1.78
	128624	BE154765	Hs.102647	ESTs, Weakly similar to TRHY_HUMAN TRICH		2.51
	128609	NM_003616	Hs.102456	survival of motor neuron protein interac	16.00	
35	128603	NM_004915	Hs.10237	ATP-binding cassette, sub-family G (WHIT	12.80	
	128598	AA305407	Hs.102308	potassium inwardly-rectifying channel, s		4.00
	128458	H55864	Hs.56340	ESTs		
	128061	AF150882	Hs.186877	sodium channel, voltage-gated, type XII,	17.20	
40	127968	AA830201	Hs.124347	ESTs	21.30	
	127959	AI302471	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L		
	127944	AI557081	Hs.262476	S-adenosylmethionine decarboxylase 1	10.60	
	127925	AA805151	Hs.3628	mitogen-activated protein kinase kinase	13.40	
	127896	AI689586	Hs.222194	ESTs		7.00
45	127859	AA761802	Hs.291559	ESTs	14.00	
	127817	AA836641	Hs.163085	ESTs	14.00	
	127742	AW293496	Hs.180138	ESTs	11.00	
	127628	AI240102	Hs.322430	NDRG family, member 4	11.10	
	127609	X80031	Hs.530	collagen, type IV, alpha 3 (Goodpasture		
50	127582	AA908954	Hs.130844	ESTs	19.60	
	127543	AK000787	Hs.157392	Homo sapiens cDNA FLJ20780 fis, clone CO	15.40	
	127535	AA568424	Hs.164450	ESTs	17.50	
	127404	AI379920	Hs.270224	ESTs	14.60	
	127396	L31968	Hs.187991	DKFZP564A122 protein	15.40	
55	127374	AA442797	Hs.312110	ESTs, Weakly similar to I38022 hypothet	14.60	
	127346	AA203616	Hs.44896	DnaJ (Hsp40) homolog, subfamily B, membe	21.00	
	127340	BE047653	Hs.119183	ESTs, Weakly similar to ZN91_HUMAN ZINC	15.80	
	127307	AW962712	Hs.126712	ESTs, Weakly similar to AF191020 1 E2IG5		
	127242	AW390395	Hs.181301	cathepsin S	22.60	
60	127167	AA625690	Hs.190272	ESTs	21.40	
	127046	AA321948	Hs.293968	ESTs	41.20	
	126928	AA480902	Hs.137401	ESTs	11.00	
	126900	AF137386	Hs.12701	plasmolipin		1.78
	126852	AA399961		gb:zu68c01.r1 Soares_testis_NHT Homo sap	5.60	
65	126816	AA248234		gb:csq2228.seq.F Human fetal heart, Lamb	12.20	
	126812	AB037860	Hs.173933	nuclear factor I/A	17.19	
	126666	AA648886	Hs.151999	ESTs	13.57	
	126645	AA316181	Hs.81635	six transmembrane epithelial antigen of	15.40	
	126592	AI611153	Hs.6093	Homo sapiens cDNA: FLJ22783 fis, clone K		4.67
70	126556	AF255303	Hs.112227	membrane-associated nucleic acid binding	18.00	
	126433	AA325606		gb:EST28707 Cerebellum II Homo sapiens c	16.77	
	126299	AW979155	Hs.298275	amino acid transporter 2	14.60	
	126218	AL049801	Hs.13849	Novel human gene mapping to chromosome 13		3.50
	126182	AA721331	Hs.293771	ESTs	13.40	
75	126177	AW752782	Hs.129750	hypothetical protein FLJ10546	18.20	
	126142	H86261	Hs.40558	ESTs	14.00	
	126077	M78772	Hs.210836	ESTs	16.59	
	125994	AI990529	Hs.270799	ESTs	17.40	
	125934	AA193325	Hs.32646	hypothetical protein FLJ21901	13.00	
80	125847	AW161885	Hs.249034	ESTs	49.57	
	125831	H04043		gb:yl45c03.r1 Soares_placenta Nb2HP Homo		
	125731	R61771	Hs.26912	ESTs	13.20	
	125676	BE612918	Hs.151973	hypothetical protein FLJ23511	11.20	
	125561	F18572	Hs.22978	ESTs, Weakly similar to ALU4_HUMAN ALU S		
85	125552	H09701	Hs.278366	ESTs, Weakly similar to I38022 hypotheti	12.60	
	125489	H49193	Hs.124984	ESTs, Moderately similar to ALU7_HUMAN A	33.40	

	125422	AA903229	Hs.153717	ESTs		1.80
	125331	AI422996	Hs.161378	ESTs	38.00	
	125309	T12411	Hs.183745	hypothetical protein FLJ13456	18.20	
5	125167	AL137540	Hs.102541	netrin 4		1.95
	125139	AW194933	Hs.9788	hypothetical protein MGC10924 similar to		1.84
	125042	T78906	Hs.269432	ESTs, Moderately similar to ALU1_HUMAN	21.80	
	124711	NM_004657	Hs.26530	serum deprivation response (phosphatidyl)	10.60	
	124631	NM_014053	Hs.270594	FLVCR protein	23.20	
	124578	N68321	Hs.231500	EST	21.43	
10	124574	AL036596	Hs.42322	A kinase (PRKA) anchor protein 2		1.77
	124472	N52517	Hs.102670	EST	37.20	
	124438	BE178536	Hs.11090	membrane-spanning 4-domains, subfamily A		
	124357	N22401		gb:yyw37g07.s1 Morton Fetal Cochlea Homo	14.64	
15	124306	AW973078	Hs.293039	ESTs		4.00
	124214	H58608	Hs.151323	ESTs		
	124097	AW298235	Hs.101689	ESTs	27.20	
	123978	T89832	Hs.170278	ESTs		2.03
	123972	T46848	Hs.70337	immunoglobulin superfamily, member 4	6.00	
	123961	AL050184	Hs.21610	DKFZP434B203 protein		1.79
20	123936	NM_004673	Hs.241519	angiotensin-like 1	15.80	
	123802	AA620448		gb:ae58c09.s1 Stratagene lung carcinoma	4.23	
	123734	AA609861	Hs.312447	ESTs	4.20	
	123619	AA602964		gb:nc97c02.s1 NCI_CGAP_Pr2 Homo sapiens	33.60	
25	123596	AA421130	Hs.112640	EST	10.93	
	123476	AA384564	Hs.108829	ESTs		2.18
	123340	AA504264	Hs.182937	peptidylprolyl isomerase A (cyclophilin	11.20	
	123190	AA489212	Hs.105228	EST	14.20	
	123136	AW451999	Hs.194024	ESTs		7.00
	123073	AA485061	Hs.105652	ESTs	31.20	
30	123055	AA482005	Hs.105102	ESTs, Weakly similar to reverse transcri		4.80
	122699	AA456130	Hs.301721	KIAA1255 protein		5.00
	122679	AA811286	Hs.192837	ESTs, Weakly similar to ALU5_HUMAN ALU S	14.40	
	122633	NM_001546	Hs.34853	inhibitor of DNA binding 4, dominant neg		
35	122553	AA451884	Hs.190121	ESTs	40.00	
	122544	AW973253	Hs.292689	ESTs	15.40	
	122485	AA524547	Hs.160318	FXRD domain-containing ion transport reg		1.81
	122211	AA300900	Hs.98849	ESTs, Moderately similar to AF161511 1 H	12.10	
	122127	AW207175	Hs.106771	ESTs		1.95
40	122011	AA431082		gb:zw78a10.s1 Soares_testis_NHT Homo sap		1.89
	121992	AI860775	Hs.98506	ESTs	3.60	
	121989	W58487	Hs.193784	Homo sapiens mRNA; cDNA DKFZp586K1922 (f		2.01
	121835	AB033030	Hs.300670	KIAA1204 protein		1.85
	121726	AF241254	Hs.178098	angiotensin I converting enzyme (peptidyl	12.43	
45	121690	AV660305	Hs.110286	ESTs		1.82
	121643	AA640987	Hs.193787	ESTs		
	121633	AA417011	Hs.98175	EST	14.00	
	121622	AA416931	Hs.126065	ESTs		16.40
	121497	AA412031	Hs.97901	EST	11.20	
50	121351	AW206227	Hs.287727	hypothetical protein FLJ23132	12.20	
	121314	W07343	Hs.182538	phospholipid scramblase 4		1.83
	121242	AA400857	Hs.97509	ESTs	22.40	
	121059	AA393283		gb:z174e03.r1 Soares_testis_NHT Homo sap	14.80	
	120934	AA226198		gb:nc26a07.s1 NCI_CGAP_Pr1 Homo sapiens	21.20	
55	120755	AA312934	Hs.190745	Homo sapiens cDNA: FLJ21326 fis, clone		1.79
	120637	AA811804		gb:ob39a05.s1 NCI_CGAP_GCB1 Homo sapiens	20.00	
	120484	AA253170	Hs.96473	EST	40.20	
	120336	N85785	Hs.181165	eukaryotic translation elongation factor		6.60
	120266	AI807264	Hs.205442	ESTs, Weakly similar to T34036 hypotheti	16.80	
60	120132	W57554	Hs.125019	ESTs		4.73
	120041	AA830882	Hs.59368	ESTs		1.75
	119996	W88996	Hs.59134	EST	7.20	
	119970	AA767718	Hs.93581	hypothetical protein FLJ10512	11.20	
	119861	W78816	Hs.49943	ESTs, Weakly similar to S65657 alpha-1C-		3.78
65	119824	W74536	Hs.184	advanced glycosylation end product-speci		
	119740	AW021407	Hs.21068	hypothetical protein	20.20	
	119271	AI081118	Hs.65328	Fanconi anemia, complementation group F	15.20	
	119221	C14322	Hs.250700	trypsin beta 1		
	119126	R45175	Hs.117183	ESTs	12.80	
70	119073	BE245360	Hs.279477	ESTs		
	118928	AA312799	Hs.283689	activator of CREM in testis		10.00
	118901	AW292577	Hs.94445	ESTs		3.96
	118661	AL137554	Hs.49927	protein kinase NYD-SP15	9.60	
	118607	AI377444	Hs.54245	ESTs, Weakly similar to S65824 reverse t	10.40	
75	118449	AI813865	Hs.164478	hypothetical protein FLJ21939 similar to		1.90
	118416	N66028	Hs.49105	FKBP-associated protein	16.20	
	118379	N64491	Hs.48990	ESTs		4.00
	118329	N63520		gb:yy62f01.s1 Soares_multiple_sclerosis_	6.60	
	118320	N63451	Hs.141600	ESTs, Weakly similar to alternatively s	3.80	
80	118253	AA497044	Hs.20887	hypothetical protein FLJ10392	17.60	
	118124	N66968	Hs.46707	chromosome 21 open reading frame 37	14.00	
	118056	AB037746	Hs.42768	hypothetical protein DKFZp76100113		1.86
	118032	N52802	Hs.47544	EST	5.00	
	117840	T26379	Hs.48802	Homo sapiens clone 23632 mRNA sequence	4.00	
85	117404	N39725	Hs.15220	zinc finger protein 106		1.90
	117314	N32498	Hs.42829	ESTs	14.20	

	117209	W03011	Hs.306881	MSTP043 protein			
	117023	AW070211	Hs.102415	Homo sapiens mRNA; cDNA DKFZp586N0121 (f		2.31	
	116814	H50834		gb:yp86a10.s1 Soares fetal liver spleen	20.20		
5	116784	AB007979	Hs.301281	Homo sapiens mRNA, chromosome 1 specific		3.51	
	116766	AI808657	Hs.95097	ESTs	16.20		
	116712	AW901618	Hs.61935	Homo sapiens mRNA; cDNA DKFZp7611071 (fr		6.80	
	116707	H10344	Hs.49050	ESTs, Weakly similar to A Chain A, Human	18.60		
	116351	AL133623	Hs.82501	similar to mouse Xrn1 / Dhm2 protein	19.40		
10	116279	AW971248	Hs.291289	ESTs, Weakly similar to ALU1_HUMAN ALU S			
	116166	AL039940	Hs.202949	KIAA1102 protein		2.13	
	116152	AL040521	Hs.15220	zinc finger protein 106		1.75	
	116117	BE613410	Hs.31575	SEC63, endoplasmic reticulum translocon	13.20		
	116107	AL133916	Hs.172572	hypothetical protein FLJ20093	30.11		
15	115965	AA001732	Hs.173233	hypothetical protein FLJ10970		2.36	
	115955	AF263613	Hs.44198	Intracellular membrane-associated calciu	18.20		
	115844	AI373062	Hs.332938	hypothetical protein MGC5370	18.57		
	115683	AF255910	Hs.54650	junctional adhesion molecule 2		23.00	
	115673	AA406341	Hs.269908	Homo sapiens cDNA FLJ11991 fls, clone HE	11.82		
20	115672	AI889110	Hs.73251	ESTs	10.60		
	115566	AI142336	Hs.43977	Human DNA sequence from clone RP11-196N1		1.76	
	115313	AA808001	Hs.184411	albumin	25.20		
	115279	AW984897	Hs.290825	ESTs		8.00	
	115230	AA278300	Hs.124292	Homo sapiens cDNA: FLJ23123 fls, clone L		1.80	
25	115110	AK001671	Hs.11387	KIAA1453 protein	14.20		
	114999	BE246481	Hs.87856	ESTs	19.20		
	114930	AA237022	Hs.188717	ESTs		5.60	
	114922	AA235672	Hs.87491	ESTs		3.60	
	114837	BE244930	Hs.166895	ESTs	43.70		
30	114769	AA149060	Hs.296100	ESTs	11.00		
	114761	AA143781	Hs.128280	hypothetical protein FLJ23393	14.00		
	114736	AI610347	Hs.103812	ESTs, Moderately similar to ALU1_HUMAN A		4.20	
	114596	AA310162	Hs.169248	cytochrome c	10.71		
	114518	AW163267	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like	20.40		
35	114455	H37908	Hs.271616	ESTs, Weakly similar to ALU8_HUMAN ALU S	20.40		
	114452	AI369275	Hs.243010	Homo sapiens cDNA FLJ14445 fls, clone HE		17.20	
	114359	NM_016929	Hs.283021	chloride intracellular channel 5		2.09	
	114357	R41677	Hs.6107	Homo sapiens cDNA FLJ14839 fls, clone OV	12.40		
	114251	H15261	Hs.21948	ESTs		2.00	
40	114138	AW384793	Hs.15740	Homo sapiens mRNA; cDNA DKFZp434E033 (fr		11.40	
	114124	W57554	Hs.125019	ESTs		6.04	
	113946	AW083883	Hs.37896	Homo sapiens cDNA FLJ13510 fls, clone PL		1.82	
	113695	T96965	Hs.17948	ESTs, Weakly similar to ALUB_HUMAN IIII			
	113606	NM_013343	Hs.278951	NAG-7 protein		2.15	
45	113590	R49642	Hs.142447	ESTs, Weakly similar to ALU1_HUMAN ALU S		3.60	
	113560	T91015	Hs.268626	ESTs	32.00		
	113552	AI654223	Hs.16026	hypothetical protein FLJ23191			
	113540	AW152618	Hs.16757	ESTs			
	113502	T89130		gb:ye12d01.s1 Stratagene lung (937210) H		8.35	
50	113288	AI076838	Hs.12967	ESTs	12.40		
	113252	NM_004469	Hs.11392	c-fos induced growth factor (vascular en		4.27	
	113238	R45467	Hs.189813	ESTs			
	113203	AA743563	Hs.10305	ESTs	21.20		
	113195	H83265	Hs.8881	ESTs, Weakly similar to S41044 chromosom		1.92	
55	113089	T40707	Hs.270862	ESTs	14.33		
	113076	AF033199	Hs.8198	zinc finger protein 204		6.00	
	113009	T23699	Hs.7246	ESTs		9.40	
	112937	AI694320	Hs.6295	ESTs, Weakly similar to T17248 hypotheti		12.20	
	112691	T03927	Hs.293147	ESTs, Moderately similar to A46010 X-li	10.57		
60	112794	R97018		gb:yy74b08.s1 Soares fetal liver spleen	26.60		
	112691	R88708	Hs.220647	ESTs	15.33		
	112602	AW004045	Hs.203365	ESTs	15.60		
	112366	AF035318	Hs.12533	Homo sapiens clone 23705 mRNA sequence	15.40		
	112210	R49645	Hs.7004	ESTs	14.00		
65	112064	AL049390	Hs.22689	Homo sapiens mRNA; cDNA DKFZp586O1318 (f	13.00		
	111998	R42379	Hs.138283	ESTs	11.00		
	111987	NM_015310	Hs.6763	KIAA0942 protein	22.40		
	111803	AA593731	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A		1.77	
	111737	H04607	Hs.9218	ESTs		1.86	
70	111605	T91061	Hs.194178	ESTs, Moderately similar to PC4259 ferri	23.00		
	111510	R07856	Hs.16355	ESTs	11.02		
	111341	AL157484	Hs.22483	Homo sapiens mRNA; cDNA DKFZp762M127 (fr		1.88	
	111280	AA373527	Hs.19385	CGL-58 protein	18.40		
	111247	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFZp554B2062 (f			
75	111232	AI247763	Hs.16928	ESTs	27.60		
	110942	R63503	Hs.28419	ESTs	14.80		
	110924	AW058463	Hs.12940	zinc-fingers and homeoboxes 1	24.71		
	110837	H03109	Hs.108920	HT018 protein		2.18	
	110824	AI767183	Hs.26942	ESTs	12.20		
80	110776	AB032417	Hs.19545	fizzled (Drosophila) homolog 4		1.75	
	110576	H60869	Hs.37889	ESTs	13.00		
	110369	AK000768	Hs.107872	hypothetical protein FLJ20761		5.60	
	110099	R44557	Hs.23748	ESTs		2.31	
	109984	AI796320	Hs.10299	Homo sapiens cDNA FLJ13545 fls, clone PL			
85	109958	AA001266	Hs.133521	ESTs	11.25		
	109893	AA884208	Hs.30484	ESTs		2.68	

	109842	AW818436	Hs.23590	solute carrier family 16 (monocarboxylic	23.83		
	109837	H00656	Hs.29792	ESTs, Weakly similar to I38022 hypothet		17.20	3.91
	109796	AI800515	Hs.12024	ESTs		9.60	
5	109688	R41900	Hs.22245	ESTs			
	109648	H17800	Hs.7154	ESTs	22.80		
	109613	H47315	Hs.27519	ESTs			
	109550	AW021488	Hs.26981	ESTs			
	109523	AW193342	Hs.24144	ESTs			1.89
10	109472	AK001989	Hs.91165	hypothetical protein		6.00	
	109355	AA524525	Hs.48297	DKFZP586C1620 protein	15.00		
	109260	AW978515	Hs.131915	KIAA0863 protein	25.60		
	108781	AA128654		gb:zn98g07.s1 Stratagene fetal retina 93	14.20		
	108663	BE219231	Hs.292653	ESTs, Weakly similar to T26845 hypothet	11.00		
	108573	AA086005		gb:z184c04.s1 Stratagene colon (937204)	26.00		
15	108480	AL133092	Hs.68055	hypothetical protein DKFZp434I0428			
	108382	NM_006770	Hs.67726	macrophage receptor with collagenous str			1.83
	108174	AA055632	Hs.303070	ESTs	15.20		
	108138	AL049990	Hs.51515	Homo sapiens mRNA; cDNA DKFZp564G112 (fr		3.60	
20	108087	AA045708	Hs.40545	ESTs	15.44		
	108048	AI797341	Hs.165195	Homo sapiens cDNA FLJ14237 fis, clone NT		11.40	
	108041	AW204712	Hs.61957	ESTs			
	107997	AL049176	Hs.82223	chordin-like		4.76	
	107994	AA036811	Hs.48469	LIM domains containing 1			
25	107922	BE153855	Hs.61460	Ig superfamily receptor LNIR	14.20		
	107581	BE379594	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN A	51.80		
	107666	AA010611	Hs.60418	EST	29.20		
	107332	T87750	Hs.183297	DKFZP566F2124 protein	10.73		
	107292	BE166479	Hs.4789	Homo sapiens serologically defined breas	32.00		
30	107230	AI034467	Hs.34650	ESTs	17.40		
	107168	W57578	Hs.237955	RAB7, member RAS oncogene family	10.43		
	107160	AA314490	Hs.27669	KIAA1563 protein	11.40		
	107054	AI076459	Hs.15978	KIAA1272 protein			
	107029	AF264750	Hs.288971	myeloid/lymphoid or mixed-lineage leukem	21.40		
35	106999	H93281	Hs.10710	hypothetical protein FLJ20417	35.80		
	106954	AF128847	Hs.204038	indolethylamine N-methyltransferase			1.76
	106870	AI983730	Hs.26530	serum deprivation response (phosphatidyl			
	106865	AW192535	Hs.19479	ESTs	13.40		
	106844	AA485055	Hs.158213	sperm associated antigen 6		7.13	
40	106820	NM_016831	Hs.12592	period (Drosophila) homolog 3		7.00	
	106818	AK002135	Hs.3542	hypothetical protein FLJ11273	13.00		
	106797	AI768801	Hs.169943	Homo sapiens cDNA FLJ13569 fis, clone PL			2.05
	106773	AA478109	Hs.188833	ESTs			
	106747	NM_007118	Hs.171957	triple functional domain (PTPRF) interact	12.60		
45	106743	BE613328	Hs.21938	hypothetical protein FLJ12492	10.60		
	106667	AW360847	Hs.16578	ESTs			
	106605	AW772298	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076 (fr			2.40
	106567	AW450408	Hs.88412	chromosome 9 open reading frame 5			1.78
	106562	AL031846	Hs.152151	plakophilin 4			1.76
50	106536	AA329648	Hs.23804	ESTs, Weakly similar to PN0099 son3 prot			2.19
	106533	AL134708	Hs.145998	ESTs	23.20		
	106507	AA259068	Hs.267819	protein phosphatase 1, regulatory (inhib	15.20		
	106490	AA404265	Hs.115537	putative dipeptidase			
	106474	BE383668	Hs.42484	hypothetical protein FLJ10618	10.44		
55	106211	AA428240	Hs.126083	ESTs		29.80	
	105986	AB037722	Hs.8707	KIAA1301 protein		3.70	
	105894	AI904740	Hs.25691	receptor (calcionin) activity modifying			1.84
	105847	AW864490	Hs.32241	ESTs, Weakly similar to S65857 alpha-1C-			1.75
	105803	AW747996	Hs.160999	ESTs, Moderately similar to A56194 throm			2.47
60	105731	AA834664	Hs.29131	nuclear receptor coactivator 2	10.71		
	105729	H46612	Hs.293815	Homo sapiens HSPC285 mRNA, partial cds			
	105688	AI299139	Hs.17517	ESTs	23.40		
	105510	Z42047	Hs.283978	Homo sapiens PRO2751 mRNA, complete cds	37.20		
	105101	H63202	Hs.38163	ESTs		8.30	
65	104989	R65998	Hs.285243	hypothetical protein FLJ22029		8.09	
	104986	AW088826	Hs.117176	poly(A)-binding protein, nuclear 1			1.92
	104969	AI670947	Hs.78406	phosphatidylinositol-4-phosphate 5-kinas		5.40	
	104903	AI436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,		7.60	
	104896	AW015318	Hs.23165	ESTs	13.80		
70	104865	T79340	Hs.22575	Homo sapiens cDNA: FLJ21042 fis, clone C			
	104825	AA035613	Hs.141883	ESTs			1.87
	104781	AA099904	Hs.21610	DKFZP434B203 protein			1.93
	104776	AA026349		gb:zj99f01.s1 Soares_pregnant_uterus_NbH		10.20	
	104691	U29690	Hs.37744	Homo sapiens beta-1 adrenergic receptor		5.69	
75	104667	AI239923	Hs.30098	ESTs		3.82	
	104404	H58762		gb:EST00057 HE6W Homo sapiens cDNA clone		4.20	
	104392	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	27.20		
	104212	AB002298	Hs.173035	KIAA0300 protein			1.91
	104074	AL162039	Hs.31422	Homo sapiens mRNA; cDNA DKFZp434M229 (fr	11.20		
80	103749	AL135301	Hs.8768	hypothetical protein FLJ10849	10.86		
	103645	AW246253	Hs.7043	succinate-CoA ligase, GDP-forming, alpha	12.00		
	103554	AI878826	Hs.323469	caveolin 1, caveolae protein, 22kD			1.80
	103541	AI815601	Hs.79197	CD83 antigen (activated B lymphocytes, i			
	103496	Y09267	Hs.132821	flavin containing monooxygenase 2			
85	103428	BE383507	Hs.78921	A kinase (PRKA) anchor protein 1	11.20		
	103353	X89399	Hs.119274	RAS p21 protein activator (GTPase activa	19.80		

5	103295	X81479	Hs.2375	egf-like module containing, mucin-like,	3.60	
	103280	U84722	Hs.76206	cadherin 5, type 2, VE-cadherin (vascula		1.76
	103100	NM_005574	Hs.184585	LIM domain only 2 (rhombotin-like 1)		2.15
	103025	NM_002837	Hs.123641	protein tyrosine phosphatase, receptor t		
	102698	M18667	Hs.1867	progastricin (pepsinogen C)		
10	102659	BE245169	Hs.211610	CUG triplet repeat, RNA-binding protein	11.00	
	102580	U60808	Hs.152981	CDP-diacylglycerol synthase (phosphatida	25.40	
	102417	AA034127	Hs.153487	signal transducing adaptor molecule (SH3	14.00	
	102363	NM_003734	Hs.198241	amine oxidase, copper containing 3 (vasc		
	102302	AA306342	Hs.69171	protein kinase C-like 2	10.86	
15	102283	AW161552	Hs.83381	guanine nucleotide binding protein 11		
	102188	U20350	Hs.78913	chemokine (C-X3-C) receptor 1	7.40	
	102151	T27013	Hs.3132	steroidogenic acute regulatory protein	16.40	
	101957	L28824	Hs.74101	spleen tyrosine kinase	15.40	
	101842	M83221	Hs.75182	mannose receptor, C type 1		
20	101771	NM_002432	Hs.153837	myeloid cell nuclear differentiation ant		
	101764	AI198550	Hs.81256	S100 calcium-binding protein A4 (calcium		1.78
	101718	AF050658	Hs.2563	tachykinin, precursor 1 (substance K, su	18.80	
	101678	M62505	Hs.2161	complement component 5 receptor 1 (C5a I		2.22
	101447	M21305		gb:Human alpha satellite and satellite 3	504.80	
25	101383	NM_000132	Hs.79345	coagulation factor VIII, procoagulant co	31.00	
	101346	AI738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N		1.75
	101345	NM_005795	Hs.152175	calcitonin receptor-like		
	101336	NM_005732	Hs.75678	FBJ murine osteosarcoma viral oncogene h		2.24
	101330	L43821	Hs.80261	enhancer of filamentation 1 (cas-like do		
30	101277	BE297626	Hs.296049	microfibrillar-associated protein 4		
	101262	L35854		gb:Human dystrophin (dp140) mRNA, 5' end	19.00	
	101168	NM_005308	Hs.211569	G protein-coupled receptor kinase 5		2.01
	101102	NM_003243	Hs.79059	transforming growth factor, beta recepto		
	101088	X70697	Hs.553	solute carrier family 6 (neurotransmitte	7.52	
35	101066	AW970254	Hs.889	Charot-Leyden crystal protein	19.38	
	100971	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte		1.91
	100893	BE245294	Hs.180789	S164 protein	15.40	
	100770	W25797.comp	Hs.177486	amyloid beta (A4) precursor protein (pro	11.20	
	100716	X89887	Hs.172350	HIR (histone cell cycle regulation defec	14.80	
40	100555	M69181		gb:Human nonmuscle myosin heavy chain-B	33.00	
	100425	NM_014747	Hs.78748	KIAA0237 gene product	16.20	
	100408	D86640	Hs.56045	src homology three (SH3) and cysteine ri	4.00	
	100382	D83407	Hs.156007	Down syndrome critical region gene 1-lik	4.24	
	100351	D64158			6.20	
45	100299	D49493	Hs.2171	growth differentiation factor 10	21.20	
	100134	AA305746	Hs.49	macrophage scavenger receptor 1		
	100108	U09577	Hs.76873	hyaluronoglucosaminidase 2		1.79
	100095	Z97171	Hs.78454	myoclin, trabecular meshwork inducible	5.40	
	100066				11.29	

TABLE 3B shows the accession numbers for those primekeys lacking unigenes for Table 3A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using *Clustering and Alignment Tools (DoubleTwist, Oakland California)*. The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT number	Accessions
123619	371681_1	AA602964 AA609200
126433	127143_1	AA325606 AA099517 N89423
125831	1522905_1	H04043 D60988 D60337
126816	122973_1	AA248234 AA090985
126852	136135_1	AA399961 AA128347
121059	273450_1	AA393283 AA398526
120637	200885_1	AA811804 AA809404 AA286907 AW977624
122011	7617_-2	AA431082
120934	177521_1	AA226198 AA226513 AA383773
123802	genbank_AA620448	AA620448
116814	genbank_H50834	H50834
118329	genbank_N63520	N63520
104404	H58762_et	H58762
104776	genbank_AA026349	AA026349
113502	genbank_T89130T89130	
101262	entrez_L35854	L35854
108573	genbank_AA086005	AA086005
101447	entrez_M21305	M21305
124357	genbank_N22401	N22401
108781	genbank_AA128654	AA128654
112794	genbank_R97018	R97018
100351	entrez_D64158	D64158
100555	Ugr_HT2245	M69181 M81105 U51039

Table 4A shows 202 genes up-regulated in samples from patients treated with chemotherapy or radiotherapy. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

5	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
	R1:	average of AI for samples from patients treated with chemotherapy or radiotherapy divided by the average of AI for normal lung samples.			
10	Pkey	ExAccn	UnigeneID	Unigene Title	R1
	100113	NM_001269	Hs.84746	chromosome condensation 1	27.20
	100187	D17793	Hs.78183	aldo-keto reductase family 1, member C3	20.60
15	100210	D26361	Hs.3104	KIAA0042 gene product	20.40
	100225	D28539	Hs.167185	glutamate receptor, metabotropic 5	20.60
	100269	NM_001949	Hs.1189	E2F transcription factor 3	29.40
	100438	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	23.50
	100877	X80821	Hs.27973	KIAA0874 protein	35.56
20	100893	BE245294	Hs.180789	S164 protein	43.40
	101273	Z11933	Hs.182505	POU domain, class 3, transcription facto	21.80
	101447	M21305		gb:Human alpha satellite and satellite 3	193.60
	101649	AW959908	Hs.1690	heparin-binding growth factor binding pr	38.40
	101724	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	198.80
25	101748	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	78.60
	101809	M68849	Hs.323733	gap junction protein, beta 2, 26kD (conn	162.20
	101879	AA176374	Hs.243886	nuclear autoantigenic sperm protein (his	50.00
	101915	AF207881	Hs.155185	cytosolic ovarian carcinoma antigen 1	26.00
	101973	U41514	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp	37.20
30	102025	U04045	Hs.78934	mutS (E. coli) homolog 2 (colon cancer,	
	102031	U04898	Hs.2156	RAR-related orphan receptor A	32.00
	102052	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	51.20
	102391	AA296874	Hs.77494	deoxyguanosine kinase	13.90
	102420	U44060	Hs.14427	Homo sapiens cDNA: FLJ21800 fis, clone H	28.80
35	102610	U65011	Hs.30743	preferentially expressed antigen in mala	110.60
	102829	NM_006183	Hs.80962	neurensin	116.80
	103000	NM_001975	Hs.146580	enolase 2, (gamma, neuronal)	2.30
	103036	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	181.40
40	103507	AJ000512	Hs.296323	serum/glucocorticoid regulated kinase	49.20
	103587	BE270266	Hs.82128	ST4 oncofetal trophoblast glycoprotein	86.60
	104660	BE298665	Hs.14846	Homo sapiens mRNA: cDNA DKFZp564D016 (fr	42.60
	104896	AW015318	Hs.23165	ESTs	29.40
	105038	AW503733	Hs.9414	KIAA1488 protein	21.50
	105298	BE387790	Hs.26369	hypothetical protein FLJ20287	32.80
45	105510	Z42047	Hs.283978	Homo sapiens PRO2751 mRNA, complete cds	20.20
	105667	AA767526	Hs.22030	paired box gene 5 (B-cell lineage specifi	28.40
	106073	AL157441	Hs.17834	downstream neighbor of SON	25.40
	106205	AW965058	Hs.111583	ESTs, Weakly similar to I38022 hypotheti	32.00
	106516	AL137311	Hs.234074	Homo sapiens mRNA: cDNA DKFZp761G02121 (40.60
50	106533	AL134708	Hs.145998	ESTs	59.80
	106575	AW970602	Hs.105421	ESTs	43.40
	106654	AW075485	Hs.286049	phosphoserine aminotransferase	50.80
	106851	AI458623		gb:tk04g09.x1 NCL_CGAP_Lu24 Homo sapiens	53.40
55	106995	AB023139	Hs.37892	KIAA0922 protein	20.88
	107332	T87750	Hs.183297	DKFZP566F2124 protein	23.60
	107532	AA443473	Hs.173684	Homo sapiens mRNA: cDNA DKFZp762G207 (fr	57.20
	107922	BE153855	Hs.61460	Ig superfamily receptor LNIR	49.00
	108609	BE409857	Hs.69499	hypothetical protein	19.67
60	108780	AU076442	Hs.117938	collagen, type XVII, alpha 1	48.17
	109166	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	59.20
	109260	AW978515	Hs.131915	KIAA0863 protein	28.60
	109280	AK001355	Hs.279610	hypothetical protein FLJ10493	22.80
	109292	AW975746	Hs.188662	KIAA1702 protein	
65	109384	AA219172	Hs.86849	ESTs	21.00
	109415	U80736	Hs.110826	trinucleotide repeat containing 9	31.60
	109445	AA232103	Hs.189915	ESTs	24.20
	109502	AW967069	Hs.211556	hypothetical protein MGC5487	21.40
	109633	AW003785	Hs.170267	ESTs	20.40
70	109786	AI989482	Hs.146286	kinesin family member 13A	19.60
	109958	AA001266	Hs.133521	ESTs	24.00
	110920	N47224	Hs.20521	HMT1 (hnRNP methyltransferase, S. cerevi	28.40
	110924	AW058463	Hs.12940	zinc-fingers and homeoboxes 1	36.00
	111084	H44186	Hs.15456	PDZ domain containing 1	61.20
75	111132	AB037807	Hs.83293	hypothetical protein	24.60
	111229	AW389845	Hs.110855	ESTs	27.20
	111337	AA837396	Hs.263925	US1-interacting protein NUDE1, rat homo	48.00
	111987	NM_015310	Hs.8763	KIAA0942 protein	37.80
	112046	AA383343	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	26.80
80	112268	W39609	Hs.22003	solute carrier family 6 (neurotransmitte	63.80
	112685	R87650	Hs.33439	ESTs, Weakly similar to ALU1_HUMAN ALU	26.40
	112871	AL110216	Hs.12285	ESTs, Weakly similar to I55214 salivary	47.64
	112897	AW206453	Hs.3782	ESTs	22.00
	112973	AB033023	Hs.318127	hypothetical protein FLJ10201	65.00
	112992	AL157425	Hs.133315	Homo sapiens mRNA: cDNA DKFZp761J1324 (f	42.00
85	113073	N39342	Hs.103042	microtubule-associated protein 1B	55.40

	113494	T91451	Hs.86538	ESTs	22.80
	113560	T91015	Hs.268626	ESTs	22.80
	113849	AA457211	Hs.8858	bromodomain adjacent to zinc finger doma	51.80
5	113950	AI267652	Hs.30504	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	28.20
	114339	AA782845	Hs.22790	ESTs	20.20
	114365	H42169	Hs.18653	hypothetical protein FLJ14627	21.00
	114455	H37908	Hs.271616	ESTs, Weakly similar to ALU8_HUMAN ALU S	25.80
	114518	AW163267	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like	23.60
10	114824	AA960961	Hs.305953	zinc finger protein 83 (HPF1)	27.20
	114837	BE244930	Hs.166895	ESTs	30.20
	114974	AW966931	Hs.179562	nucleosome assembly protein 1-like 1	20.80
	115075	AA814043	Hs.88045	ESTs	30.60
	115084	BE383668	Hs.42484	hypothetical protein FLJ10618	28.86
	115291	BE545072	Hs.122579	hypothetical protein FLJ10461	38.00
15	115313	AA808001	Hs.184411	albumin	22.60
	115697	D31382	Hs.63325	transmembrane protease, serine 4	173.60
	115909	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	27.77
	116090	AI591147	Hs.61232	ESTs	20.80
	116107	AL133916	Hs.172572	hypothetical protein FLJ20093	164.20
20	116399	AA889120	Hs.110637	homeo box A10	38.00
	117099	H93699		gb:yv16a11.s1 Soares fetal liver spleen	21.60
	117881	AF161470	Hs.260622	butyrate-induced transcript 1	49.40
	118091	AW006054	Hs.47883	ESTs, Weakly similar to KCC1_HUMAN CALCI	22.40
	118138	AA374756	Hs.93560	Homo sapiens mRNA for KIAA1771 protein,	22.00
25	118720	N73515		gb:za49d07.s1 Soares fetal liver spleen	20.00
	118873	AI824009	Hs.44577	ESTs	19.40
	119126	R45175	Hs.117183	ESTs	111.20
	119717	AA918317	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	33.00
30	119940	AL050097	Hs.272531	DKFZP586B0319 protein	31.00
	120266	AI807264	Hs.205442	ESTs, Weakly similar to T34036 hypotheti	20.20
	120515	AA258356		gb:zr59c10.s1 Soares_NhHMPu_S1 Homo sapi	25.00
	120859	AA826434	Hs.1819	achaete-scute complex (Drosophila) homol	95.40
	120983	AA398209	Hs.97587	EST	105.20
35	121054	AW976570	Hs.97387	ESTs	38.80
	121369	AW450737	Hs.128791	CGI-09 protein	41.60
	122335	AA443258	Hs.241551	chloride channel, calcium activated, fam	30.80
	122612	AA974832	Hs.128708	ESTs	19.60
	123130	AA487200		gb:ab19f02.s1 Stratagene lung (937210) H	33.20
40	123440	AI733692	Hs.112488	ESTs	23.17
	123596	AA421130	Hs.112640	EST	23.00
	123619	AA602964		gb:nc97c02.s1 NCL_CGAP_Pr2 Homo sapiens	28.80
	124006	AI147155	Hs.270016	ESTs	77.60
	124169	BE079334	Hs.271630	ESTs	22.20
45	124281	AI333756	Hs.111801	arsenate resistance protein ARS2	42.20
	124472	N52517	Hs.102670	EST	32.60
	124617	AW628168	Hs.152684	ESTs	21.80
	124631	NM_014053	Hs.270594	FLVCR protein	30.40
	124839	R55784	Hs.140942	ESTs	21.20
50	125186	AA610620	Hs.181244	major histocompatibility complex, class	42.80
	125321	T86652	Hs.178294	ESTs	27.00
	125535	NM_013243	Hs.22215	secretogranin III	23.80
	125646	AA628962	Hs.75209	protein kinase (cAMP-dependent, catalyti	23.20
	125684	AW589427	Hs.158849	Homo sapiens cDNA: FLJ21663 fis, clone C	21.20
55	125724	AL360190	Hs.295978	Homo sapiens mRNA full length insert cDN	48.80
	125847	AW161885	Hs.249034	ESTs	31.00
	125934	AA193325	Hs.32646	hypothetical protein FLJ21901	21.20
	126077	M78772	Hs.210836	ESTs	49.80
	126299	AW979155	Hs.298275	amino acid transporter 2	21.80
60	126395	AI468004	Hs.276956	hypothetical protein FLJ12929	71.00
	126433	AA325606		gb:EST28707 Cerebellum II Homo sapiens c	23.20
	126509	R47400	Hs.23850	ESTs	23.80
	126538	AB030656	Hs.17377	coronin, actin-binding protein, 1C	23.10
	126666	AA648886	Hs.151999	ESTs	36.00
65	126812	AB037860	Hs.173933	nuclear factor I/A	20.80
	126872	AW450979		gb:U1-H-B13-ata-a-12-0-UI.s1 NCL_CGAP_Su	46.29
	127046	AA321948	Hs.293968	ESTs	22.80
	127431	AW771958	Hs.175437	ESTs, Moderately similar to PC4259 ferri	30.00
	127489	AA650250	Hs.272076	ESTs	20.80
70	127521	AW297206	Hs.164018	ESTs	25.20
	127742	AW293496	Hs.180138	ESTs	28.00
	127925	AA805151	Hs.3628	mitogen-activated protein kinase kinase	21.20
	127930	AA809672	Hs.123304	ESTs	20.64
	127968	AA830201	Hs.124347	ESTs	28.20
75	127987	AI022103	Hs.124511	ESTs	19.60
	128116	H07103	Hs.286014	Homo sapiens, clone IMAGE:3867243, mRNA	20.40
	128609	NM_003616	Hs.102456	survival of motor neuron protein interac	34.40
	128777	AI878918	Hs.10526	cysteine and glycine-rich protein 2	53.80
	128949	AA009647	Hs.8850	a disintegrin and metalloproteinase doma	23.00
80	129168	AI132968	Hs.109052	chromosome 14 open reading frame 2	37.60
	129404	AI267700	Hs.317584	ESTs	28.60
	129527	AA769221	Hs.270847	delta-tubulin	40.80
	129574	AA026815	Hs.11463	UMP-CMP kinase	31.20
	128598	N30436	Hs.11556	Homo sapiens cDNA FLJ12566 fis, clone NT	29.60
85	129785	H19006	Hs.184780	ESTs	72.20
	129970	AV655806	Hs.296198	chromosome 12 open reading frame 4	22.20

	130149	AW067805	Hs.172665	methylenetetrahydrofolate dehydrogenase	29.60
	130199	Z48579	Hs.172028	a disintegrin and metalloproteinase domain	27.60
	130441	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	28.36
5	130466	W19744	Hs.180059	Homo sapiens cDNA FLJ20653 fis, clone KA	20.20
	130482	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	22.40
	130617	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	19.60
	130703	R77776	Hs.18103	ESTs	19.40
	130732	AW890487	Hs.63984	cadherin 13, H-cadherin (heart)	21.40
10	130867	NM_001072	Hs.284239	UDP glycosyltransferase 1 family, polype	110.00
	131028	AI879165	Hs.2227	CCAAT/enhancer binding protein (C/EBP),	25.20
	131086	AL035461	Hs.2281	chromogranin B (secretogranin 1)	40.60
	131284	NM_001429	Hs.25272	E1A binding protein p300	24.60
	131775	AB014548	Hs.31921	KIAA0648 protein	21.00
15	131860	BE383676	Hs.334	Rho guanine nucleotide exchange factor (33.40
	131945	NM_002918	Hs.35120	replication factor C (activator 1) 4 (37	60.80
	132040	NM_001196	Hs.315689	Homo sapiens cDNA: FLJ22373 fis, clone H	20.40
	132084	NM_002267	Hs.3886	karyopherin alpha 3 (importin alpha 4)	29.40
	132389	AA310393	Hs.190044	ESTs	32.40
	132437	AA152106	Hs.4859	cyclin L an/a-6a	27.40
20	132550	AW969263	Hs.170195	bone morphogenetic protein 7 (osteogenic	75.60
	132617	AF037335	Hs.5338	carbonic anhydrase XII	31.36
	132632	AU076916	Hs.5398	guanine monophosphate synthetase	32.40
	132672	W27721	Hs.54897	Cdc42 guanine exchange factor (GEF) 9	23.40
25	132742	AA025480	Hs.292812	ESTs, Weakly similar to T33468 hypotheti	61.20
	132771	Y10275	Hs.56407	phosphoserine phosphatase	22.33
	133070	U92649	Hs.64311	a disintegrin and metalloproteinase domain	23.50
	133153	AF070592	Hs.66170	HSKM-B protein	30.00
	133181	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	23.80
30	133282	AA449015	Hs.286145	SRB7 (suppressor of RNA polymerase B, ye	51.60
	133350	AI499220	Hs.71573	hypothetical protein FLJ10074	33.00
	133592	AV652066	Hs.75113	general transcription factor IIA	82.00
	133658	AA319146	Hs.75426	secretogranin II (chromogranin C)	
	133865	AB011155	Hs.170290	discs, large (Drosophila) homolog 6	69.33
35	134032	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibitor	33.20
	134125	NM_014781	Hs.50421	KIAA0203 gene product	31.60
	134158	U15174	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	30.60
	134321	BE538082	Hs.8172	ESTs, Moderately similar to A46010 X-in	23.40
	134367	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	49.20
40	134570	U66615	Hs.172280	SWI/SNF related, matrix associated, acti	20.20
	134753	NM_006482	Hs.173135	dual-specificity tyrosine-(Y)-phosphoryl	20.80
	135002	AA448542	Hs.251677	G antigen 7B	37.60
	135029	H58818	Hs.187579	hydroxysteroid (17-beta) dehydrogenase	53.40
	135047	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	31.60
45	135345	X53655	Hs.99171	neurotrophin 3	28.80

TABLE 4B shows the accession numbers for those primekeys lacking unigenelD's for Table 4A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT number	Accessions
123619	371681_1	AA602964 AA609200
126433	127143_1	AA325606 AA099517 N89423
126872	142696_1	AW450979 AA136653 AA136656 AW419381 AA984358 AA492073 BE168945 AA809054 AW238038 BE011212 BE011359 BE011367 BE011368 BE011362 BE011215 BE011365 BE011363
106851	322947_1	AI458623 AA639708 AA485409 R22065 AA485570
118720	genbank_N73515	N73515
120515	genbank_AA258356	AA258356
117099	321871_1	H93699 H97976 H80036
101447	entrez_M21305	M21305
123130	genbank_AA487200	AA487200

Table 5A shows 680 genes up-regulated in squamous cell carcinoma or adenocarcinoma lung tumors relative to normal lung and chronically diseased lung. These genes were selected from 59680 probesets on the Eos/Arraymatrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

5	Pkey:	Unique Eos probeset identifier number							
	ExAccn:	Exemplar Accession number, Genbank accession number							
	UnigeneID:	Unigene number							
	Unigene Title:	Unigene gene title							
10	R1:	70th percentile of AI for squamous cell carcinoma and adenocarcinoma lung tumor samples divided by the 90th percentile of AI for normal and chronically diseased lung samples.							
	R2:	80th percentile of AI adenocarcinoma lung tumor samples divided by the 90th percentile of AI for normal and chronically diseased lung samples.							
	R3:	80th percentile of AI squamous cell carcinoma lung tumor samples divided by the 90th percentile of AI for normal and chronically diseased lung samples.							
	R4:	80th percentile of AI adenocarcinoma lung tumor samples divided by the 80th percentile of AI for squamous cell carcinoma lung tumor samples.							
15	R5:	70th percentile of AI for squamous cell carcinoma and adenocarcinoma lung tumor samples minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples divided by 90th percentile of AI for normal and chronically diseased lung samples minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples							
20	Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2	R3	R4	R5
	100035			AFFX control: GAPDH					6.76
	100036			AFFX control: GAPDH					5.77
	100037			AFFX control: GAPDH					5.75
25	100071	A28102		Human GABAA receptor alpha-3 subunit		8.00			
	100114	X02308	Hs.82962	thymidylate synthetase					5.71
	100154	H60720	Hs.81892	KIAA0101 gene product	3.84				
	100187	D17793	Hs.78183	aldo-keto reductase family 1, member C3	3.33				
	100188	AW247090	Hs.57101	minichromosome maintenance deficient (S.					4.52
	100202	BE294407	Hs.99910	phosphofructokinase, platelet					5.49
30	100216	AA489908	Hs.1390	proteasome (prosome, macropain) subunit, E2F transcription factor 3	2.55				5.67
	100269	NM_001949	Hs.1189	chaperonin containing TCP1, subunit 5 (e					5.66
	100287	AU076657	Hs.1600	protein disulfide isomerase-related prot					3.81
	100297	AU077258	Hs.182429	minichromosome maintenance deficient (S.					4.50
35	100330	AW410976	Hs.77152	platelet-activating factor acetylhydrola	5.07				
	100336	AW247629	Hs.6793	uridine monophosphate kinase					4.82
	100360	W70171	Hs.75939	KIAA0175 gene product					3.79
	100372	NM_014791	Hs.184339	amylase, alpha 2A; pancreatic				15.65	
	100474	NM_000699	Hs.300280	RAN, member RAS oncogene family					5.49
40	100486	T19006	Hs.10842	non-metastatic cells 2, protein (NM23B)					4.17
	100491	D56165	Hs.275163	carcinoembryonic antigen-related cell ad		7.20			
	100516	D90278	Hs.11	prolactin-induced protein				14.20	
	100522	X51501	Hs.99949	collagen, type VII, alpha 1 (epidermolys	3.10				
	100559	NM_000094	Hs.1640	calcitonin/calcitonin-related polypeptid				9.30	
45	100576	X00356	Hs.37058	mitogen-activated protein kinase kinase				20.60	
	100629	AA015693	Hs.21291	Homo sapiens ribosomal protein L39 mRNA,	3.85				
	100661	BE623001	Hs.132748	zinc ribbon domain containing, 1		8.60			
	100677	AA353686	Hs.57813	general transcription factor IIA, 1 (37k				10.00	
	100696	D14887	Hs.121686	myeloid/lymphoid or mixed-lineage leukem			24.80		
50	100709	N26539	Hs.100469	KIAA0618 gene product		7.60			
	100761	BE208491	Hs.295112	flap structure-specific endonuclease 1					7.99
	100830	AC004770	Hs.4756	gb:Human transketolase-like protein gene		10.20			
	100867	U14622		ret proto-oncogene (multiple endocrine n		8.00			
	100902	M16029	Hs.287270	guanine monophosphate synthetase					5.16
55	100906	AU076916	Hs.5398	keratin 14 (epidermolysis bullosa simple	2.57				
	100960	J00124	Hs.117729	gb:Human proliferating cell nuclear anti					4.69
	101045	J05614		glucose phosphate isomerase					4.19
	101061	NM_000175	Hs.180532	potassium voltage-gated channel, Shab-re		12.91			
	101071	L02840	Hs.84244	protease inhibitor 3, skin-derived (SKAL	3.12				
60	101124	L10343	Hs.112341	melanoma antigen, family A, 2	3.50				
	101175	U82671	Hs.36980	macrophage migration inhibitory factor (5.69
	101181	BE262621	Hs.73798	ataxia-telangiectasia group D-associated	4.08				
	101204	L24203	Hs.82237	opioid receptor, mu 1			6.40		
	101210	L29301	Hs.2353	cyclin-dependent kinase inhibitor 3 (CDK	2.53				
65	101216	AA284166	Hs.84113	chaperonin containing TCP1, subunit 6A (7.90
	101228	AA333387	Hs.82916	sorbitol dehydrogenase					4.45
	101233	AL135173	Hs.878	POU domain, class 3, transcription facto	8.50				
	101273	Z11933	Hs.182505	interleukin-1 receptor-associated kinase					4.17
	101342	U52112	Hs.182018	hydroxyprostaglandin dehydrogenase 15-(N				21.89	
70	101346	A1738616	Hs.77348	kalikrein B, plasma (Fletcher factor) 1				12.80	
	101389	NM_000892	Hs.1901	proliferating cell nuclear antigen	3.24				
	101396	BE267931	Hs.78996	small proline-rich protein 1B (cornifin)					7.90
	101431	BE185289	Hs.1076	keratin 5 (epidermolysis bullosa simplex	8.31				
	101448	NM_000424	Hs.195850	bone morphogenetic protein 2				38.80	
75	101462	AL035668	Hs.73853	glutamic-oxaloacetic transaminase 2, mit					4.01
	101466	BE262660	Hs.170197	interferon-induced protein with tetrabi				12.00	
	101484	AA053486	Hs.20315	gb:Human parathyroid hormone-related pro	10.50				
	101502	M26958		asparagine synthetase					4.46
	101505	AA307680	Hs.75692	aconitase 1, soluble	4.02				
80	101526	NM_002197	Hs.154721	fibrillarin					4.65
	101535	X57152	Hs.99853	v-ros avian UR2 sarcoma virus oncogene h				9.09	
	101577	M34353	Hs.1041	heparin-binding growth factor binding pr	54.00				
	101649	AW959908	Hs.1690	H2B histone family, member Q	5.59				
	101663	NM_003528	Hs.2178	H2A histone family, member A	7.00				
85	101664	AA436989	Hs.121017	growth arrest and DNA-damage-inducible,		7.60			
	101669	L24498	Hs.80409						

	101695	M69136	Hs.135626	chymase 1, mast cell	4.79		
	101724	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	15.21		
	101748	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	55.50		
5	101759	M80244	Hs.184601	solute carrier family 7 (cationic amino		18.57	4.10
	101771	NM_002432	Hs.153837	myeloid cell nuclear differentiation ant			
	101804	M86699	Hs.169840	TTK protein kinase	4.50		
	101809	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	140.00		
	101833	AU076442	Hs.117938	collagen, type XVII, alpha 1	2.56		
10	101842	M93221	Hs.75182	mannose receptor, C type 1		12.80	
	101851	BE260964	Hs.82045	midkine (neurite growth-promoting factor			5.88
	102002	NM_002484	Hs.81469	nucleotide binding protein 1 (E.coli Min	7.80		
	102039	AL134223	Hs.306098	aldo-keto reductase family 1, member C1			4.35
	102072	U09410	Hs.78743	zinc finger protein 131 (clone pHZ-10)	7.40		
	102083	T35901	Hs.75117	interleukin enhancer binding factor 2, 4			5.12
15	102111	L36196	Hs.81884	sulfotransferase family, cytosolic, 2A,		12.00	
	102123	NM_001809	Hs.1594	centromere protein A (17kD)	6.20		
	102154	U17760	Hs.75517	laminin, beta 3 (niclin (125kD), kalinin	2.62		
	102193	AL036335	Hs.313	secreted phosphoprotein 1 (osteopontin,	5.85		
	102217	AA825978	Hs.301613	JTV1 gene			6.18
20	102224	NM_002810	Hs.148495	proteasome (prosome, macropain) 26S subu			4.49
	102234	AW163390	Hs.278554	heterochromatin-like protein 1			5.80
	102251	NM_004398	Hs.41706	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	4.50		
	102305	AL043202	Hs.90073	chromosome segregation 1 (yeast homolog)			5.15
	102330	BE298063	Hs.77254	chromobox homolog 1 (Drosophila HP1 beta			4.17
25	102340	U37055	Hs.278657	macrophage stimulating 1 (hepatocyte gro		9.33	
	102348	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	8.87		
	102368	U39817	Hs.36820	Bloom syndrome	15.91		
	102394	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma		19.20	
30	102404	NM_005429	Hs.79141	vascular endothelial growth factor C			14.00
	102537	U57094	Hs.50477	RAB27A, member RAS oncogene family			12.00
	102581	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2			4.57
	102605	AI435128	Hs.181369	ubiquitin fusion degradation 1-like			3.98
	102610	U65011	Hs.30743	preferentially expressed antigen in meta	77.50		
	102623	AW249285	Hs.37110	melanoma antigen, family A, 9	12.50	22.00	
35	102642	AA205847	Hs.23016	G protein-coupled receptor			
	102654	AV649989	Hs.24385	Human hbc647 mRNA sequence		12.00	
	102659	BE245169	Hs.211610	CUG triplet repeat, RNA-binding protein			12.80
	102669	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	6.50		
	102672	U72066	Hs.29287	retinoblastoma-binding protein 8	8.50		
40	102687	NM_007019	Hs.93002	ubiquitin carrier protein E2-C			9.24
	102696	BE540274	Hs.239	forkhead box M1			5.54
	102768	U82321		gb:Homo sapiens clone 14.9B mRNA sequenc	6.60		
	102781	BE258778	Hs.108809	chaperonin containing TCP1, subunit 7 (e			3.78
45	102784	U85658	Hs.61796	transcription factor AP-2 gamma (activat		14.40	4.26
	102824	U90916	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H			
	102829	NM_006183	Hs.80962	neurotensin	8.00		
	102888	AI346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1			5.50
	102892	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin		6.70	
50	102913	NM_002275	Hs.80342	keratin 15	4.64		
	102935	BE561850	Hs.80508	small nuclear ribonucleoprotein polypept	2.93		
	102951	X15218	Hs.2969	v-ski avian sarcoma viral oncogene homol		11.40	
	102983	BE387202	Hs.118638	non-metastatic cells 1, protein (NM23A)			7.26
	103023	AW500470	Hs.117950	multifunctional polypeptide similar to S	3.01		
55	103036	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	27.90		
	103038	AA926960	Hs.334883	CDC28 protein kinase 1			8.79
	103060	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin			4.27
	103099	AI693251	Hs.8248	NADH dehydrogenase (ubiquinone) Fe-S pro	9.80		
	103119	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	4.05		
60	103168	X53463	Hs.2704	glutathione peroxidase 2 (gastric/intestin	3.07		
	103185	NM_006825	Hs.74368	transmembrane protein (63kD), endoplasm			5.62
	103192	M22440	Hs.170009	transforming growth factor, alpha	7.40		
	103223	BE275607	Hs.1708	chaperonin containing TCP1, subunit 3 (g			4.70
	103242	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu o		100.00	
65	103316	X83301	Hs.324728	SMA5			9.80
	103375	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	9.71		
	103376	AL036166	Hs.323378	coated vesicle membrane protein	14.00		
	103385	NM_007069	Hs.37189	similar to rat HREV107		11.00	
	103391	X94453	Hs.114366	pyrroline-5-carboxylate synthetase (glut	2.93		
70	103404	BE394784	Hs.78596	proteasome (prosome, macropain) subunit,			5.15
	103430	BE564090	Hs.20716	translocase of inner mitochondrial membr			3.98
	103446	X98834	Hs.79971	sal (Drosophila)-like 2		21.40	
	103476	Y07701	Hs.293007	aminopeptidase puromycin sensitive		13.00	
	103477	AJ011812	Hs.119018	transcription factor NRF		6.40	
75	103478	BE514982	Hs.38991	S100 calcium-binding protein A2	5.02		
	103515	Y10275	Hs.56407	phosphoserine phosphatase	10.50		
	103558	BE816547	Hs.2785	keratin 17	6.41		
	103580	AA328046	Hs.46405	polymerase (RNA) II (DNA directed) polyp			3.84
	103587	BE270266	Hs.82128	ST4 oncofetal trophoblast glycoprotein	78.50		
80	103594	AI368680	Hs.816	SRY (sex determining region Y)-box 2	6.51		
	103636	NM_006235	Hs.2407	POU domain, class 2, associating factor	3.50		
	103768	AF086009		gb:Homo sapiens full length insert cDNA			4.48
	103841	AA314821	Hs.38178	hypothetical protein FLJ23468	8.00		
	103847	AF219946	Hs.102237	tubby super-family protein	10.40		
85	103913	AW967500	Hs.133543	ESTs		15.60	
	104094	AA418187	Hs.330515	ESTs	6.60		

WO 02/086443

PCT/US02/12476

104150	AL122044	Hs.331633	hypothetical protein DKFZp566N034		26.00
104257	BE560621	Hs.9222	estrogen receptor binding site associate	6.80	
104261	AW248364	Hs.5409	RNA polymerase I subunit		3.98
104331	AB040450	Hs.279862	cdk inhibitor p21 binding protein	6.80	
104415	BE410992	Hs.258730	heme-regulated initiation factor 2-alpha	10.29	
104558	R56678	Hs.88959	hypothetical protein MGC4816	4.21	
104590	AW373062	Hs.83623	nuclear receptor subfamily 1, group I, m		15.79
104658	AA350954	Hs.27268	Homo sapiens cDNA: FLJ21933 fis, clone H		17.40
104660	BE298665	Hs.14846	Homo sapiens mRNA; cDNA DKFZp564D016 (fr	6.40	
104689	AA420450	Hs.292911	ESTs, Highly similar to S60712 band-6-pr		6.55
104754	AI206234	Hs.155924	cAMP responsive element modulator		10.00
104758	BE560269	Hs.7010	NPD002 protein		4.47
104971	BE311926	Hs.15830	hypothetical protein FLJ12691	2.87	
105011	BE091926	Hs.16244	mitotic spindle coiled-coil related prot	3.83	
105012	AF098158	Hs.9329	chromosome 20 open reading frame 1	2.86	
105026	AA809485	Hs.124219	hypothetical protein FLJ12934	11.00	
105076	AI598262	Hs.37810	hypothetical protein MGC14833		5.01
105132	AA148164	Hs.247280	HBV associated factor		3.99
105143	AI368836	Hs.24808	ESTs, Weakly similar to I38022 hypotheti		11.00
105158	AW976357	Hs.234545	hypothetical protein NUF2R	16.00	
105175	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	4.32	
105200	AA328102	Hs.24641	cytoskeleton associated protein 2	3.00	
105264	AA227934		gb:zr57e08.s1 Soares_NhHMPu_S1 Homo sapi		10.00
105298	BE387790	Hs.26369	hypothetical protein FLJ20287	3.69	
105409	AW505076	Hs.301855	DiGeorge syndrome critical region gene 8		9.20
105460	AW296078	Hs.271721	Homo sapiens, clone IMAGE:4179986, mRNA,		7.80
105667	AA767526	Hs.22030	paired box gene 5 (B-cell lineage specif	4.12	
105743	BE246502	Hs.9598	sema domain, immunoglobulin domain (Ig),	3.82	
105782	H09748	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro		27.00
105848	AW954054	Hs.24951	ESTs		7.60
105891	U55984	Hs.289088	heat shock 90kD protein 1, alpha		4.14
106019	AF221993	Hs.46743	McKusick-Kaufman syndrome		16.80
106069	BE586623	Hs.29899	ESTs, Weakly similar to G02075 transcrip		23.40
106073	AL157441	Hs.17834	downstream neighbor of SON	9.50	
106126	AA576953	Hs.22972	hypothetical protein FLJ13352	6.00	
106159	AK001301	Hs.3487	hypothetical protein FLJ10439		3.95
106220	D61329	Hs.32196	mitochondrial ribosomal protein L36		6.04
106260	AI097144	Hs.5250	ESTs, Weakly similar to ALU1_HUMAN ALU S		13.20
106300	Y10043	Hs.19114	high-mobility group (nonhistone chromoso		5.02
106307	AA436174	Hs.37751	ESTs, Weakly similar to putative p150 [6.60	
106318	AA025610	Hs.9605	cleavage and polyadenylation specific fa		5.04
106341	AF191020	Hs.5243	hypothetical protein, estradiol-induced		7.25
106440	AA448553	Hs.151393	glutamate-cysteine ligase, catalytic sub		13.80
106481	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	4.75	
106586	AA243837	Hs.57787	ESTs		10.84
106605	AW772298	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076 (fr		45.60
106654	AW075485	Hs.286049	phosphoserine aminotransferase	28.00	
106785	Y15227	Hs.20149	deleted in lymphocytic leukemia, 1	3.00	
106813	C05766	Hs.181022	CGI-07 protein		11.40
106895	AK001826	Hs.25245	hypothetical protein FLJ11269		6.00
106913	AI219346	Hs.86178	M-phase phosphoprotein 9	6.56	
106919	AW043637	Hs.21766	ESTs, Weakly similar to ALU5_HUMAN ALU S		4.27
107054	AI076459	Hs.15978	KIAA1272 protein		34.80
107059	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	4.71	
107098	AI823593	Hs.27688	ESTs		24.80
107104	AU076640	Hs.15243	nucleolar protein 1 (120kD)		7.05
107129	AC004770	Hs.4756	flap structure-specific endonuclease 1	2.60	
107198	AV657225	Hs.9846	KIAA1040 protein		19.20
107203	D20426	Hs.41639	programmed cell death 2	7.60	
107217	AL080235	Hs.35861	DKFZP586E1621 protein	9.50	
107284	NM_005629	Hs.187958	solute carrier family 6 (neurotransmitte	2.71	
107318	T74445	Hs.5957	Homo sapiens clone 24416 mRNA sequence		8.71
107516	X57152	Hs.99853	fibrillarin		4.33
107529	BE515065	Hs.296585	nucleolar protein (KKE/D repeat)		4.00
107728	AA019551	Hs.294151	Homo sapiens, clone IMAGE:3603836, mRNA,	10.80	
107851	AA022953	Hs.61172	EST		8.00
107901	L42612	Hs.335952	keratin 6B	3.40	
107922	BE153855	Hs.61460	Ig superfamily receptor LNIR	2.88	
107932	AW392555	Hs.18878	hypothetical protein FLJ21620	7.50	
108015	AW298357	Hs.49927	protein kinase NYD-SP15		23.40
108056	AA043675	Hs.62633	ESTs		12.80
108075	AI867370	Hs.139709	hypothetical protein FLJ12572		12.80
108187	BE245374	Hs.27842	hypothetical protein FLJ11210	7.00	
108296	N31256	Hs.161623	ESTs	6.60	
108305	AA071391		gb:zm61a06.r1 Stratagene fibroblast (937		11.80
108393	AA075211		gb:zm86a08.r1 Stratagene ovarian cancer		11.80
108480	AL133092	Hs.68055	hypothetical protein DKFZp434I0428		20.80
108554	AA084948		gb:zn13b09.s1 Stratagene hNT neuron (937	6.40	
108573	AA086005		gb:zlb4c04.s1 Stratagene colon (937204)		25.40
108584	AA088326	Hs.120905	Homo sapiens cDNA FLJ11448 fis, clone HE	9.60	
108597	AK000292	Hs.278732	hypothetical protein FLJ20285		14.60
108695	AB029000	Hs.70823	KIAA1077 protein	3.00	
108699	AA121514	Hs.70832	ESTs		10.00
108700	AA121518	Hs.193540	ESTs, Moderately similar to 2109260A B c		11.00
108780	AU076442	Hs.117938	collagen, type XVII, alpha 1	11.21	

5	108810	AW295647	Hs.71331	hypothetical protein MGC5350	8.50			
	108816	AA130884	Hs.270501	ESTs, Moderately similar to ALU2_HUMAN		7.40		
	108857	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	4.00			
	108860	AA133334	Hs.129911	ESTs	6.09			
	108937	AL050107	Hs.24341	transcriptional co-activator with PDZ-bl	3.00			
10	109010	NM_007240	Hs.44229	dual specificity phosphatase 12	2.69			
	109121	BE389387	Hs.49767	NADH dehydrogenase (ubiquinone) Fe-S pro			4.53	
	109166	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rakines	10.58			
	109227	AA766998	Hs.85874	Human DNA sequence from clone RP11-16L21		9.00		
	109415	U80736	Hs.110826	trinucleotide repeat containing 9		51.40		
15	109418	AI866946	Hs.161707	ESTs			11.00	
	109454	AA232255	Hs.295232	ESTs, Moderately similar to A46010 X-II		17.60		
	109502	AW967069	Hs.211556	hypothetical protein MGC5487		9.49		
	109543	AA564994	Hs.222851	ESTs		12.67		
	109548	H17800	Hs.7154	ESTs			10.40	
20	109680	AB037734	Hs.4993	KIAA1313 protein		33.20		
	109700	F09609		gb:HSC33H092 normalized infant brain cDN			16.00	
	109704	AI743880	Hs.12876	ESTs		11.00		
	109792	R49625		gb:yg61f03.s1 Soares infant brain 1NIB H			12.60	
	109981	BE548208	Hs.26090	hypothetical protein FLJ20272	4.00			
25	109998	AL042201	Hs.21273	transcription factor NYD-sp10		7.80		
	110039	H11938	Hs.21907	histone acetyltransferase		7.00		
	110156	AA581322	Hs.4213	hypothetical protein MGC16207			4.24	
	110500	AA907723	Hs.36962	ESTs	4.50			
	110551	AW450381	Hs.14529	ESTs		8.60		
30	110561	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	3.06			
	110854	BE612992	Hs.27931	hypothetical protein FLJ10607 similar to		6.80		
	110886	AW274992	Hs.72249	three-PDZ containing protein similar to		8.80		
	110916	BE178102	Hs.24349	ESTs		6.80		
	111003	N52980	Hs.83765	dihydrofolate reductase			16.80	
35	111337	AA837396	Hs.263925	LIS1-interacting protein NUDE1, rat homo	2.54			
	111434	R01608	Hs.142736	ESTs			9.80	
	111439	AI476429	Hs.19238	ESTs			10.40	
	111540	U82670	Hs.9786	zinc finger protein 275		15.40		
	111597	R11499	Hs.189716	ESTs			9.20	
40	111895	T80581	Hs.12723	Homo sapiens clone 25153 mRNA sequence		6.80		
	111929	AF027208	Hs.112360	prominin (mouse)-like 1			14.67	
	112054	R43590		gb:yc85g02.s1 Soares infant brain 1NIB H		10.80		
	112210	R49645	Hs.7004	ESTs			10.20	
	112244	AB029000	Hs.70823	KIAA1077 protein	2.99			
45	112382	R59604		gb:yh07g12.s1 Soares infant brain 1NIB H		6.60		
	112392	R60763	Hs.193274	ESTs, Moderately similar to I57588 HSrel		7.10		
	112442	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	3.00			
	112539	R70318	Hs.339730	ESTs			37.20	
	112772	AI992283	Hs.35437	ESTs, Moderately similar to I38026 MLN 6			14.60	
50	112869	BE261750	Hs.4747	dyskeratosis congenita 1, dyskerin				4.83
	112935	R71449	Hs.268760	ESTs	2.73			
	112970	AA694010	Hs.6932	Homo sapiens clone 23809 mRNA sequence			12.00	
	112973	AB033023	Hs.318127	hypothetical protein FLJ10201	11.50			
	112992	AL157425	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (f		10.89		
55	113063	W15573	Hs.5027	ESTs, Weakly similar to A47582 B-cell gr	15.00			
	113073	N39342	Hs.103042	microtubule-associated protein 1B		15.31		
	113078	T40444	Hs.118354	CAT56 protein		7.00		
	113238	R45467	Hs.189813	ESTs			41.20	
	113591	T91881	Hs.200597	KIAA0583 gene product			9.40	
60	113702	T97307		gb:ye53h05.s1 Soares fetal liver spleen	25.00			
	113844	AI369275	Hs.243010	Homo sapiens cDNA FLJ14445 fts, clone HE			13.91	
	113984	R96696	Hs.35588	ESTs		7.80		
	114073	R44953	Hs.22908	Homo sapiens mRNA; cDNA DKFZp434J1027 (f	3.42			
	114162	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase		7.20		
65	114208	AL049466	Hs.7859	ESTs		6.74		
	114251	H15261	Hs.21948	ESTs			33.20	
	114285	R44338	Hs.22974	ESTs			13.20	
	114313	H18456	Hs.27946	ESTs			10.00	
	114339	AA782845	Hs.22790	ESTs		7.80		
70	114407	BE539976	Hs.103305	Homo sapiens mRNA; cDNA DKFZp434B0425 (f				4.14
	114560	AI452469	Hs.165221	ESTs			9.80	
	114699	AA127386		gb:zn90d09.r1 Stratagene lung carcinoma		7.60		
	114767	AI859865	Hs.154443	minichromosome maintenance deficient (S	3.21			
	114793	AA158245		gb:zo76c03.s1 Stratagene pancreas (93720		6.00		
75	114833	AI417215	Hs.87159	hypothetical protein FLJ12577			11.40	
	115047	BE270930	Hs.82916	chaperonin containing TCP1, subunit 6A (4.31
	115060	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3				4.03
	115097	AA256213	Hs.72010	ESTs			35.40	
	115113	AA256460		gb:zr81a04.s1 Soares_NhHMPu_S1 Homo sapi			15.20	
80	115123	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m				4.19
	115134	AW968073	Hs.194331	ESTs, Highly similar to A55713 inositol			12.40	
	115291	BE545072	Hs.122579	hypothetical protein FLJ10461	25.00			
	115347	AA356792	Hs.334824	hypothetical protein FLJ14825		7.00		
	115414	AA662240	Hs.283099	AF15q14 protein	3.25			
85	115522	BE614387	Hs.333893	c-Myc target JPO1	3.68			
	115536	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	10.50			
	115566	AI142336	Hs.43977	Human DNA sequence from clone RP11-196N1			24.40	
	115645	AI207410	Hs.69280	Homo sapiens, clone IMAGE:3636299, mRNA,	4.17			
	115648	AW016811	Hs.234478	Homo sapiens cDNA: FLJ22648 fts, clone H		6.00		

5	115652	BE093589	Hs.38178	hypothetical protein FLJ23468	3.81			
	115697	D31382	Hs.63325	transmembrane protease, serine 4	62.14			
	115793	AA424883	Hs.70333	hypothetical protein MGC10753			11.80	
	115816	BE042915	Hs.287588	Homo sapiens cDNA FLJ13675 fis, clone PL			9.71	
	115882	AA291377	Hs.50831	ESTs		27.40		
10	115906	AI767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	2.53			
	115909	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	11.82			
	115965	AA001732	Hs.173233	hypothetical protein FLJ10970			34.29	
	115978	AL035864	Hs.69517	cDNA for differentially expressed CO16 g			8.23	
	115985	AA447709	Hs.268115	ESTs, Weakly similar to T08599 probable	3.00			
15	116090	AI591147	Hs.61232	ESTs	5.17			
	116096	AA682382	Hs.59982	ESTs		8.20		
	116127	AF126743	Hs.279884	DNAJ domain-containing		10.60		
	116157	BE439838	Hs.44298	mitochondrial ribosomal protein S17			5.82	
	116190	AI949095	Hs.67776	ESTs, Weakly similar to T22341 hypotheti			4.08	
20	116278	NM_003686	Hs.47504	exonuclease 1	9.50			
	116335	AK001100	Hs.41690	desmocollin 3	3.67			
	116496	AW450694	Hs.21433	hypothetical protein DKFZp547J036		7.00		
	116503	AI925316	Hs.212617	ESTs			12.60	
	116674	AI768015	Hs.92127	ESTs		32.00		
25	116929	AA586922	Hs.80475	polymerase (RNA) II (DNA directed) polyp	7.60			
	116973	AI702054	Hs.166982	phosphatidylinositol glycan, class F	9.80			
	116993	AI417023	Hs.40478	ESTs			10.20	
	117079	H92325		gb:ys85f05.s1 Soares retina N2b4HR Homo			15.20	
	117317	AI263517	Hs.43322	ESTs			13.40	
30	117326	N23629	Hs.241420	Homo sapiens mRNA for KIAA1756 protein,			20.60	
	117396	W20128	Hs.296039	ESTs			10.60	
	117412	N32536	Hs.42645	ESTs			16.00	
	117519	N32528	Hs.146286	kinesin family member 13A			9.11	
	117693	AW179019	Hs.112110	mitochondrial ribosomal protein L42			4.01	
35	117721	N46100	Hs.93939	EST			19.80	
	117881	AF161470	Hs.260622	butyrate-induced transcript 1	2.71			
	117903	AA768283	Hs.47111	ESTs			17.80	
	117992	AI015709	Hs.172089	Homo sapiens mRNA; cDNA DKFZp586i2022 (f			10.60	
	118013	AI674126	Hs.94031	ESTs			4.17	
40	118017	AI813444	Hs.42197	ESTs		8.82		
	118186	N22886	Hs.42380	ESTs		7.00		
	118325	AI868065	Hs.166184	intersectin 2			13.80	
	118367	N84269	Hs.48946	EST		6.14		
	118368	N64339	Hs.48956	gap junction protein, beta 6 (connexin 3	3.14			
45	118472	AL167545	Hs.42179	bromodomain and PHD finger containing, 3		12.40		
	118709	AA232970	Hs.293774	ESTs			12.20	
	119025	BE003760	Hs.55209	Homo sapiens mRNA; cDNA DKFZp434K0514 (f	4.50			
	119027	AF086161	Hs.114611	hypothetical protein FLJ11808	3.22			
	119052	R10889		gb:yf38d02.s1 Soares fetal liver spleen		9.60		
50	119164	AF221993	Hs.46743	McKusick-Kaufman syndrome		6.60		
	119186	AI979147	Hs.101265	hypothetical protein FLJ22593			10.80	
	119243	T12603		gb:CHR90123 Chromosome 9 exon II Homo sa			9.44	
	119490	AA195276	Hs.263858	ESTs, Moderately similar to B34087 hypot			11.80	
	119499	AI918906	Hs.55080	ESTs		14.80		
55	119599	W45552		gb:zc26d03.s1 Soares_senescent_fibroblas		12.60		
	119780	NM_016625	Hs.191381	hypothetical protein	17.00			
	119845	W79123	Hs.58561	G protein-coupled receptor 87	13.50			
	119941	AA699485	Hs.58896	ESTs		8.00		
	119994	AA642402	Hs.59142	ESTs	7.73			
60	120102	W67353	Hs.170218	KIAA0251 protein		39.60		
	120104	AK000123	Hs.180479	hypothetical protein FLJ20118	2.91			
	120294	AK000059	Hs.153881	Homo sapiens NY-REN-62 antigen mRNA, par		8.20		
	120486	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	8.73			
	120599	AA804448	Hs.104463	ESTs		7.00		
65	120699	AI683243	Hs.97258	ESTs, Moderately similar to S29539 ribos		9.40		
	120715	AA292700		gb:zs59a06.s1 NCL_CGAP_GCB1 Homo sapiens			10.00	
	120821	Y19062	Hs.96870	staufer (Drosophila, RNA-binding protein			13.80	
	120859	AA826434	Hs.1619	achaete-scute complex (Drosophila) homol		9.00		
	120880	AA360240	Hs.97019	EST	15.60			
70	120983	AA398209	Hs.97587	EST		27.66		
	121034	AL389951	Hs.271623	nucleoporin 50kD		20.80		
	121121	AA399371	Hs.189095	similar to SALL1 (sal (Drosophila))-like		22.80		
	121313	AA402713	Hs.97872	ESTs			10.00	
	121369	AW450737	Hs.128791	CGI-09 protein	25.71			
75	121376	AA448103	Hs.187958	solute carrier family 6 (neurotransmitte			5.42	
	121476	AA412311	Hs.97903	ESTs		8.30		
	121509	AA868939	Hs.97888	ESTs		8.59		
	121553	AA412488	Hs.48820	TATA box binding protein (TBP)-associat	18.50			
	121753	AK000552	Hs.323518	WD repeat domain 5	7.00			
80	121838	AA425680	Hs.98441	ESTs			10.40	
	121857	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	6.00			
	121991	AA430058	Hs.98649	EST			12.20	
	122089	AW016543	Hs.98682	hypothetical protein FKSG32		8.60		
	122105	AW241685	Hs.98699	ESTs		6.14		
85	122163	AA435702	Hs.98829	EST			10.40	
	122318	AA429743		gb:zv60b05.r1 Soares_testis_NHT Homo sap			18.20	
	122335	AA443258	Hs.241551	chloride channel, calcium activated, fam	13.50			
	122338	AA443311	Hs.98998	ESTs	4.80			
	122414	AK13473	Hs.99087	ESTs, Weakly similar to S47073 finger pr		8.00		

5	122512	AF053305	Hs.98658	budding uninhibited by benzimidazoles 1	8.80		
	122516	AA449352	Hs.99217	ESTs		9.20	9.40
	122702	AI220089	Hs.99439	ESTs			
	122852	AI580056	Hs.98992	ESTs			10.40
	122925	AW268962	Hs.111335	ESTs	6.80		
10	123005	AW369771	Hs.52620	integrin, beta 8		12.60	
	123044	AK001035	Hs.130881	B-cell CLL/lymphoma 11A (zinc finger pro			5.35
	123160	AA488687	Hs.284235	ESTs, Weakly similar to 138022 hypothe		6.06	
	123315	AA496369		gb:zv37d10.s1 Soares ovary tumor NbHOT H		12.40	
	123329	Z47542	Hs.179312	small nuclear RNA activating complex, po		11.80	
15	123497	AA765256	Hs.135191	ESTs, Weakly similar to unnamed protein	12.00		
	123518	AL035414	Hs.21068	hypothetical protein		13.00	
	123519	AW015887	Hs.112574	ESTs	12.20		
	123614	AK000492	Hs.98806	hypothetical protein		7.80	
	123616	AA680003	Hs.109363	Homo sapiens cDNA: FLJ23603 fis, clone L			10.60
20	123673	BE550112	Hs.158549	ESTs, Weakly similar to T2D3_HUMAN TRANS	23.00		
	123727	AI083986	Hs.282977	hypothetical protein FLJ13490	7.00		
	123731	AA609839		gb:ae62f01.s1 Stralagene lung carcinoma		9.80	
	123752	AA227714	Hs.179703	KIAA0129 gene product	3.50		
	123900	AA621223	Hs.112953	EST			12.80
25	124006	AI147155	Hs.270016	ESTs	97.00		
	124059	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypothe	3.02		
	124069	AF134160	Hs.7327	claudin 1		27.80	
	124181	T96509	Hs.248549	ESTs, Moderately similar to S65657 alpha			35.80
	124273	AA457211	Hs.8858	bromodomain adjacent to zinc finger doma	7.20		
30	124297	AL080215	Hs.102301	Homo sapiens mRNA; cDNA DKFp586J0323 (f			11.00
	124305	AW963221		gb:EST375294 MAGe resequences, MAGH Homo			16.00
	124676	AI360119.comp	Hs.181013	phosphoglycerate mutase 1 (brain)			6.08
	124874	BE550182	Hs.127826	RaiGEF-like protein 3, mouse homolog		21.00	
	124904	AK000483	Hs.93872	KIAA1682 protein	9.40		
35	124969	AI650360	Hs.100256	ESTs			10.80
	125000	T58615	Hs.110640	ESTs			9.80
	125201	AA693960	Hs.103158	ESTs, Weakly similar to T33296 hypothe	7.60		
	125266	W90022	Hs.186809	ESTs, Highly similar to LCT2_HUMAN LEUKO	6.59		
	125299	T32982	Hs.102720	ESTs			9.57
40	125356	AI057052	Hs.133554	ESTs, Weakly similar to Z195_HUMAN ZINC			14.00
	125370	AA256743	Hs.134168	Homo sapiens, Similar to KIAA0092 gene p	8.20		
	125418	AA777690	Hs.188501	ESTs			13.20
	125433	AL162066	Hs.54320	hypothetical protein DKFp762D096	21.40		
	125437	AI609449	Hs.140197	ESTs	6.98		
45	125446	BE219987	Hs.166982	phosphatidylinositol glycan, class F	8.80		
	125711	AA305800	Hs.5672	hypothetical protein AF140225		11.20	
	125756	BE174587	Hs.289721	growth arrest specific transcript 5			4.31
	125757	AI274906	Hs.166835	ESTs, Highly similar to 1814460A p53-ass			15.60
	125769	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	3.20		
50	125839	AW836261	Hs.337717	ESTs	8.20		
	125850	W85858	Hs.99804	ESTs	2.65		
	125875	H14480		gb:ym18b09.r1 Soares infant brain 1N1B H	7.40		
	125924	BE272506	Hs.82109	syndecan 1			4.23
	125972	AI927475	Hs.35406	ESTs, Highly similar to unnamed protein			3.98
55	126034	H60340		gb:yr39b04.r1 Soares fetal liver spleen		10.60	
	126327	AA432266	Hs.44648	ESTs	11.60		
	126345	N49713		gb:yv23f06.s1 Soares fetal liver spleen	6.67		
	126435	AW614529	Hs.285847	CGI-19 protein		10.60	
	126487	AA283809	Hs.184601	solute carrier family 7 (cationic amino			4.38
60	126521	AI475110	Hs.203933	ESTs	6.60		
	126522	W31912		gb:zc76d03.s1 Pancreatic Islet Homo sapi		14.80	
	126543	AL035864	Hs.69517	cDNA for differentially expressed CO16 g			4.01
	126567	AA058394	Hs.57887	ESTs, Weakly similar to KIAA0758 protein	7.80		
	126605	AA676910		gb:zj65h07.s1 Soares_fetal_liver_spleen_		11.60	
65	126627	AA497044	Hs.20887	hypothetical protein FLJ10392		14.60	
	126628	N49776	Hs.170994	hypothetical protein MGC10946	8.00		
	126737	AW976516	Hs.283707	Homo sapiens cDNA: FLJ21354 fis, clone C	2.92		
	126795	AW976076	Hs.172589	nuclear phosphoprotein similar to S. cer	7.50		
	126802	AW805510	Hs.97056	hypothetical protein FLJ21634	11.60		
70	126892	AF121856	Hs.284291	sorting nexin 6	3.50		
	126928	AA480902	Hs.137401	ESTs			22.83
	126979	AA210954		gb:zq89h10.r1 Stralagene hNT neuron (937			11.80
	126986	AI279892	Hs.46801	sorting nexin 14			11.60
	126992	AI809521		gb:wf30e03.x1 Soares_NFL_T_GBC_S1 Homo s			20.80
75	127066	R25066		gb:yg42c07.r1 Soares Infant brain 1N1B H			27.60
	127099	AA347668		gb:EST54026 Fetal heart II Homo sapiens			21.60
	127139	AA830233	Hs.293585	ESTs			11.20
	127209	AA305023	Hs.81964	SEC24 (S. cerevisiae) related gene famil	3.10		
	127221	BE062109	Hs.241551	chloride channel, calcium activated, fam	2.76		
80	127225	AA315933	Hs.120879	ESTs			16.80
	127313	AK002014	Hs.47546	Homo sapiens cDNA FLJ11458 fis, clone HE	14.00		
	127444	AW978474	Hs.7560	Homo sapiens mRNA for KIAA1729 protein,			13.60
	127500	AW971353	Hs.162115	ESTs	11.20		
	127524	AI243596	Hs.94830	ESTs, Moderately similar to T03094 A-kin		7.80	
85	127540	N45572	Hs.105362	Homo sapiens, clone MGC:18257, mRNA, com	3.53		
	127599	AA613204	Hs.150399	ESTs			13.80
	127609	X80031	Hs.530	collagen, type IV, alpha 3 (Goodpasture			28.00
	127662	W80755	Hs.8294	KIAA0195 gene product			19.80
	127668	AI343257	Hs.139993	ESTs			11.20

	127746	AI239495	Hs.120189	ESTs			14.18
	127812	AA741368	Hs.291434	ESTs	4.50		
	127817	AA836841	Hs.163085	ESTs			24.60
5	127959	AI302471	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L			9.20
	127960	AI613226	Hs.41569	phosphatidic acid phosphatase type 2A			16.83
	127969	F06498	Hs.93748	Homo sapiens cDNA FLJ14676 fis, clone NT	13.60		
	128015	Z21169	Hs.334659	hypothetical protein MGC14139	7.00		
	128027	AI433721	Hs.164153	ESTs			37.40
	128077	AI310330	Hs.128720	ESTs			9.60
10	128168	NM_008147	Hs.11801	interferon regulatory factor 6			9.24
	128226	AI284940	Hs.289082	GM2 ganglioside activator protein	19.00		
	128305	AI954968	Hs.279009	matrix Gla protein			10.40
	128341	AA191420	Hs.185030	ESTs	9.00		
	128527	AA504583	Hs.101047	transcription factor 3 (E2A immunoglobul			4.30
15	128539	R46163	Hs.258618	ESTs	12.60		
	128568	H12912	Hs.274691	adenylate kinase 3			4.56
	128572	AA933022	Hs.256583	interleukin enhancer binding factor 3, 9		10.00	
	128777	AI878918	Hs.10526	cysteine and glycine-rich protein 2	16.80		
	128781	N71826	Hs.105465	small nuclear ribonucleoprotein polypept			4.48
20	128786	AJ000152	Hs.105924	defensin, beta 2	8.12		
	128920	AA622037	Hs.166468	programmed cell death 5			4.62
	128924	BE279383	Hs.26557	plakophilin 3			4.04
	128971	H05132	Hs.107510	ESTs	12.60		
	129008	AL079648	Hs.301088	ESTs	8.80		
25	129041	BE382756	Hs.169902	solute carrier family 2 (facilitated glu			6.05
	129075	BE250162	Hs.83765	dihydrofolate reductase	2.59		
	129105	AI769160	Hs.108681	Homo sapiens brain tumor associated prot		6.67	
	129189	AB023179	Hs.9059	KIAA0962 protein	8.00		
	129229	AF013758	Hs.109643	polyadenylate binding protein-interactin	4.00		
30	129241	AI878857	Hs.109706	hematological and neurological expressed			4.06
	129300	W94197	Hs.110165	ribosomal protein L26 homolog	2.55		
	129404	AI267700	Hs.317584	ESTs	18.00		
	129457	X61959	Hs.207776	aspartylglucosaminidase	6.50		
	129466	L42583	Hs.334309	keratin 6A	12.94		
35	129494	AI148976	Hs.112062	ESTs			11.00
	129605	AF061812	Hs.115947	keratin 16 (focal non-epidermolytic palm			4.46
	129641	AI911527	Hs.11805	ESTs			12.00
	129665	AW163331	Hs.118778	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic			4.70
40	129703	BE388665	Hs.179999	Homo sapiens, clone IMAGE:3457003, mRNA			4.02
	129720	AA156214	Hs.12162	APMCF1 protein			5.71
	129748	M16707	Hs.123053	H4 histone, family 2	3.50		
	129890	AI868872	Hs.282804	hypothetical protein FLJ22704			4.21
	129896	BE295568	Hs.13225	UDP-Gal:betaGlcNAc beta 1,4- galactosyl	2.56		
45	129945	BE514376	Hs.165998	PAI-1 mRNA-binding protein		7.00	
	130010	AA301116	Hs.142838	nucleolar phosphoprotein Nopp34			4.03
	130026	T40480	Hs.332112	EST	6.40		
	130080	X14850	Hs.147097	H2A histone family, member X			4.65
	130149	AW067805	Hs.172665	methyleneletrahydrofolate dehydrogenase	2.74		
50	130285	AA063546	Hs.75981	ubiquitin specific protease 14 (tRNA-gua		7.40	
	130441	U63630	Hs.155637	protein kinase, DNA-activated, catalytic			3.91
	130482	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	4.87		
	130500	AB007913	Hs.158291	KIAA0444 protein			9.60
	130524	U89995	Hs.159234	forkhead box E1 (thyroid transcription f		13.40	
	130541	X05608	Hs.211584	neurofilament, light polypeptide (68kD)		8.20	
55	130553	AF062649	Hs.252587	pituitary tumor-transforming 1			6.06
	130567	AA383092	Hs.1608	replication protein A3 (14kD)		7.00	
	130577	M69241	Hs.162	insulin-like growth factor binding prote	3.04		
	130627	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	3.87		
60	130648	AI458165	Hs.17296	hypothetical protein MGC2376			16.20
	130697	L29472	Hs.1802	major histocompatibility complex, class			17.80
	130744	H59696	Hs.18747	POP7 (processing of precursor, S. cerevi			5.28
	130800	AI187292	Hs.19574	hypothetical protein MGC5469			4.43
	130867	NM_001072	Hs.284239	UDP glycosyltransferase 1 family, polype	16.84		
65	130869	J03626	Hs.2057	uridine monophosphate synthetase (orotat			4.92
	130925	AF093419	Hs.169378	multiple PDZ domain protein			9.60
	130994	W17044	Hs.327337	ESTs	12.40		
	131028	AI879165	Hs.2227	CCAAT/enhancer binding protein (C/EBP),	10.21		
	131031	NM_001650	Hs.288650	aquaporin 4			9.80
70	131041	T15767	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,			9.60
	131058	W28545	Hs.101514	hypothetical protein FLJ10342			17.00
	131090	AI143139	Hs.2288	visinin-like 1	2.74		
	131112	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (f		8.80	
	131148	AW953575	Hs.303125	p53-induced protein PIGPC1	3.12		
75	131185	BE280074	Hs.23960	cyclin B1	3.07		
	131200	BE540516	Hs.293732	hypothetical protein MGC3195	3.07		
	131219	W25005	Hs.24395	small inducible cytokine subfamily B (Cy	2.87		
	131257	AW339037	Hs.24908	ESTs			14.67
	131375	AW293165	Hs.143134	ESTs		19.20	
80	131460	NM_003729	Hs.27076	RNA 3'-terminal phosphate cyclase	3.50		
	131476	AI521663	Hs.334644	hypothetical protein FLJ14668	15.00		
	131510	BE245374	Hs.27842	hypothetical protein FLJ11210		7.80	
	131646	BE302464	Hs.30057	MRS2 (S. cerevisiae)-like, magnesium hom		7.00	
	131786	BE000971	Hs.306083	Novel human gene mapping to chromosome 22	2.65		
85	131839	AB014533	Hs.33010	KIAA0633 protein			35.20
	131843	AA192315	Hs.184062	putative Rab5-interacting protein			4.11

	131877	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	19.00			
	131885	BE502341	Hs.3402	ESTs	6.48			
	131921	AA456093	Hs.34720	ESTs		8.40		
5	131945	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	56.00			
	131958	NM_014062	Hs.3566	ART-4 protein			3.82	
	131965	W79283	Hs.35962	ESTs	3.03			
	132000	AW247017	Hs.36978	melanoma antigen, family A, 3		9.80		
	132040	NM_001196	Hs.315589	Homo sapiens cDNA: FLJ22373 fis, clone H	3.30			
10	132109	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	21.00			
	132114	NM_006152	Hs.40202	lymphoid-restricted membrane protein		8.40		
	132162	AA315805	Hs.94560	desmoglein 2			12.25	
	132164	AI752235	Hs.41270	procollagen-lysine, 2-oxoglutarate 5-dio	2.70			
	132180	NM_004460	Hs.418	fibroblast activation protein, alpha	2.71			
	132181	AW961231	Hs.16773	Homo sapiens clone TCCCA00427 mRNA sequ	3.83			
15	132182	NM_014210	Hs.70499	ecotropic viral integration site 2A			13.20	
	132231	AA662910	Hs.42635	hypothetical protein DKFZp434K2435	9.50			
	132277	AK001745	Hs.184628	hypothetical protein FLJ10883	4.50			
	132328	NM_014787	Hs.44896	DnaJ (Hsp40) homolog, subfamily B, membe			9.20	
	132394	AK001680	Hs.30488	DKFZP434F091 protein			19.80	
20	132424	AA417878	Hs.48401	ESTs, Moderately similar to ALU8_HUMAN A		8.60		
	132528	T78736	Hs.50758	SMC4 (structural maintenance of chromoso		27.40		
	132543	BE568452	Hs.5101	protein regulator of cytokinesis 1	4.38			
	132544	L19778	Hs.51011	H2A histone family, member P		7.00		
25	132550	AW969253	Hs.170195	bone morphogenetic protein 7 (osteogenic	2.64			
	132552	BE621985	Hs.296922	thiopurine S-methyltransferase			15.83	
	132581	AK000631	Hs.52256	hypothetical protein FLJ20624		6.60		
	132617	AF037335	Hs.5338	carbonic anhydrase XII	4.95			
	132638	AI798870	Hs.54277	DNA segment on chromosome X (unique) 992		8.20		
30	132653	Z15008	Hs.54451	laminin, gamma 2 (nicotin (100kD), kalni	4.38			
	132669	W38586	Hs.293981	guanine nucleotide binding protein (G pr			4.36	
	132710	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	4.60			
	132771	Y10275	Hs.56407	phosphoserine phosphatase	3.71			
	132799	W73311	Hs.169407	SAC2 (suppressor of actin mutations 2,			9.48	
35	132833	U78525	Hs.57783	eukaryotic translation initiation factor			5.83	
	132892	AW834050	Hs.9973	tensin			12.00	
	132906	BE613337	Hs.234896	germinin	3.09			
	132959	AW014195	Hs.61472	ESTs, Weakly similar to YAE6_YEAST HYPOT			3.87	
	132962	AA576635	Hs.6153	CGI-48 protein	3.50			
40	132990	X77343	Hs.334334	transcription factor AP-2 alpha (activat	6.18			
	132994	AA112748	Hs.279905	clone HQ0310 PRO0310p1	3.19			
	133000	AL042444	Hs.62402	p21/Cdc42/Rac1-activated kinase 1 (yeast	2.96			
	133050	X73424	Hs.63788	propionyl Coenzyme A carboxylase, beta p	2.55			
	133083	BE244588	Hs.6456	chaperonin containing TCP1, subunit 2 (b			4.00	
45	133086	L17131	Hs.139800	high-mobility group (nonhistone chromoso			8.96	
	133134	AF198620	Hs.65648	RNA binding motif protein 8A			4.28	
	133155	M58583	Hs.662	cerebellin 1 precursor			10.60	
	133181	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	3.00			
	133204	BE267696	Hs.254105	enolase 1, (alpha)			4.63	
50	133412	U41493	Hs.73112	guanine nucleotide binding protein (G pr		12.50		
	133421	AF134160	Hs.7327	claudin 1	2.85			
	133451	AW970026	Hs.73818	ubiquinol-cytochrome c reductase hinge p			4.66	
	133453	AI659306	Hs.73826	protein tyrosine phosphatase, non-recept		6.80		
	133504	NM_004416	Hs.74316	desmoplakin (DPI, DPII)	6.14			
55	133506	BE562958	Hs.74346	hypothetical protein MGC14353			4.55	
	133615	M62843	Hs.75236	ELAV (embryonic lethal, abnormal vision,			17.80	
	133627	NM_002047	Hs.75280	glycyl-tRNA synthetase			4.85	
	133649	U25849	Hs.75393	acid phosphatase 1, soluble			6.34	
	133669	NM_006925	Hs.166975	splicing factor, arginine/serine-rich 5			14.00	
60	133749	L20852	Hs.10018	solute carrier family 20 (phosphate tran		6.11		
	133776	BE268649	Hs.177766	ADP-ribosyltransferase (NAD+; poly (ADP-			4.91	
	133865	AB011155	Hs.170290	discs, large (Drosophila) homolog 5	3.07			
	133946	AJ001258	Hs.173878	NIPSNAP, C. elegans, homolog 1			4.60	
	133973	N55540	Hs.78026	ESTs, Weakly similar to similar to ankyr			13.00	
65	134047	BE262529	Hs.78771	phosphoglycerate kinase 1			3.85	
	134098	BE513171	Hs.79086	mitochondrial ribosomal protein L3	2.56			
	134107	NM_005629	Hs.187958	solute carrier family 6 (neurotransmitte		8.20		
	134112	AW449809	Hs.79150	chaperonin containing TCP1, subunit 4 (d			4.08	
	134158	U15174	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	31.00			
70	134160	T98152	Hs.79432	fibrillin 2 (congenital contractual ara		24.60		
	134168	AA398908	Hs.181634	Homo sapiens cDNA: FLJ23602 fis, clone L			6.71	
	134185	AA285136	Hs.301914	neuronal specific transcription factor D			14.74	
	134201	L35035	Hs.79886	ribose 5-phosphate isomerase A (ribose 5		8.40		
	134272	X76040	Hs.278614	protease, serine, 15	4.50			
75	134276	BE083936	Hs.80976	antigen identified by monoclonal antibod		9.00		
	134353	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, m			16.40	
	134367	AA339449	Hs.82265	phosphoryl-glycinamide formyltransfer	2.80			
	134380	AU077143	Hs.179565	minichromosome maintenance deficient (S.	4.68			
	134423	H53497	Hs.83006	CGI-139 protein			3.84	
	134469	AA279661	Hs.83753	small nuclear ribonucleoprotein polypept			5.81	
80	134470	X54942	Hs.83758	CDC28 protein kinase 2			4.21	
	134498	AW246273	Hs.84131	threonyl-tRNA synthetase			7.30	
	134502	BE148534	Hs.84168	UV-B repressed sequence, HUR 7		13.60		
	134510	NM_002757	Hs.250870	mitogen-activated protein kinase kinase			9.70	
85	134548	N95406	Hs.333495	Deleted in split-hand/split-foot 1 regio			4.63	
	134654	AK001741	Hs.8739	hypothetical protein FLJ10879	6.00			

WO 02/086443

PCT/US02/12476

134724	AF045239	Hs.321576	ring finger protein 22			12.00
134743	AA044163	Hs.89463	potassium large conductance calcium-acti	4.00		
134781	AA374372	Hs.89626	parathyroid hormone-like hormone		25.20	
134806	AD001628	Hs.89718	spermine synthase			4.58
134853	BE268326	Hs.90280	5-aminimidazole-4-carboxamide ribonucle			4.79
134859	D26488	Hs.90315	KIAA0007 protein		6.20	
134891	R51083	Hs.90787	ESTs		7.40	
134960	BE246400	Hs.285178	acetyl-Coenzyme A transporter	4.00		
134993	BE409809	Hs.301005	purine-rich element binding protein B			4.48
135047	AL134187	Hs.93597	cyclin-dependent kinase 5, regulatory su	9.50		
135080	AI761180	Hs.94211	cd1 (required for cell differentiation,	5.00		
135103	NM_003428	Hs.9450	zinc finger protein 84 (HPF2)		11.00	
135145	AW014729	Hs.95282	nuclear factor related to kappa B bindin			4.01
135184	U13222	Hs.96028	forkhead box D1		7.00	
135242	AI583187	Hs.9700	cyclin E1	13.50		
135288	AW023482	Hs.97849	ESTs	6.46		
135289	AW372569	Hs.9788	hypothetical protein MGC10924 similar to		8.80	
135355	AK001652	Hs.99423	ATP-dependent RNA helicase	10.00		
135371	NM_006025	Hs.997	protease, serine, 22	8.00		
135393	L11244	Hs.99886	complement component 4-binding protein,			14.60

TABLE 5B shows the accession numbers for those primekeys lacking unigenelD's for Table 5A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Key: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Key	CAT number	Accessions
117079	1621717_1	H92325 T97125
124305	242183_1	AW963221 AA344870 AA344871 H93331
101502	18202_6	M26958
109792	754958_1	R49625 F10674
126034	1598157_1	H60340 N91637
102768	44641_1	U82321 H66077
126345	1653833_1	N49713 N49819 W03810
127066	1703458_1	R25066 R20144 R20145 Z43845
127099	244301_1	AA347668 AW956810 Z44271 F07064 R13506
119243	1774795_1	T12603 T12604
125875	1566433_1	H14480 N98295
112054	1638292_1	R43590 F10439
126979	171411_1	AA210954 AA211007
126992	880655_1	AI809521 H12174 Z42556
122318	292419_1	AA429743 AA442754
114699	135322_1	AA127386 R15644 AA127404
114793	150742_1	AA158245 AA158235
108305	111550_1	AA071391 AA069892 AA069891
108393	113411_1	AA075211 AA075245 AA075126 AA074946
100867	Ugr_HT4586	U14622
123731	genbank_AA609839	AA609839
109700	genbank_F09609	F09609
120715	genbank_AA292700	AA292700
113702	genbank_T97307	T97307
115113	genbank_AA256460	AA256460
101045	entrez_J05614	J05614
108554	genbank_AA084948	AA084948
108573	genbank_AA086005	AA086005
119052	149538_1	R10889 R10888
126522	416020_1	W31912 AI167491
126605	439280_1	AA676910 AA778853 AA778865 W86800
103768	46922_1	W42667 AI580740 AI690440 AI561350 AW467906 AW151450 AI825927 AL041716 AI885600 AI742213 AW248624 AI955498 AA033947 AA845593 AI623711 N68583 C00064 AA193567 AW083868 AW163216 AA191595 AA522778 AI628008 AI915518 AA843508 AI926195 AA176265 AW167963 AA992115 W93647 AW103572 AI862994 AI342059 AA911719 AA176155 AA024712 AA089988 AA205591 AI591107 AI199673 AI811766 AI275832 AI422233 AI191852 AI096682 AI580124 AI683612 AA582453 AA927559 AA486415 T32414 AI084978 H44849 H44848 H20477 T91695 W47039 AA070055 AA024795 AA328855 AA379248 AA379330 AA385580 W25920 W03688 AA448359 AA093881 AW362477 AA089997 AI350265 W93479 N99688 AA932257 AW351469 H68590 AA663402 AA069771 AW087986 AI858420 AA600214 AI970774 AI857712 AI683081 AI885584 AW131150 AI567981 AW002714 AW189973 AW075495 AW168303 AA953714 AW516881 AI357375 AI566663 AW512676 AI570580 AI023690 AA448216 AI079853 AI422707 AA779516 AW026972 AW130082 AW162307 AW438646 AA709332 AW192394 AI167350 AI217879 AI129152 AA719509 AI350480 AA663418 AI003634 AW118546 AA180261 AA442833 AI268625 AA888881 AI038759 AA846723 AI248770 AA993694 AI280335 AI885107 AW518649 AA641563 AA995835 AA582521 AI276744 AA436478 AI017360 AI620763 AI859887 N73926 AI076327 AI741615 AI160617 AW172819 AI492005 AA677429 AA996334 AI693771 AI950039 AI245629 AI288515 AI866186 T93293 AA173262 AA599779 AI690092 AW439316 AI084555 AI272672 AI583507 AW473219 AA738132 AW473283 AI367492 AA995410 AI689624 AA206353 AI033095 AI040382 AA873630 AI221074 AI934840 AI418680 AA844306 R94503 AA773520 AA843169 AA219425 AA629658 AI811719 AW411275 AI590981 W37907 AI591178 AI684051 AA983238 AA669347 AA976239 AA704570 AI628339 AI884391 AI241580 AI003539 AW176687 AA009650 N34566 AI333493 AI186070 AA070827 AA411683 AI280884 AA872023 AA207255 AA021576 N71953 AI885888 AW076039 T15777 AI537673 AW248048 H09554 W93480 W47001 AW079114 AA063160 AA757453 R60788 AI859431 H20478 AA218882 AA757465 AA100995 AI864135 AI934209 AA070503 H47008 AA219646 W61039 W93907 AW385050 W37967 W78028 AA189007 AA479136 R93650 AA442312 T30287 AA847628 AA180262 AA009649 C03892 AW149464 AA310963 AA219693 AA069747 R29207 AA094784 AA293615 AA447848 AI984167 N90393 C05097 N56499 AW292351 AW149681 AW473258 AA629322 AI004409 AW105577 AI954937 AI811070 AA902422 AW514437 AA535460 AA916877 AW517122 AA974657 AA975649 AW517130 AW517129 F31737 W07688 AA193645 AA378994 AA489273 F32267 W39303 AA021181 N86810 AA406524 AA062553 AA436801 H08985 H15979 N40310

AA436789 AA232172 AW360778 W25862 R60282 AA436530 AA378894 AA187461 AI940535 AA604210 AA089514 AA360421 N88243 N84281
 AA209340 N56174 N88374 AA191088 AW247691 AA249013 AA093111 AA972536 AW298594 AA375893 T12139 W28186 AW243849
 A1288629 AA843996 W15260 A188286 AW248079 R15836

5 119599 genbank_W45552 W45552
 112382 genbank_R59904 R59904
 105264 genbank_AA227934 AA227934
 100071 entrez_A28102 A28102
 123315 714071_1 AA496369 AA496646

10

Table 6A shows 99 genes up-regulated nonsmokers with lung cancer relative to smokers with lung cancer. These genes were selected from 59680 probesets on the Eos/Atfy matrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

15

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title

20

R1: average of AI for samples from non-smokers with adenocarcinoma divided by the 90th percentile of AI for samples from smokers with adenocarcinoma
 R2: average of AI for samples from non-smokers with squamous cell carcinoma divided by the 90th percentile of AI for samples from smokers with squamous cell carcinoma

	Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2
25	100971	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte		3.64
	101174	L17330	Hs.280	pre-T/NK cell associated protein	15.00	
	101296	Y12490	Hs.85092	thyroid hormone receptor interactor 11		2.46
	101304	AA001021	Hs.6685	thyroid hormone receptor interactor 8		12.00
	101806	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias)		2.68
30	101972	S82472		gb:beta-pol=DNA polymerase beta (exon a		2.11
	102274	U30930	Hs.158540	UDP glycosyltransferase 8 (UDP-galactose	7.50	
	102394	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	7.50	
	102832	U92015		gb:Human clone 143789 defective mariner	13.50	
	103010	X52509	Hs.161640	tyrosine aminotransferase	9.50	
35	103439	X98266		gb:H.sapiens mRNA for ligase like protel		2.50
	103563	L02911	Hs.150402	activin A receptor, type I	9.00	
	103857	AI076795	Hs.45033	lacrimal proline rich protein		3.94
	104239	AB002367	Hs.21355	doublecortin and CaM kinase-like 1	13.50	
	104590	AW373062	Hs.83623	nuclear receptor subfamily 1, group 1, m		12.66
40	104907	AA055829	Hs.196701	ESTs, Weakly similar to ALU1_HUMAN ALU	16.50	
	106131	BE514788	Hs.296244	SNARE protein		2.17
	106872	H47233	Hs.30643	ESTs	7.00	
	106872	T56887	Hs.18282	KIAA1134 protein	11.50	
	106960	AA156238	Hs.32501	ESTs		2.38
45	106971	Z43846	Hs.194478	Homo sapiens mRNA; cDNA DKFZp434O1572 (f	9.50	
	107982	AA035375	Hs.57887	ESTs, Weakly similar to KIAA0758 protel		2.95
	108562	AA100796		gb:zmn26c06.s1 Stratagene pancreas (93720	16.50	
	108599	AB018549	Hs.69328	MD-2 protein	13.00	
	108663	BE219231	Hs.292653	ESTs, Weakly similar to T26845 hypothel		2.40
50	109247	AA314907	Hs.85950	ESTs	7.00	
	109630	R44607	Hs.22672	ESTs		5.00
	110193	AI004874	Hs.310764	Homo sapiens mRNA; cDNA DKFZp434M082 (fr	12.50	
	110234	H24458	Hs.32085	EST	16.50	
	110644	R94207	Hs.268889	ESTs, Highly similar to type II CALM/AF1	8.00	
55	110886	AW274992	Hs.72249	three-PDZ containing protein similar to	17.00	
	111057	T79639	Hs.14629	ESTs	16.50	
	111850	AF071594	Hs.110457	Wolf-Hirschhorn syndrome candidate 1	11.00	
	112291	R53972	Hs.26026	ESTs		3.00
	112956	Z43784	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)		2.79
60	113009	T23699	Hs.7246	ESTs		4.50
	113060	BE564162	Hs.250820	hypothetical protein FLJ14827	9.79	
	113073	N39342	Hs.103042	microtubule-associated protein 1B	32.50	
	113074	AK001335	Hs.31137	protein tyrosine phosphatase, receptor t		3.82
	113121	T48011	Hs.8764	EST		2.21
65	113125	AA968672	Hs.8929	hypothetical protein FLJ11362	19.50	
	113757	AA703095	Hs.18631	ESTs		2.65
	113848	W52654	Hs.27099	hypothetical protein FLJ23293 similar to	6.00	
	113884	AI333076	Hs.28529	chromosome 12 open reading frame 2		6.00
	113936	W17056	Hs.83623	nuclear receptor subfamily 1, group 1, m		4.63
70	114875	AA235609	Hs.236443	Homo sapiens mRNA; cDNA DKFZp564N1063 (7.00
	114987	AA251016	Hs.87808	EST		6.00
	115460	AW958439	Hs.38613	ESTs		2.27
	115722	W91892	Hs.59609	ESTs		9.00
	116261	AA481788	Hs.190150	ESTs	9.50	
75	116830	H61037	Hs.70404	ESTs, Weakly similar to ALU2_HUMAN ALU	8.50	
	116970	AB023179	Hs.9059	KIAA0962 protein	7.50	
	117178	H98675	Hs.269034	ESTs		2.68
	117757	AF088019	Hs.46732	EST	7.50	
	118283	AA287747	Hs.173012	ESTs, Weakly similar to A46010 X-linked	16.50	
80	118384	AF217525	Hs.49002	Down syndrome cell adhesion molecule		2.50
	118657	AI822106	Hs.49902	ESTs		2.39
	120328	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi		3.50
	120404	AB023230	Hs.96427	KIAA1013 protein	7.00	
	120524	AA261852	Hs.192905	ESTs	6.00	
85	120688	AW207555	Hs.97093	Homo sapiens cDNA: FLJ23004 fis, clone L	17.92	

	121558	AA412497	gb:z185g12.s1 Soares_testis_NHT Homo sap		2.95
	121676	H56037	Hs.108146 ESTs	10.00	
	121936	AI024600	Hs.98612 ESTs	15.00	
5	121938	AA428659	Hs.98610 ESTs	14.00	
	122177	AA435789	Hs.98833 EST	8.93	
	123442	AA299652	Hs.111496 Homo sapiens cDNA FLJ11643 fis, clone HE	13.04	
	123551	AA608837	gb:af03h12.s1 Soares_testis_NHT Homo sap	11.50	
	123756	AA609971	Hs.112795 EST	11.00	
10	123861	AA620840	gb:af89g01.s1 Soares_testis_NHT Homo sap		2.50
	124371	N24924	Hs.188601 ESTs	6.50	
	127477	BE328720	Hs.280651 ESTs		4.33
	127591	AI190540	Hs.131092 ESTs		3.02
	128252	AA455924	Hs.192228 ESTs	7.00	
15	128426	AI265784	Hs.145197 ESTs		2.08
	128925	R67419	Hs.21851 Homo sapiens cDNA FLJ12900 fis, clone NT		2.11
	128945	AI990506	Hs.8077 Homo sapiens mRNA; cDNA DKFZp547E184 (fr	10.00	
	129105	AI769160	Hs.108681 Homo sapiens brain tumor associated prot	15.50	
	129235	AW977238	Hs.126084 KIAA1055 protein		4.25
	129506	AB020684	Hs.11217 KIAA0877 protein	6.50	
20	129595	U09550	Hs.1154 oviductal glycoprotein 1, 120kD (mucin 9		10.00
	130160	AA305688	Hs.267695 UDP-Gal:betaGlcNAc beta 1,3-galactosyltr	20.00	
	130340	D82326	Hs.239106 solute carrier family 3 (cystine, dibasi	11.50	
	131220	AB023194	Hs.300855 KIAA0977 protein	17.50	
	131430	AI879148	Hs.26770 fatty acid binding protein 7, brain	6.10	
25	132114	NM_006152	Hs.40202 lymphoid-restricted membrane protein		6.15
	132458	AA935315	Hs.48965 Homo sapiens cDNA: FLJ21693 fis, clone C		5.58
	132647	NM_006927	Hs.54432 sialyltransferase 4B (beta-galactosidase	7.50	
	132655	D49372	Hs.54460 small inducible cytokine subfamily A (Cy		2.53
	132682	AI077500	Hs.54900 serologically defined colon cancer antig		2.50
30	132747	AA345241	Hs.55950 ESTs, Weakly similar to KIAA1330 protein		2.83
	132812	R50333	Hs.92186 Leman coiled-coil protein		3.82
	133337	AF085983	Hs.293676 ESTs		5.00
	133876	AL134908	Hs.771 phosphorylase, glycogen; liver (Hers dis		3.00
	134119	AW157837	Hs.79226 fasciculation and elongation protein zet		2.06
35	134464	AA302983	Hs.239720 CCR4-NOT transcription complex, subunit		2.27
	134542	M14156	Hs.85112 insulin-like growth factor 1 (somatomedi		11.50
	135002	AA448542	Hs.251677 G antigen 7B	87.00	
	135305	AA203555	Hs.98288 Homo sapiens cDNA FLJ14903 fis, clone PL		6.50

TABLE 6B show the accession numbers for those primekeys lacking unigenelD's for Table 6A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT number	Accessions
108562	36375_1	AA100796 AF020589 AA074629 AA075946 AA100849 AA085347 AA126309 AA079311 AA079323 AA085274
103439	35330_1	X98266 N41124
123551	genbank_AA608837	AA608837
123861	genbank_AA620840	AA620840
102832	entrez_U92015	U92015
101972	entrez_S82472	S82472
121558	genbank_AA412497	AA412497

Table 7A shows 98 genes down-regulated in non-smokers with lung cancer relative to smokers with lung cancer. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

5	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
10	R1:	90th percentile of AI for samples from smokers with adenocarcinoma divided by the average of AI for samples from non-smokers with adenocarcinoma.			
	R2:	90th percentile of AI for samples from smokers with squamous cell carcinoma divided by the average of AI for samples from non-smokers with squamous cell carcinoma.			
	Pkey	ExAccn	UnigeneID	Unigene Title	R1 R2
15	100187	D17793	Hs.78183	aldo-keto reductase family 1, member C3	164.10
	100380	D82343	Hs.18551	neuroblastoma (nerve tissue) protein	77.40
	100576	X00356	Hs.37058	calcitonin/calcitonin-related polypeptid	102.40
	100971	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte	463.80
	101046	K01160		(NONE)	672.00
20	101066	AW970254	Hs.889	Charot-Leyden crystal protein	66.00
	101175	U82671	Hs.36980	melanoma antigen, family A, 2	77.20
	101497	W05160	Hs.37034	homeo box A5	62.80
	101663	NM_003528	Hs.2178	H2B histone family, member Q	78.00
	101677	NM_000715	Hs.1012	complement component 4-binding protein,	186.20
25	101745	M88700	Hs.150403	dopa decarboxylase (aromatic L-amino acid	80.08
	101941	S77583		gb:HERVK10/HUMMTV reverse transcriptase	99.20
	102125	NM_006456	Hs.288215	sialyltransferase	103.10
	102242	U27185	Hs.82547	retinoic acid receptor responder (tazaro	67.00
	102340	U37055	Hs.278657	macrophage stimulating 1 (hepatocyte gro	71.60
30	102369	U39840	Hs.299867	hepatocyte nuclear factor 3, alpha	69.70
	102457	NM_001394	Hs.2359	dual specificity phosphatase 4	153.00
	102669	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	65.70
	102796	AL079848	Hs.107019	sympkalin; Huntingtin interacting protei	58.80
	102829	NM_006183	Hs.80962	neurotensin	268.80
35	103207	X72790		gb:Human endogenous retrovirus mRNA for	70.00
	103242	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu o	212.10
	103260	X78416	Hs.3155	casein, alpha	130.70
	103351	X89211		gb:H.sapiens DNA for endogenous retrovir	64.60
	104212	AB002298	Hs.173035	KIAA0300 protein	66.80
40	104252	AF002246	Hs.210863	cell adhesion molecule with homology to	63.80
	104258	AF007216	Hs.5462	solute carrier family 4, sodium bicarbon	94.40
	105024	AA126311	Hs.9879	ESTs	68.20
	106260	AI097144	Hs.5260	ESTs, Weakly similar to ALU1_HUMAN ALU S	74.60
	106440	AA449563	Hs.151393	glutamate-cysteine ligase, catalytic sub	71.10
45	106566	BE298210		gb:601118016F1 NIH_MGC_17 Homo sapiens c	73.20
	106605	AW772298	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076 (fr	83.80
	106614	AA648459	Hs.335951	hypothetical protein AF301222	62.30
	106654	AW075485	Hs.286049	phosphoserine aminotransferase	202.40
	106999	H93281	Hs.10710	hypothetical protein FLJ20417	89.60
50	108700	AA121518	Hs.193540	ESTs, Moderately similar to 2109260A B c	66.40
	108810	AW295647	Hs.71331	hypothetical protein MGCS350	95.50
	108857	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	63.40
	109597	AA989362	Hs.293780	ESTs	85.00
	109591	T65568	Hs.12860	ESTs	58.70
55	109704	AI743880	Hs.12876	ESTs	60.60
	110942	R63503	Hs.28419	ESTs	76.40
	111722	R23924	Hs.23596	EST	74.60
	112891	T03927	Hs.293147	ESTs, Moderately similar to A46010 X-II	64.80
60	112992	AL157425	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (f	76.70
	113073	N39342	Hs.103042	microtubule-associated protein 1B	120.20
	114251	H15261	Hs.21948	ESTs	127.20
	115230	AA278300	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	174.00
	115291	BE545072	Hs.122579	hypothetical protein FLJ10461	91.00
	115815	AW905328	Hs.180842	ribosomal protein L13	66.40
65	115909	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	226.60
	115965	AA001732	Hs.173233	hypothetical protein FLJ10970	82.80
	116107	AL133916	Hs.172572	hypothetical protein FLJ20093	361.60
	116552	D20508	Hs.164649	hypothetical protein DKFZp434H247	69.00
	116571	D45652		gb:HUMGS02848 Human adult lung 3' direct	64.20
70	118466	N66741		gb:yz33g08.s1 Morton Fetal Cochlea Homo	63.50
	120484	AA253170	Hs.96473	EST	81.60
	120983	AA398209	Hs.97587	EST	81.10
	121034	AL389951	Hs.271623	nucleoporin 50kD	66.20
	121423	AW973352	Hs.290585	ESTs	64.40
75	122553	AA451884	Hs.190121	ESTs	60.40
	122946	AI718702	Hs.308026	major histocompatibility complex, class	188.60
	123130	AA487200		gb:ab19f02.s1 Stratagene lung (937210) H	80.20
	124472	N52517	Hs.102670	EST	71.00
	124528	N62096	Hs.293185	ESTs, Weakly similar to J7328 amino acid	104.90
80	125489	H49193	Hs.124984	ESTs, Moderately similar to ALU7_HUMAN A	72.00
	125731	R61771	Hs.26912	ESTs	69.90
	125747	NM_002884	Hs.865	RAP1A, member of RAS oncogene family	69.00
	126020	H79863	Hs.114243	ESTs	62.40
	126547	U47732	Hs.84072	transmembrane 4 superfamily member 3	62.80
85	126956	R38438	Hs.182575	solute carrier family 15 (H+/peptide tra	60.10

	127472	AA761378	Hs.192013	ESTs	70.20	
	127610	AA960867	Hs.150271	ESTs, Highly similar to unnamed protein	64.00	
	127742	AW293496	Hs.180138	ESTs	85.20	
	127987	AI022103	Hs.124511	ESTs	98.60	
5	128233	AW889132	Hs.11916	ribokinase		78.90
	128420	AA650274	Hs.41296	fibronectin leucine rich transmembrane p		106.90
	128766	AW160432	Hs.296460	craniofacial development protein 1	66.80	
	129014	AW935187	Hs.170162	KIAA1357 protein		58.53
10	129215	AB040930	Hs.126085	KIAA1497 protein	64.20	
	130090	H97878	Hs.132390	zinc finger protein 36 (KOX 18)	63.80	
	130385	AW067800	Hs.155223	stanniocalcin 2		139.60
	130732	AW890487	Hs.63994	cadherin 13, H-cadherin (heart)		64.60
	131025	AB040900	Hs.6189	KIAA1467 protein	64.40	
15	131241	BE501914	Hs.24654	Homo sapiens cDNA FLJ11640 fis, clone HE	76.20	
	131775	AB014548	Hs.31921	KIAA0848 protein	97.80	
	132240	AB018324	Hs.42676	KIAA0781 protein		71.00
	132856	NM_001448	Hs.58367	glypican 4		88.40
	132977	AA093322	Hs.301404	RNA binding motif protein 3	133.20	
20	133749	L20852	Hs.10018	solute carrier family 20 (phosphate tran		69.30
	133818	AI110584	Hs.7645	fibrinogen, B beta polypeptide	341.00	
	134264	AF149297	Hs.8087	NAG-5 pplein		64.30
	134265	M83772	Hs.80876	flavin containing monooxygenase 3		232.53
	134346	X84002	Hs.82037	TATA box binding protein (TBP)-associate	66.00	
25	134395	AA456539	Hs.8262	lysosomal-associated membrane protein 2		75.80
	135047	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su		108.30
	135056	N75765	Hs.93765	lipoma HMGIC fusion partner	71.40	
	135309	AI564123	Hs.42500	ADP-ribosylation factor-like 5	70.40	

30 TABLE 7B shows the accession numbers for those primekeys lacking unigenal D's for Table 7A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

35 Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

40	Pkey	CAT number	Accessions
	103207	30635_4	X72790
	106566	120358_1	BE298210 AI672315 AW086489 BE298417 AA455921 AA902537 BE327124 R14963 AA085210 AW274273 AI333584 AI369742 AI039658 AI885095 AI476470 AI287650 AI885299 AI985381 AW592624 AW340136 AI266556 AA456390 AI310815 AA484951
45	116571	genbank_D45652	D45652
	118466	genbank_N66741	N66741
	101046	entrez_K01160 K01160	
	101941	entrez_S77583 S77583	
	103351	entrez_X89211 X89211	
50	123130	genbank_AA487200	AA487200

Table 8A shows 1720 genes either up or down-regulated in lung tumors or chronically diseased lung relative to a broad collection of over 40 distinct normal body tissues. Chronically diseased lung samples represent chronic non-malignant lung diseases such as fibrosis, emphysema, and bronchitis. These genes were selected from 39494 probesets on the Eos/Affymetrix Hu02 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Pkey: Unique Eos probeset identifier number

ExAccn: Exemplar Accession number, Genbank accession number

UnigeneID: Unigene number

Unigene Title: Unigene gene title

R1: 70th percentile of AI for lung tumors divided by 90th percentile of AI for normal lung

R2: 70th percentile of AI for chronically diseased lung divided by 90th percentile of AI for normal lung

Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2
300097	AI916973	Hs.213603	ESTs	5.46	4.69
300117	AW189787	Hs.147474	ESTs	0.58	0.56
300197	AI686661	Hs.218286	ESTs	4.26	5.44
300201	AI308300		gb:ta90c06.x1 NCI_CGAP_Bm20 Homo sapien	0.62	0.83
300225	AI989963	Hs.197505	ESTs	1.68	1.75
300247	AW274682	Hs.161394	ESTs	1.08	2.28
300256	AI469095	Hs.298241	Transmembrane protease, serine 3	0.86	1.00
300337	AI707881	Hs.202090	ESTs	5.80	9.09
300362	Z42308		gb:HSC0FB121 normalized infant brain cDN	4.18	12.78
300374	AI859947	Hs.314158	ESTs	2.99	4.38
300387	AW270150	Hs.254516	ESTs	1.50	2.53
300440	AI421541	Hs.146164	ESTs	3.98	5.25
300441	R10387	Hs.307921	EST, Weakly similar to Z232_HUMAN ZINC F	3.18	6.80
300449	AI362967	Hs.132221	hypothetical protein FLJ12401	0.43	0.62
300469	AW135830	Hs.233955	hypothetical protein FLJ20401	0.16	0.83
300552	X85711	Hs.21838	hypothetical protein FLJ11191	4.10	9.75
300627	W27363		gb:ab37d01.r1 Stratagene HeLa cell s3 93	4.60	12.60
300630	AW118822	Hs.128757	ESTs	2.91	5.86
300716	AI216113	Hs.126280	hypothetical protein FLJ23393	1.00	0.92
300738	AI623332	Hs.130541	KIAA1542 protein	1.82	1.71
300777	AA235361	Hs.96840	KIAA1527 protein	4.48	8.22
300790	AI492471	Hs.188270	ESTs	1.29	1.18
300832	AI688147	Hs.220615	ESTs, Weakly similar to T03829 transcrip	5.51	8.56
300836	Z44942	Hs.22958	calcium channel alpha2-delta3 subunit	4.90	6.34
300838	AI582897	Hs.192570	hypothetical protein FLJ22028	1.70	2.81
300878	AW449802	Hs.285901	Homo sapiens cDNA FLJ20428 fis, clone KA	4.56	7.91
300897	AI890356	Hs.127804	ESTs, Weakly similar to T17233 hypotheti	2.23	1.58
300926	AA504860		gb:ab03a10.s1 Stratagene fetal retina 93	2.13	3.50
300960	AI041019	Hs.152454	ESTs	2.74	4.46
300961	AW204069	Hs.312716	ESTs, Weakly similar to unnamed protein	1.00	1.00
300962	AA593373	Hs.293744	ESTs	1.46	1.51
300967	AA565209	Hs.269439	ESTs	0.39	1.30
300987	AW450840	Hs.148590	ESTs, Weakly similar to AF208846 1 BM-00	1.49	1.08
300988	AI927208	Hs.208952	ESTs	0.16	0.37
301050	AW136973	Hs.288518	ESTs, Weakly similar to S69890 mitogen I	3.23	1.94
301098	AA677570	Hs.185918	ESTs	6.76	14.28
301157	AA729905	Hs.231916	ESTs	3.16	8.85
301162	AI142118	Hs.129004	ESTs	1.68	7.18
301170	AA737594	Hs.247606	ESTs	4.40	6.42
301192	AI808751	Hs.121188	ESTs	6.38	11.59
301193	AA758115	Hs.128350	ESTs, Weakly similar to JC5423 2-hydroxy	4.35	7.78
301267	AW297782	Hs.255690	ESTs	1.56	1.61
301281	AA843986	Hs.190586	ESTs	2.19	1.78
301341	AI819198	Hs.208229	ESTs	0.76	0.76
301382	AA912839	Hs.163369	ESTs	1.00	1.81
301407	AW450466	Hs.126830	ESTs	1.48	1.51
301452	AA975688	Hs.159955	ESTs	0.51	1.46
301483	AW272467	Hs.254655	Untitled	2.40	5.02
301494	AI678034	Hs.131099	ESTs	2.79	3.41
301521	AI733621	Hs.133011	zinc finger protein 117 (HPF9)	0.67	0.67
301531	AI077462	Hs.134084	ESTs	2.52	3.76
301580	AI878959	Hs.73737	splicing factor, arginine/serine-rich 1	7.41	11.92
301676	Z43570	Hs.27453	ESTs, Moderately similar to G01251 Rar p	8.31	10.70
301690	F05865	Hs.108323	ubiquitin-conjugating enzyme E2E 2 (homo	2.70	4.22
301718	F07744	Hs.7987	DKFZP434F162 protein	4.20	8.78
301799	AA384252	Hs.286132	D15F37 (pseudogene)	5.93	7.04
301804	AA581004	Hs.62180	anillin (Drosophila Scraps homolog), act	1.70	0.76
301822	X17033	Hs.271986	Integrin, alpha 2 (CD49B, alpha 2 subunl	1.58	1.36
301846	R20002	Hs.6823	hypothetical protein FLJ10430	1.00	1.00
301868	T71508	Hs.13861	ESTs, Weakly similar to pH sensitive max	2.88	5.49
301882	T78054		gb:yc97g09.r1 Soares infant brain 1N18 H	2.28	3.80
301905	AI991127	Hs.117202	ESTs	1.00	1.00
301948	AA344647	Hs.116724	aldo-keto reductase family 1, member B11	5.28	2.28
301960	AW070252	Hs.27973	KIAA0874 protein	5.38	6.48
302011	T91418	Hs.125156	transcriptional adaptor 2 (ADA2, yeast,	3.03	3.42
302016	N40834	Hs.23495	hypothetical protein FLJ11252	1.00	1.25
302041	NM_001501	Hs.129715	gonadotrophin-releasing hormone 2	0.71	0.99
302072	AJ238381	Hs.132575	paired box gene 9	1.60	1.71
302094	AI286176	Hs.6786	ESTs	0.52	1.20
302095	AW044300	Hs.137506	Homo sapiens BAC clone RP11-120J2 from 7	2.75	4.93
302148	AW269618	Hs.23244	ESTs	3.04	3.87

	302155	AI088485	Hs.144759	ESTs	0.45	1.15
	302201	AJ006276	Hs.159003	transient receptor potential channel 6	0.33	0.84
	302202	AF097159	Hs.159140	UDP-Gal:betaGlcNAc beta 1,4- galactosylt	0.52	0.94
5	302206	AI937193	Hs.41143	phospholipid-specific phospholipase	2.76	3.65
	302209	AF047445	Hs.159297	killer cell lectin-like receptor subfam1	1.00	1.00
	302235	AL049987	Hs.168361	Homo sapiens mRNA; cDNA DKFZp564F112 (fr	1.68	1.50
	302290	AL117607	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N0763 (f	1.00	2.11
	302328	AA354849	Hs.23240	Homo sapiens cDNA FLJ13496 fis, clone PL	9.38	13.08
10	302346	AL039101	Hs.194625	dynein, cytoplasmic, light intermediate	3.27	7.24
	302360	AJ010901	Hs.198267	mucin 4, tracheobronchial	2.54	1.88
	302384	Y08982	Hs.202678	synaptonemal complex protein 2	1.00	0.91
	302406	U86751	Hs.211956	CD3-epsilon-associated protein; antisens	2.63	2.67
	302409	AF155156	Hs.218028	adaptor-related protein complex 4, epsil	5.82	9.34
	302423	AB028977	Hs.225974	KIAA1054 protein	3.66	3.18
15	302432	AL080068	Hs.272534	Homo sapiens mRNA; cDNA DKFZp564J062 (fr	2.44	6.77
	302435	AF092047	Hs.227277	sine oculus homeobox (Drosophila) homolo	0.44	0.84
	302437	AB024730	Hs.227473	UDP-N-acetylglucosamine:alpha-1,3-D-mannosid	4.18	6.64
	302456	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 2	1.85	0.92
	302472	AA317451	Hs.6335	SWI/SNF related, matrix associated, acti	2.04	2.13
20	302476	AF182294	Hs.241578	U6 snRNA-associated Sm-like protein LSM8	1.44	1.89
	302489	T80680	Hs.230424	Homo sapiens cDNA FLJ13540 fis, clone PL	0.51	1.10
	302490	AA885502	Hs.187032	ESTs	2.64	4.87
	302562	AJ005585	Hs.48956	gap junction protein, beta 6 (connexin 3	5.34	2.68
25	302566	AA085996	Hs.248572	hypothetical protein FLJ22965	1.00	1.21
	302630	AB029488	Hs.272100	SMS3 protein	0.52	1.24
	302634	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	1.00	1.00
	302638	AA463798	Hs.102696	MCT-1 protein	1.58	1.02
	302647	X57723	Hs.198273	NADH dehydrogenase (ubiquinone) 1 beta s	2.72	6.85
	302655	AJ227892	Hs.146274	ESTs	1.00	4.32
30	302656	AW293005	Hs.70704	Homo sapiens, clone IMAGE:2823731, mRNA,	2.97	0.93
	302668	AA580691	Hs.180789	S164 protein	0.80	0.95
	302679	H65022		gb:yu66g11.1 r1 Weizmann Olfactory Epithel	1.68	5.04
	302680	AW192334	Hs.38218	ESTs	2.70	7.98
35	302697	AJ001408		gb:Homo sapiens mRNA for Immunoglobulin	4.25	8.13
	302705	U09080		gb:Human immunoglobulin heavy chain, V-r	3.91	8.68
	302711	L08442		gb:Human autonomously replicating sequen	2.20	2.73
	302719	W69724	Hs.288959	hypothetical protein FLJ20920	0.54	1.02
	302742	L12089		gb:Homo sapiens (clone WR4.10VH) anti-th	4.28	11.57
40	302755	AW384815	Hs.149208	KIAA1555 protein	1.57	2.38
	302771	H98478	Hs.42522	ESTs	2.94	4.68
	302789	AJ245067		gb:Homo sapiens mRNA for immunoglobulin	3.49	6.31
	302795	AJ245313	Hs.272838	hypothetical protein FLJ10494	0.80	2.74
	302802	Y08250		gb:H.sapiens mRNA for variable region of	1.13	0.77
45	302803	AA442824	Hs.293961	ESTs, Moderately similar to putative DNA	3.14	10.68
	302812	N31301	Hs.162664	hypothetical protein FLJ20051	3.04	8.24
	302847	X98940		gb:H.sapiens rearranged Ig heavy chain (1.80	1.92
	302885	AL137763	Hs.132127	hypothetical protein LOC57822	1.00	1.00
	302943	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypothell	0.53	0.67
50	302977	AW263124	Hs.315111	hypothetical protein FLJ12894	2.45	2.62
	303006	AF078950	Hs.24139	Homo sapiens cDNA: FLJ23137 fis, clone L	4.88	8.61
	303011	AF090405		gb:Homo sapiens clone 2A1 acFV antibody	1.41	1.86
	303013	F07898	Hs.288968	RAB22A, member RAS oncogene family	1.51	1.19
	303061	AF151882	Hs.27693	peptidylprolyl isomerase (cyclophilin)-I	0.72	0.76
55	303077	AF163305		gb:H.sapiens T-cell receptor mRNA	1.17	3.90
	303090	AA443259	Hs.146288	kinesin family member 13A	4.08	6.46
	303091	AF192913	Hs.130683	zinc finger protein 180 (HHZ168)	2.50	4.37
	303094	AF195513	Hs.278953	Pur-gamma	5.38	8.38
	303095	AF202051	Hs.134079	NM23-H8	3.26	4.08
60	303131	AW081061	Hs.103180	DC2 protein	2.02	1.83
	303195	AA082211	Hs.233936	myosin, light polypeptide, regulatory, n	1.32	3.95
	303196	AA082298	Hs.59710	ESTs	0.77	0.53
	303216	AA581439	Hs.152328	ESTs	0.24	0.63
	303222	AA333538	Hs.204501	hypothetical protein FLJ10534	3.56	6.22
65	303234	AA132255	Hs.143951	ESTs	2.28	3.17
	303251	AW340037	Hs.115897	protocadherin 12	0.38	1.02
	303295	AA205625	Hs.208067	ESTs	2.30	1.00
	303297	T80072	Hs.13423	Homo sapiens clone 24468 mRNA sequence	1.86	4.48
	303316	AF033122	Hs.14125	p53 regulated PA26 nuclear protein	0.10	0.80
70	303467	AA398801	Hs.323397	ESTs	4.54	9.65
	303506	AA340805	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	0.09	0.04
	303552	AA359799	Hs.224652	ESTs, Weakly similar to unnamed protein	1.00	1.72
	303598	AA382814		gb:EST96097 Testis I Homo sapiens cDNA 5	4.96	9.14
	303637	AF056083	Hs.24879	phosphatidic acid phosphatase type 2C	2.05	2.02
75	303655	AA504702	Hs.258802	ATPase, (Na+)/K+ transporting, beta 4 po	1.00	1.24
	303756	AI738488	Hs.115838	ESTs	1.08	1.43
	303858	AA968589	Hs.180532	glucose phosphate isomerase	1.76	1.31
	303893	N88597	Hs.113503	karyopherin (importin) beta 3	2.30	2.57
	303907	AW467774	Hs.171880	polymerase (RNA) II (DNA directed) polyp	3.10	5.79
80	303946	AW474196	Hs.306637	Homo sapiens cDNA FLJ12363 fis, clone MA	5.06	11.86
	303978	AW513315		gb:xa43c12.x1 NCI_CGAP_U11 Homo sapiens	5.14	7.31
	303981	AW513804	Hs.278834	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.83	4.06
	303990	AW515465		gb:xu71a11.x1 NCI_CGAP_Kd8 Homo sapiens	1.15	2.35
	303998	AW516449		gb:xt68f05.x1 NCI_CGAP_U12 Homo sapiens	2.20	9.35
85	303999	AW516611		gb:xp70b11.x1 NCI_CGAP_Ov39 Homo sapiens	4.85	6.28
	304006	AW517947		gb:xt68h02.x1 NCI_CGAP_U12 Homo sapiens	3.21	4.07

	304008	AW518198	Hs.3297	ribosomal protein S27a	6.50	11.08
	304009	AW518206	Hs.181165	eukaryotic translation elongation factor	1.88	3.27
	304024	T03036		gb:FB2187 Fetal brain, Stratagene Homo s	2.15	3.55
5	304026	T03160		gb:FB26F2 Fetal brain, Stratagene Homo s	5.88	11.80
	304028	T03266		gb:FB7C1 Fetal brain, Stratagene Homo sa	5.59	13.46
	304036	T16855	Hs.244621	ribosomal protein S14	6.55	14.43
	304046	T54803		gb:yb42d06.s1 Stratagene fetal spleen (9	6.18	12.19
	304061	T61521		gb:yb73g01.s1 Stratagene ovary (937217)	2.64	8.23
10	304063	T62536		gb:yc04c12.s1 Stratagene lung (937210) H	0.53	1.61
	304097	R25376	Hs.177592	ribosomal protein, large, P1	6.49	11.67
	304114	R78946		gb:yi87g02.s1 Soares placenta Nb2HP Homo	2.90	4.18
	304122	H28966		gb:ym31a06.s1 Soares infant brain 1NIB H	1.00	2.76
	304155	H68696		gb:yr78b06.s1 Soares fetal liver spleen	0.79	1.18
	304203	N56929		gb:yy82d08.s1 Soares_multiple_sclerosis_	4.28	11.34
15	304234	W81608		gb:zd88h06.s1 Soares_fetal_heart_NbHH19W	6.47	11.03
	304267	AA064862	Hs.73742	ribosomal protein, large, P0	1.34	1.16
	304270	AA069711	Hs.297753	vimentin	3.40	5.40
	304287	AA079286	Hs.78466	proteasome (prosome, macropain) 26S sub	2.93	4.42
20	304348	AA179868		gb:zp38g12.s1 Stratagene muscle 937209 H	3.98	10.96
	304415	AA290747	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	3.32	5.99
	304430	AA347682		gb:EST54044 Fetal heart II Homo sapiens	1.00	1.00
	304455	AA411240		gb:zv26g05.s1 Soares_NhHMPu_S1 Homo sapi	1.42	3.33
	304521	AA464716		gb:zx82c11.s1 Soares ovary tumor NbHOT H	2.18	1.15
25	304526	AA476427		gb:zx02c05.s1 Soares_total_fetus_Nb2HF8_	5.38	14.11
	304542	AA482602	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	4.16	8.23
	304546	AA486074	Hs.297681	serine (or cysteine) proteinase inhibitor	0.55	1.20
	304607	AA513322		gb:nh85e08.s1 NCI_CGAP_Br1.1 Homo sapien	1.95	2.10
	304640	AA524440	Hs.111334	ferritin, light polypeptide	2.10	2.83
30	304650	AA527489	Hs.3463	ribosomal protein S23	3.33	12.62
	304735	AA576453		gb:nm75h11.s1 NCI_CGAP_Co9 Homo sapiens	1.33	0.88
	304760	AA580401		gb:nn13g09.s1 NCI_CGAP_Co12 Homo sapiens	3.68	8.14
	304849	AA588157	Hs.13801	KIAA1695 protein	2.77	3.70
	304917	AA602685	Hs.284136	PRO2047 protein	7.16	11.01
35	304921	AA603092	Hs.297753	vimentin	2.47	4.24
	304968	AA613893	Hs.282435	ESTs	6.78	11.66
	304987	AA618044	Hs.300697	immunoglobulin heavy constant gamma 3 (G	0.90	1.23
	305016	AA626876		gb:zu89h06.s1 Soares_testis_NHT Homo sap	6.46	10.17
	305034	AA630128		gb:ab99c04.s1 Stratagene lung (937210) H	1.00	1.00
40	305072	AA641012		gb:nr72a12.s1 NCI_CGAP_Pr24 Homo sapiens	6.68	11.59
	305111	AA644187	Hs.303405	ESTs	1.48	1.37
	305148	AA654070		gb:nt01g08.s1 NCI_CGAP_Lym3 Homo sapiens	1.76	4.61
	305159	AA659166	Hs.275668	EST, Weakly similar to EF1D_HUMAN ELONG	1.00	2.15
	305190	AA665955		gb:ag57d12.s1 Gessler Wilms tumor Homo s	5.31	8.14
45	305232	AA670052	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	0.78	1.18
	305235	AA670480		gb:ag37e01.s1 Jia bone marrow stroma Hom	3.11	8.66
	305245	AA676695	Hs.81328	nuclear factor of kappa light polypeptid	4.38	7.53
	305312	AA700201		gb:zj44f07.s1 Soares_fetal_liver_spleen_	2.13	2.66
	305322	AA701597	Hs.163019	EST	1.20	1.40
50	305394	AA720942	Hs.300697	immunoglobulin heavy constant gamma 3 (G	1.16	0.68
	305413	AA724659		gb:al10f08.s1 Soares_parathyroid_tumor_N	5.86	9.87
	305447	AA737856		gb:mx10c08.s1 NCI_CGAP_GC3 Homo sapiens	2.21	2.86
	305476	AA745664	Hs.287445	hypothetical protein FLJ11726	3.38	6.54
	305483	AA748030	Hs.303512	EST	1.00	2.02
55	305528	AA769156		gb:nz12e05.s1 NCI_CGAP_GCB1 Homo sapiens	6.44	9.10
	305612	AA782347	Hs.272572	hemoglobin, alpha 2	0.19	0.79
	305614	AA782866		gb:aj09h02.s1 Soares_parathyroid_tumor_N	1.00	1.00
	305616	AA782884	Hs.275665	ribosomal protein S18	7.57	10.20
	305637	AA806124		gb:oe29a12.s1 NCI_CGAP_Pr25 Homo sapiens	4.78	12.42
60	305639	AA806138		gb:oe29c12.s1 NCI_CGAP_Pr25 Homo sapiens	0.89	0.70
	305650	AA807709		gb:nw31e04.s1 NCI_CGAP_GCB0 Homo sapiens	4.49	8.71
	305690	AA813477		gb:ai67a05.s1 Soares_testis_NHT Homo sap	4.91	9.40
	305726	AA828156	Hs.73742	ribosomal protein, large, P0	0.19	0.81
	305728	AA828209		gb:of34a02.s1 NCI_CGAP_Kid6 Homo sapiens	5.12	9.29
65	305759	AA835353		gb:ak72b06.s1 Barstead spleen HPLRB2 Hom	1.66	4.11
	305792	AA845256		gb:ak84a08.s1 Barstead spleen HPLRB2 Hom	2.34	4.25
	305864	AA845374	Hs.73742	ribosomal protein, large, P0	0.30	1.40
	305901	AA872968		gb:oh63h08.s1 NCI_CGAP_Kid5 Homo sapiens	2.10	5.21
	305910	AA875981		gb:nx21h02.s1 NCI_CGAP_GC3 Homo sapiens	0.32	1.01
70	306015	AA897116		gb:am09b07.s1 Soares_NFL_T_GBC_S1 Homo s	1.56	1.12
	306017	AA897221	Hs.109058	ribosomal protein S6 kinase, 90kD, poly	5.21	7.90
	306020	AA897630	Hs.130027	EST	1.96	6.59
	306063	AA906316		gb:ok03g03.s1 Soares_NFL_T_GBC_S1 Homo s	7.38	20.69
	306065	AA906725		gb:ok78g02.s1 NCI_CGAP_GC4 Homo sapiens	7.19	13.48
75	306104	AA910956		gb:ok85h11.s1 NCI_CGAP_Kid3 Homo sapiens	6.50	9.13
	306109	AA911861		gb:og21a07.s1 NCI_CGAP_PNS1 Homo sapiens	4.21	5.25
	306148	AA917409	Hs.288036	tRNA isopentenylpyrophosphate transfera	2.20	2.70
	306242	AA932805		gb:oe60g04.s1 NCI_CGAP_Lu5 Homo sapiens	2.84	5.35
	306288	AA936900		gb:of53h05.s1 NCI_CGAP_HN3 Homo sapiens	1.60	1.12
80	306325	AA953072	Hs.210546	interleukin 21 receptor	1.65	2.26
	306353	AA961382	Hs.275865	ribosomal protein S18	3.78	6.32
	306375	AA968650	Hs.276018	EST, Moderately similar to JC4662 ribos	4.30	5.74
	306396	AA970223		gb:op09d05.s1 NCI_CGAP_Kid6 Homo sapiens	0.95	2.45
	306428	AA975110	Hs.191228	hypothetical protein FLJ20284	3.19	4.10
85	306442	AA976899		gb:og35e09.s1 NCI_CGAP_GC4 Homo sapiens	4.67	7.44
	306446	AA977348		gb:og72e12.s1 NCI_CGAP_Kid6 Homo sapiens	3.92	6.27

5	306458	AA978186		gb:op33c06.s1 Soares_NFL_T_GBC_S1 Homo s	3.35	5.77
	306467	AA983508	Hs.163593	ribosomal protein L18a	3.72	5.37
	306510	AA988546		gb:cr84d07.s1 NCI_CGAP_Lu5 Homo sapiens	1.00	1.00
	306555	AA994304	Hs.276083	EST, Weakly similar to RL23_HUMAN 60S R	6.61	10.91
	306557	AA994530		gb:rou57e08.s1 NCI_CGAP_Br2 Homo sapiens	16.20	31.83
10	306572	AA995686		gb:ros25c12.s1 NCI_CGAP_Kid5 Homo sapiens	2.51	6.52
	306582	AA996248		gb:ros18c10.s1 NCI_CGAP_Kid5 Homo sapiens	1.42	3.13
	306598	AI000320	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	4.91	8.68
	306605	AI000497	Hs.119500	ribosomal protein, large P2	1.96	8.60
	306656	AI004024		gb:ou11b07.x1 Soares_NFL_T_GBC_S1 Homo s	0.11	0.45
15	306676	AI005603	Hs.284136	PRO2047 protein	9.56	17.28
	306686	AI015615		gb:ov29f10.x1 Soares_testis_NHT Homo sap	1.86	3.60
	306702	AI022565	Hs.307670	EST	1.47	1.19
	306728	AI027359	Hs.272572	hemoglobin, alpha 2	1.28	2.83
	306751	AI032589		gb:ow70h12.s1 Soares_fetal_liver_spleen_	3.91	5.21
20	306767	AI038963	Hs.249118	ESTs	3.33	6.06
	306892	AI092465		gb:qa75h12.x1 Soares_fetal_heart_NbHH19W	3.77	7.46
	306897	AI093967		gb:qa33c06.s1 Soares_NhHMPu_S1 Homo sapi	2.12	2.85
	306956	AI125111		gb:am66f03.s1 Barstead spleen HPLRB2 Hom	6.10	10.52
	306958	AI125152		gb:am55e09.x1 Johnston frontal cortex Ho	1.72	1.56
25	307035	AI142774	Hs.119122	ribosomal protein L13a	2.00	4.70
	307041	AI144243		gb:qb85b12.x1 Soares_fetal_heart_NbHH19W	9.12	12.56
	307091	AI167439		gb:xx70h06.s1 Soares_NhHMPu_S1 Homo sapi	4.88	8.52
	307181	AI189251		gb:qc99g06.x1 Soares_pregnant_uterus_NbH	3.65	6.44
	307297	AI205798	Hs.111334	ferritin, light polypeptide	2.46	4.65
30	307317	AI208303	Hs.147333	EST	5.64	10.13
	307327	AI214142	Hs.246381	CD68 antigen	3.18	5.15
	307382	AI223158	Hs.147885	ESTs	2.02	3.73
	307410	AI241715	Hs.77039	ribosomal protein S3A	0.72	0.48
	307415	AI242118		gb:qh92b02.x1 Soares_NFL_T_GBC_S1 Homo s	2.38	3.51
35	307423	AI243206	Hs.179573	collagen, type I, alpha 2	2.60	5.44
	307428	AI243364		gb:qh30g11.x1 Soares_NFL_T_GBC_S1 Homo s	3.18	7.67
	307517	AI275055		gb:qx72d03.x1 Soares_NhHMPu_S1 Homo sapi	1.00	1.00
	307551	AI281556		gb:qu52f11.x1 NCI_CGAP_Lym6 Homo sapiens	3.40	11.20
	307561	AI282207		gb:qp65a12.x1 Soares_fetal_lung_NbHL19W	4.74	15.51
40	307608	AI290295		gb:qm01f02.x1 Soares_NhHMPu_S1 Homo sapi	3.50	7.19
	307657	AI306428	Hs.298262	ribosomal protein S19	1.76	2.44
	307691	AI318285		gb:lb17b01.x1 NCI_CGAP_Ov37 Homo sapiens	1.59	1.31
	307701	AI318583	Hs.276672	EST, Weakly similar to RL6_HUMAN 60S RI	1.90	2.13
	307718	AI333406	Hs.83753	small nuclear ribonucleoprotein polypept	0.45	0.99
45	307730	AI336092		gb:ql43b07.x1 Soares_fetal_lung_NbHL19W	1.51	0.99
	307760	AI342387		gb:ql27f07.x1 Soares_pregnant_uterus_NbH	1.00	1.00
	307764	AI342731		gb:qo26a07.x1 NCI_CGAP_Lu5 Homo sapiens	4.52	12.58
	307783	AI347274		gb:tc05d02.x1 NCI_CGAP_Co16 Homo sapiens	1.42	1.00
	307796	AI350556		gb:xt18f09.x1 NCI_CGAP_GC4 Homo sapiens	6.57	9.61
50	307807	AI351799		gb:xl09d02.x1 NCI_CGAP_GC4 Homo sapiens	3.38	7.68
	307808	AI351826		gb:xl09g03.x1 NCI_CGAP_GC4 Homo sapiens	0.33	0.86
	307820	AI355761		gb:xl94a11.x1 NCI_CGAP_Co14 Homo sapiens	7.94	21.57
	307830	AI358722	Hs.276737	EST, Weakly similar to R5HU22 ribosomal	2.05	3.32
	307852	AI365541		gb:qz08g05.x1 NCI_CGAP_CLL1 Homo sapiens	3.18	5.21
55	307902	AI380462		gb:tg02h05.x1 NCI_CGAP_CLL1 Homo sapiens	3.13	4.99
	307997	AI434512	Hs.181165	eukaryotic translation elongation factor	1.00	3.01
	308002	AI435240	Hs.283442	ESTs	5.86	12.64
	308011	AI439473		gb:ti60a08.x1 NCI_CGAP_Lym12 Homo sapien	3.79	5.83
	308023	AI452732	Hs.251577	hemoglobin, alpha 1	0.38	0.88
60	308041	AI458824	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	4.36	6.06
	308059	AI468938	Hs.276877	EST, Weakly similar to RL10_HUMAN 60S R	1.80	1.98
	308085	AI474135	Hs.181165	eukaryotic translation elongation factor	3.38	4.14
	308101	AI475950	Hs.181165	eukaryotic translation elongation factor	1.30	3.87
	308106	AI476803		gb:jl77e12.x1 Soares_NSF_F8_9W_OT_PA_P_S238		8.72
65	308122	AI480123	Hs.309411	EST	2.70	3.86
	308154	AI500600		gb:tn93d08.x1 NCI_CGAP_UI2 Homo sapiens	0.66	1.33
	308171	AI523632	Hs.298766	ESTs, Weakly similar to schlafen4 [M.mu	2.48	4.86
	308211	AI557029	Hs.278572	anaplastic lymphoma kinase (K1-1)	2.43	2.14
	308213	AI557041		gb:PT2.1_12_E04.r tumor2 Homo sapiens cD	3.34	3.79
70	308216	AI557135		gb:PT2.1_13_H06.r tumor2 Homo sapiens cD	4.61	4.78
	308219	AI557246		gb:PT2.1_15_D07.r tumor2 Homo sapiens cD	4.87	7.94
	308271	AI567844	Hs.252259	ribosomal protein S3	2.40	6.35
	308319	AI583983	Hs.181165	eukaryotic translation elongation factor	2.45	3.33
	308362	AI613519	Hs.105749	KIAA0553 protein	1.24	1.41
75	308413	AI636253	Hs.198511	ESTs	3.16	4.82
	308450	AI660860	Hs.96840	KIAA1527 protein	1.79	2.68
	308464	AI672425	Hs.277117	EST, Moderately similar to I38055 myosi	4.87	8.27
	308588	AI718299		gb:as51g12.x1 Barstead aorta HPLRB6 Homo	3.90	5.64
	308599	AI719893		gb:as47d07.x1 Barstead aorta HPLRB6 Homo	3.32	5.12
80	308615	AI738593	Hs.101774	hypothetical protein FLJ23045	3.11	2.36
	308643	AI745040		gb:tr19a12.x1 NCI_CGAP_Ov23 Homo sapiens	3.98	3.69
	308673	AI760864		gb:wi09c10.x1 NCI_CGAP_CLL1 Homo sapiens	0.82	0.99
	308697	AI767143		gb:wi97a07.x1 NCI_CGAP_Kid12 Homo sapien	2.76	5.59
	308762	AI807405	Hs.259408	ESTs	3.17	6.30
85	308778	AI811109		gb:tr04c11.x1 NCI_CGAP_Ov23 Homo sapiens	1.00	1.00
	308782	AI811767	Hs.2186	eukaryotic translation elongation factor	2.94	5.15
	308808	AI818289		gb:wk52c01.x1 NCI_CGAP_Pr22 Homo sapiens	4.41	8.34
	308823	AI824118	Hs.217493	annexin A2	1.85	1.92
	308875	AI832332		gb:at48g03.x1 Barstead colon HPLRB7 Homo	2.52	3.80

	308879	AI832763	Hs.75968	thymosin, beta 4, X chromosome	3.38	7.96
	308886	AI833240		gb:al76d10.x1 Barstead colon HPLRB7 Homo	3.06	2.65
	308898	AI858845		gb:w32d10.x1 NCI_CGAP_U11 Homo sapiens	2.45	3.44
5	308934	AI865023	Hs.177	phosphatidylinositol glycan, class H	4.14	6.76
	308966	AI870704		gb:w47h01.x1 NCI_CGAP_U11 Homo sapiens	1.00	1.00
	308979	AI873111		gb:w52h05.x1 NCI_CGAP_Bm25 Homo sapien	7.15	11.10
	309045	AI910902		gb:tg39f01.x1 NCI_CGAP_U11 Homo sapiens	0.61	0.59
	309051	AI911975		gb:wd78d01.x1 NCI_CGAP_Lu24 Homo sapiens	1.78	4.42
10	309069	AI917366	Hs.78202	SWI/SNF related, matrix associated, act	3.27	5.88
	309083	AI922426	Hs.119598	ribosomal protein L3	2.39	3.34
	309105	AI925503	Hs.265884	ESTs	5.54	17.78
	309122	AI928178		gb:wo95a11.x1 NCI_CGAP_Kld11 Homo sapien	1.00	2.92
	309128	AI928816	Hs.180842	ribosomal protein L13	1.38	5.55
15	309164	AI937761		gb:wp84b09.x1 NCI_CGAP_Bm25 Homo sapien	2.43	3.11
	309177	AI951118		gb:wx63g05.x1 NCI_CGAP_Br18 Homo sapiens	0.81	0.97
	309288	AI991525	Hs.299426	ESTs	4.86	7.46
	309299	AW003478		gb:wq66c06.x1 NCI_CGAP_GC6 Homo sapiens	4.36	9.43
	309303	AW004823		gb:ws93a08.x1 NCI_CGAP_Co3 Homo sapiens	2.88	7.54
20	309411	AW085201	Hs.244144	EST	4.30	7.14
	309437	AW090702	Hs.278242	tubulin, alpha, ubiquitous	2.49	3.11
	309459	AW117645	Hs.65114	keratin 18	2.88	4.55
	309476	AW129368		gb:xe14b05.x1 NCI_CGAP_U14 Homo sapiens	2.08	6.60
	309499	AW136325	Hs.279771	Homo sapiens clone PP1596 unknown mRNA	2.82	3.55
25	309529	AW150807	Hs.181357	laminin receptor 1 (67kD, ribosomal pro	4.78	3.95
	309532	AW151119		gb:xx33e10.x1 NCI_CGAP_U11 Homo sapiens	1.18	4.40
	309626	AW192004	Hs.297681	serine (or cysteine) proteinase inhibit	4.46	12.06
	309641	AW194230	Hs.253100	EST, Moderately similar to GHU Ig gamm	1.47	1.39
	309675	AW205681	Hs.253506	EST, Moderately similar to ATPN_HUMAN A	5.68	15.20
30	309693	AW237221	Hs.181357	laminin receptor 1 (67kD, ribosomal prot	1.00	1.00
	309695	AW238011	Hs.295605	mannosidase, alpha, class 2A, member 2	5.45	9.61
	309700	AW241170	Hs.179661	tubulin, beta polypeptide	1.41	1.25
	309747	AW264889		gb:xq36h02.x1 NCI_CGAP_Lu28 Homo sapiens	5.00	8.35
	309769	AW272346		gb:xs13c10.x1 NCI_CGAP_Kld11 Homo sapien	5.76	11.90
35	309782	AW275156	Hs.156110	immunoglobulin kappa constant	0.42	0.69
	309783	AW275401	Hs.254798	EST	1.00	4.11
	309799	AW276964		gb:xp58h01.x1 NCI_CGAP_Ov39 Homo sapiens	1.68	1.44
	309866	AW299916		gb:xs44c01.x1 NCI_CGAP_Kld11 Homo sapien	3.02	5.04
40	309903	AW330071	Hs.300697	immunoglobulin heavy constant gamma 3 (G	1.05	1.18
	309923	AW340684		gb:bhd05g08.x1 Soares_NFL_T_GBC_S1 Homo s	2.30	3.67
	309928	AW341418		gb:bhd08c03.x1 Soares_NFL_T_GBC_S1 Homo s	7.41	13.71
	309931	AW341683		gb:bhd13d01.x1 Soares_NFL_T_GBC_S1 Homo s	1.20	12.70
	309933	AW341936		gb:hb73f10.x1 NCI_CGAP_U12 Homo sapiens	4.90	18.29
	309964	AW449111	Hs.257111	hypothetical protein MGC3265	1.99	3.07
45	310002	AI439096	Hs.323079	Homo sapiens mRNA; cDNA DKFZp554P116 (fr	0.20	0.47
	310096	AW136822	Hs.172824	ESTs, Weakly similar to B48013 proline-r	1.51	1.22
	310098	AI685841	Hs.161354	ESTs	0.31	0.76
	310109	AI203094	Hs.148633	ESTs	2.06	5.83
	310112	AW197233	Hs.147253	ESTs	2.92	3.55
50	310116	AI611317	Hs.223796	ESTs	1.25	0.84
	310121	AW195642	Hs.148901	ESTs	1.00	2.71
	310148	AI206614	Hs.197422	ESTs	9.50	15.31
	310193	AI627653	Hs.147562	ESTs	2.85	4.18
	310255	AW450439	Hs.153378	ESTs	4.26	10.63
55	310261	AI240483	Hs.201217	ESTs	3.28	4.40
	310264	AI915771	Hs.74170	metallothionein 1E (functional)	0.26	0.86
	310275	AI242102	Hs.213636	ESTs	5.43	8.19
	310282	AI243332	Hs.156065	ESTs	3.15	8.06
60	310290	AW013815	Hs.149103	ESTs	2.19	3.12
	310333	AI253200	Hs.145402	ESTs	1.17	1.91
	310346	AI261340	Hs.145517	ESTs	4.81	9.95
	310385	AI263392	Hs.156151	ESTs	5.96	7.79
	310443	AW119018	Hs.164231	ESTs	2.90	4.63
	310444	AW196632	Hs.252956	ESTs	0.85	1.01
65	310446	AI275715	Hs.145926	ESTs	2.18	3.85
	310468	AI984074	Hs.196398	ESTs	3.39	5.19
	310477	AI948801	Hs.171073	ESTs	1.00	1.00
	310512	AW275603	Hs.200712	ESTs	3.87	8.12
	310514	AI681145	Hs.160724	ESTs	3.30	7.33
70	310524	AW082270	Hs.12496	ESTs, Highly similar to AC004836 1 simil	0.72	1.44
	310547	AI302654	Hs.208024	ESTs	3.26	3.46
	310584	AI653007	Hs.156304	ESTs	2.39	4.08
	310608	AI962234	Hs.195102	ESTs	5.60	6.49
	310624	AI341594		gb:Human endogenous retrovirus H proteas	4.91	9.09
75	310636	AI814373	Hs.164175	ESTs	1.85	1.71
	310648	AI347863	Hs.156672	ESTs	0.17	0.69
	310694	AI654370	Hs.157752	Homo sapiens mRNA full length insert cDN	5.40	13.22
	310695	AI472124	Hs.157757	ESTs	4.82	6.27
	310714	AI418446	Hs.157882	ESTs	1.76	3.51
80	310722	AI989803	Hs.157289	ESTs	1.14	6.85
	310756	AI916560	Hs.158707	ESTs	8.46	13.01
	310764	AI376769	Hs.167172	ESTs	4.76	7.37
	310848	AI459554	Hs.161286	ESTs	2.84	1.96
	310851	AW291714	Hs.221703	ESTs	1.00	2.32
85	310854	AI421677	Hs.161332	ESTs	6.37	7.94
	310858	AI871000	Hs.161330	ESTs	6.07	9.84

	310864	AI924558	Hs.161399	ESTs	0.87	0.78
	310875	T47764	Hs.132917	ESTs	1.00	3.63
	310896	AW157731	Hs.270982	ESTs, Moderately similar to ALU7_HUMAN A	7.07	16.68
5	310922	AW195634	Hs.170401	ESTs	1.00	1.00
	310955	AI560210	Hs.263912	ESTs	10.08	17.86
	310957	AW190974	Hs.196918	ESTs	2.18	3.18
	311000	AI521830	Hs.171050	ESTs	3.08	6.64
	311012	AW298070	Hs.241097	ESTs	1.23	3.77
10	311034	AI564023	Hs.311389	ESTs, Moderately similar to PT0375 natur	2.44	2.09
	311074	AW290922	Hs.199848	ESTs	6.04	14.19
	311134	AI990849	Hs.198971	ESTs	3.54	6.96
	311174	AW450552	Hs.205457	periakin	0.65	0.95
	311187	AI638374	Hs.224189	ESTs	2.46	2.78
15	311220	AI656040	Hs.196532	ESTs	1.10	2.52
	311230	AI989808	Hs.197663	ESTs	1.41	1.75
	311236	AI653378	Hs.197674	ESTs	2.18	2.11
	311242	AW016812	Hs.200266	ESTs	0.63	5.11
	311258	AI671221	Hs.199887	ESTs	1.00	1.41
20	311277	AW072813	Hs.270868	ESTs, Moderately similar to ALU4_HUMAN A	2.56	1.94
	311294	AA826425	Hs.291829	ESTs	1.04	2.69
	311308	F12664	Hs.49000	ESTs	1.96	6.70
	311351	AI682303	Hs.201274	ESTs	4.77	9.38
	311390	AW392997	Hs.202280	ESTs	2.80	6.06
25	311405	AW290961	Hs.201815	ESTs	3.80	11.66
	311409	AI698839		gb:wd31f02.x1 Soares_NFL_T_GBC_S1 Homo s	3.84	6.94
	311420	AI936291	Hs.208867	ESTs	5.30	12.56
	311443	AI791521	Hs.192206	ESTs	4.39	6.09
	311467	AI934909	Hs.175377	ESTs	1.00	1.04
30	311479	AI933672	Hs.211399	ESTs	2.76	5.61
	311488	R57390	Hs.301064	arfaplin 1	2.50	5.73
	311495	AW300077	Hs.221358	ESTs	3.63	6.09
	311511	AW444568	Hs.210303	ESTs	2.00	2.87
	311534	AW130351	Hs.243549	ESTs	0.31	1.33
35	311537	AI805121	Hs.211828	ESTs	3.69	5.85
	311543	AI681360	Hs.201259	ESTs	1.73	1.34
	311551	AW449774	Hs.296380	POM (POM121 rat homolog) and ZP3 fusion	3.31	6.12
	311557	AI819230	Hs.211238	interleukin-1 homolog 1	1.00	1.00
	311558	Z44432	Hs.63128	KIAA1292 protein	2.25	3.41
40	311559	AW008271	Hs.265848	similar to rat myomegalin	2.68	5.90
	311563	AI922143	Hs.211334	ESTs	2.39	3.32
	311586	AI827834	Hs.211227	ESTs	2.47	3.85
	311616	AW450575	Hs.212709	ESTs	1.00	1.00
	311621	AI924307	Hs.213464	ESTs	4.16	6.74
45	311635	AI928456	Hs.213081	ESTs	2.17	3.76
	311668	AW193674	Hs.240044	ESTs	2.60	3.12
	311672	R11807	Hs.20914	hypothetical protein FLJ23056	2.79	5.18
	311683	AW183738	Hs.232644	ESTs	0.19	0.96
	311700	R49601	Hs.171495	retinoic acid receptor, beta	6.28	8.83
50	311714	AW131785	Hs.246831	ESTs, Weakly similar to CIKG_HUMAN VOLTA	5.00	8.17
	311735	AW294416	Hs.144687	Homo sapiens cDNA FLJ12981 fis, clone NT	0.96	0.72
	311743	T99079	Hs.191194	ESTs	1.00	1.95
	311783	AI682478	Hs.13528	hypothetical protein FLJ14054	0.16	0.77
	311785	AI056769	Hs.133512	ESTs	1.34	3.97
55	311799	AA780791	Hs.14014	ESTs, Weakly similar to KIAA0973 protein	8.52	13.32
	311819	AW265275	Hs.254325	ESTs	3.58	3.91
	311823	AI089422	Hs.131297	ESTs	1.40	1.72
	311877	AA349893	Hs.85339	G protein-coupled receptor 39	0.95	0.91
	311886	AA522738	Hs.132554	ESTs	0.88	0.87
60	311896	AW205447		gb:U1-H-B11-afg-g-02-0-U1.s1 NCI_CGAP_Su	1.66	1.13
	311910	N28365	Hs.22579	Homo sapiens clone CDABP0036 mRNA sequen	1.66	2.30
	311923	T60843	Hs.189679	ESTs	0.42	2.63
	311933	AI597963	Hs.118726	ESTs	1.88	3.02
	311959	T67262	Hs.124733	ESTs	2.02	2.33
65	311960	AW440133	Hs.189690	ESTs	3.87	6.62
	311967	AI382726	Hs.182434	ESTs	5.80	8.14
	311975	AA804374	Hs.272203	Homo sapiens cDNA FLJ20843 fis, clone AD	0.98	3.26
	312005	T78450	Hs.13941	ESTs	0.12	1.39
	312028	T78886	Hs.284450	ESTs	3.78	4.92
70	312046	AI580018	Hs.268591	ESTs	4.11	7.32
	312058	T83748	Hs.268594	ESTs	2.36	3.08
	312064	AA676713	Hs.191155	ESTs	3.34	5.28
	312088	AW303760	Hs.13685	ESTs	1.60	1.15
	312093	T91809	Hs.121296	ESTs	0.68	0.85
75	312094	Z78390		gb:HSZ78390 Human fetal brain S. Meier-E	3.05	4.48
	312097	AI352096	Hs.112180	zinc finger protein 148 (pH2-52)	4.52	9.70
	312118	T85332	Hs.178294	ESTs	2.40	2.60
	312128	AI052609	Hs.17631	Homo sapiens cDNA FLJ20118 fis, clone CO	2.39	3.53
	312147	T89855	Hs.195648	ESTs	0.67	1.03
80	312175	AA953383	Hs.127554	ESTs	5.85	10.60
	312179	AI052572	Hs.269864	ESTs	2.41	3.32
	312201	AI928365	Hs.91139	solute carrier family 1 (neuronal/epithe	0.24	0.89
	312207	H90213	Hs.191330	ESTs	2.20	4.55
	312220	N74613		gb:za55a07.s1 Soares fetal liver spleen	4.28	11.13
85	312252	AI128388	Hs.143655	ESTs	1.64	1.57
	312304	AA491949	Hs.269392	ESTs	0.12	2.47

	312318	AW235092	Hs.143981	ESTs	3.46	5.69
	312319	AA216698	Hs.180780	TERA protein	5.78	4.46
	312321	R66210	Hs.186937	ESTs	0.44	1.74
5	312331	AA825512	Hs.289101	glucose regulated protein, 58kD	3.73	5.96
	312339	AA524394	Hs.165544	ESTs	3.07	0.95
	312363	AI675558	Hs.181867	ESTs	10.08	16.73
	312375	AI375096	Hs.172405	cell division cycle 27	2.78	3.71
	312376	R52089	Hs.172717	ESTs	1.00	1.00
10	312389	AI863140		gb:tz43h12.x1 NCL_CGAP_Bm52 Homo sapien	2.37	3.98
	312437	AA995028		gb:RC4-BT0629-120200-011-b10 BT0629 Homo	4.06	5.41
	312440	AI051133	Hs.133315	Homo sapiens mRNA: cDNA DKFZp761J1324 (f	1.00	1.00
	312451	R59989	Hs.176539	ESTs	4.96	10.04
	312458	AI167637	Hs.146924	ESTs	1.11	1.00
15	312507	AI168177	Hs.143653	ESTs	5.89	8.24
	312520	AI742591	Hs.205392	ESTs	3.30	8.92
	312548	AI566228	Hs.159426	hypothetical protein PRO2121	1.38	1.65
	312564	H21520	Hs.35088	ESTs	0.40	0.77
	312583	AI193122	Hs.124141	ESTs	0.13	0.94
20	312599	AI865073	Hs.125720	ESTs	3.75	5.29
	312602	AA046451	Hs.165200	ESTs	6.78	12.93
	312645	H52121	Hs.193007	ESTs	0.38	1.13
	312666	AI240682	Hs.214678	ESTs	0.98	2.03
	312689	AW450461	Hs.203965	ESTs	0.21	0.61
	312817	H75459	Hs.233425	ESTs	1.51	0.85
25	312846	AW152104	Hs.200879	ESTs	8.93	13.78
	312873	AI690071	Hs.283552	ESTs, Weakly similar to unnamed protein	4.20	6.23
	312893	AI016204	Hs.172922	ESTs	2.67	3.15
	312902	AW292797	Hs.130316	ESTs, Weakly similar to T2D3_HUMAN TRANS	1.19	0.71
30	312925	N90888	Hs.271695	ESTs	2.50	4.25
	312936	AI681581	Hs.121525	ESTs	1.00	1.17
	312975	AI640506	Hs.293119	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.30	4.80
	312978	N24887	Hs.292500	ESTs	0.80	1.05
	312980	AA497043	Hs.115685	ESTs	3.12	3.60
35	312984	N25871	Hs.177337	ESTs	2.03	2.13
	313000	AI147412	Hs.146657	ESTs	5.52	8.42
	313029	AA731520	Hs.170504	ESTs	0.96	1.39
	313039	AI419290	Hs.149990	ESTs, Weakly similar to unnamed protein	6.48	13.20
	313049	AW293055	Hs.119357	ESTs	6.44	10.73
40	313056	AI651930	Hs.135684	ESTs	1.51	2.04
	313058	DB1015	Hs.125382	ESTs	0.25	1.50
	313070	AI422023	Hs.161338	ESTs	8.56	11.60
	313097	AI676164	Hs.204339	ESTs	3.72	4.56
	313130	AW449171	Hs.168677	ESTs	3.28	5.06
45	313136	N59284	Hs.288010	ESTs	0.49	1.36
	313153	AI240838	Hs.132750	ESTs	5.36	5.52
	313210	N74077	Hs.197043	ESTs	0.30	0.66
	313236	AW238169	Hs.83513	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.16	8.76
	313239	W19632	Hs.124170	ESTs	1.00	3.87
50	313265	N93466	Hs.121764	ESTs, Weakly similar to testicular tekti	0.74	2.06
	313267	AI770008	Hs.129583	ESTs	0.23	1.30
	313275	AI027604	Hs.159650	ESTs	6.68	9.57
	313290	AI753247	Hs.29643	Homo sapiens cDNA FLJ13103 fls, clone NT	1.34	1.07
	313292	AI362991	Hs.202121	ESTs, Weakly similar to env protein [H.s	2.00	4.32
55	313325	AI420611	Hs.127832	ESTs	1.20	2.27
	313357	AW074848	Hs.201501	ESTs	4.02	5.33
	313393	AI674685	Hs.200141	ESTs	1.36	2.84
	313399	AW376889	Hs.194097	ESTs	2.58	5.26
	313414	AI241540	Hs.132933	ESTs	6.57	15.07
60	313417	AA741151	Hs.137323	ESTs	0.63	3.01
	313457	AA576052	Hs.193223	Homo sapiens cDNA FLJ11646 fls, clone HE	2.78	4.70
	313499	AI261390	Hs.146085	KIAA1345 protein	0.91	2.37
	313516	AA029058	Hs.135145	ESTs	3.41	7.08
	313558	AA628517	Hs.118502	ESTs	0.23	0.70
65	313569	AI273419	Hs.135146	hypothetical protein FLJ13984	1.88	1.00
	313570	AA041455	Hs.209312	ESTs	0.73	2.27
	313638	AI753075	Hs.104627	Homo sapiens cDNA FLJ10158 fls, clone HE	1.00	1.72
	313662	AA740151	Hs.130425	ESTs	0.20	1.42
	313671	W49823	Hs.104813	RP42 homolog	1.00	1.00
70	313672	AW468891	Hs.122948	ESTs	3.46	5.80
	313690	AI493591	Hs.78146	platelet/endothelial cell adhesion molec	0.51	0.97
	313711	AA398070	Hs.133471	ESTs	0.18	1.01
	313723	AA070412		gb:zm68c10.s1 Stratagene neuroepithelium	1.08	1.03
	313726	AI744687	Hs.257806	ESTs	2.13	2.99
75	313774	AW136836	Hs.144583	ESTs	1.38	1.19
	313784	AA910514	Hs.134905	ESTs	3.88	5.78
	313790	AW078569	Hs.177043	ESTs	0.22	2.06
	313832	AW271022	Hs.133294	ESTs	1.15	0.91
	313834	AW418779	Hs.114889	ESTs	0.68	3.14
80	313835	AI538438	Hs.159087	ESTs	5.74	8.88
	313852	H18633	Hs.123641	protein tyrosine phosphatase, receptor t	0.16	1.14
	313854	AW470806	Hs.275002	ESTs	2.09	4.06
	313865	AA731470	Hs.163839	ESTs	3.41	4.09
	313871	AW471088	Hs.145950	ESTs	5.28	6.83
85	313883	AI949384		gb:nu76d01.s1 NCL_CGAP_Alv1 Homo sapiens	2.90	10.91
	313915	AI969390	Hs.163443	Homo sapiens cDNA FLJ11576 fls, clone HE	1.00	1.00

	313926	AW473830	Hs.171442	ESTs	3.40	4.11
	313948	AW452823	Hs.135268	ESTs	5.77	9.15
	313978	AI870175	Hs.13957	ESTs	0.46	0.75
5	313983	AI829133	Hs.226780	ESTs	4.10	6.40
	314035	AA164199	Hs.270152	ESTs	5.88	7.90
	314037	AW300048	Hs.275272	ESTs	1.00	3.79
	314040	AA166970	Hs.118748	ESTs	7.60	11.33
	314067	AW293538	Hs.51743	KIAA1340 protein	1.86	1.21
10	314103	AI028477	Hs.132775	ESTs	2.90	5.29
	314107	AA806113	Hs.189025	ESTs	2.00	1.66
	314113	AA218985	Hs.118854	ESTs	0.91	4.17
	314124	AW118745	Hs.9460	Homo sapiens mRNA; cDNA DKFZp547C244 (fr	2.53	3.32
	314126	AA226431		gb:nc18b12.s1 NCI_CGAP_Pr1 Homo sapiens	3.13	5.08
15	314128	AA935633	Hs.194628	ESTs	2.90	6.35
	314161	AA236163	Hs.202430	ESTs	4.15	6.45
	314184	AW081795	Hs.233465	ESTs	3.44	4.65
	314192	AW290975	Hs.118923	ESTs	1.00	1.23
	314244	AL036450	Hs.103238	ESTs	2.88	3.67
20	314253	AA278679	Hs.189510	ESTs	4.98	7.16
	314262	AW086215	Hs.246096	ESTs	0.38	1.94
	314320	AA811598	Hs.275809	ESTs	3.34	5.66
	314332	AL037551	Hs.95612	ESTs	2.85	2.09
	314335	AA287443	Hs.142570	Homo sapiens clone 24629 mRNA sequence	4.35	4.78
25	314340	AW304350	Hs.130879	ESTs, Moderately similar to putative p15	0.77	0.86
	314351	AA292275	Hs.193746	ESTs	3.07	3.77
	314376	AI628633	Hs.324679	ESTs	4.10	6.11
	314443	AA827125	Hs.192043	ESTs	6.20	13.67
	314458	AI217440	Hs.143873	ESTs	0.58	2.49
30	314466	AA767818	Hs.122707	ESTs	2.53	2.62
	314478	AI521173	Hs.125507	DEAD-box protein	3.94	5.65
	314482	AL043807	Hs.134182	ESTs	1.30	1.44
	314506	AA833655	Hs.206868	Homo sapiens cDNA FLJ14056 fis, clone HE	3.28	3.47
	314519	R42554	Hs.210862	T-box, brain, 1	3.12	6.16
35	314529	AL046412	Hs.202151	ESTs	3.43	6.87
	314546	AW007211	Hs.16131	hypothetical protein FLJ12876	1.38	1.00
	314562	AI564127	Hs.143493	ESTs	2.29	5.27
	314579	AW197442	Hs.116998	ESTs	3.87	5.75
	314580	AW451832	Hs.255938	ESTs, Moderately similar to KIAA1200 pro	0.10	0.71
40	314585	AA918474	Hs.216363	ESTs	1.08	1.40
	314589	AW384790	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	1.00	1.00
	314592	AA435761	Hs.192148	ESTs	0.90	2.60
	314803	AA418024	Hs.270870	ESTs	4.56	6.29
	314604	AA946582	Hs.8700	deleted in liver cancer 1	3.42	3.92
45	314606	AA418241	Hs.188767	ESTs	2.97	4.55
	314648	AA878419		gb:EST391378 MAGE resequences, MAGP Homo1.42	1.36	1.36
	314699	AI038719	Hs.132801	ESTs	3.66	4.97
	314701	AI754634	Hs.131987	ESTs	0.03	0.90
	314710	AI669131	Hs.290989	EST	3.40	7.52
50	314750	AI095005	Hs.135174	ESTs	2.80	6.54
	314767	AW135412	Hs.164002	ESTs	3.20	4.26
	314801	AA481027	Hs.109045	hypothetical protein FLJ10498	1.00	1.00
	314817	AI694139	Hs.192855	ESTs	0.91	0.99
	314835	AI281370	Hs.76064	ribosomal protein L27a	5.75	7.44
55	314852	AI903735		gb:MR-BT035-200199-031 BT035 Homo sapien	1.68	4.34
	314853	AA729232	Hs.153279	ESTs	0.60	1.85
	314940	AW452768	Hs.162045	ESTs	10.10	16.20
	314941	AA515802	Hs.130650	ESTs	0.31	1.02
	314943	AI476797	Hs.184572	cell division cycle 2, G1 to S and G2 to	2.18	0.37
60	314955	AA521382	Hs.192534	ESTs	2.59	3.90
	314973	AW273128	Hs.300268	ESTs	1.05	1.25
	315004	AA527941	Hs.325351	EST	5.64	13.63
	315006	AI538613	Hs.298241	Transmembrane protease, serine 3	0.52	1.78
	315033	AI493046	Hs.146133	ESTs	2.46	1.00
65	315035	AI569476	Hs.177135	ESTs	0.34	1.33
	315056	AI202703	Hs.152414	ESTs	2.10	2.64
	315069	AI821517	Hs.105866	ESTs	1.00	1.30
	315071	AA552690	Hs.152423	Homo sapiens cDNA: FLJ21274 fis, clone C	1.78	1.00
	315073	AW452948	Hs.257631	ESTs	1.17	1.52
70	315078	AA568548	Hs.190616	ESTs	3.00	3.79
	315080	AA744550	Hs.136345	ESTs	1.00	1.00
	315120	AA564991	Hs.269477	ESTs	0.64	1.44
	315175	AI025842	Hs.152530	ESTs	0.61	1.91
	315193	AI241331	Hs.131765	ESTs	1.06	0.97
75	315196	AA972756	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	0.48	1.96
	315200	AI808235	Hs.307686	EST	3.76	9.40
	315254	AI474433	Hs.179556	ESTs	5.37	9.36
	315353	AW452608	Hs.279610	hypothetical protein FLJ10493	1.00	1.30
	315397	AA218940	Hs.137516	fidgetin-like 1	3.38	2.24
80	315403	AW362980	Hs.163924	ESTs	2.04	5.23
	315431	AA622104	Hs.184838	ESTs	2.36	8.04
	315454	AI239473		gb:qh36f02.x1 Soares_NFL_T_GBC_S1 Homo s	3.46	7.64
	315455	AW393391	Hs.156919	ESTs	3.78	5.76
	315473	AI681671	Hs.312671	ESTs, Moderately similar to OVCA1	0.89	2.15
85	315483	AW512763	Hs.222024	transcription factor BMAL2	2.32	1.96
	315526	AI193048	Hs.128685	ESTs	1.67	1.78

	315530	AI200852	Hs.127780	ESTs	1.05	1.01
	315541	AI168233	Hs.123159	sperm associated antigen 4	0.85	0.56
	315552	AW445034	Hs.255578	ESTs	1.00	2.22
5	315562	AA737415	Hs.152826	ESTs	2.68	2.48
	315577	AW513545	Hs.17283	hypothetical protein FLJ10890	2.20	2.25
	315587	AI268399	Hs.140489	ESTs	1.00	1.04
	315589	AW072387	Hs.158258	Homo sapiens mRNA; cDNA DKFZp434B1272 (f	0.14	1.05
	315623	AA364078	Hs.258189	ESTs	7.44	12.55
10	315634	AA837085	Hs.220685	ESTs	0.50	1.40
	315668	AA912347	Hs.136585	ESTs	0.43	1.22
	315677	AI932662	Hs.164073	ESTs	0.60	1.39
	315706	AW440742	Hs.155556	hypothetical protein FLJ20202	2.18	3.77
	315707	AI418055	Hs.161160	ESTs	2.88	2.63
	315730	H25899	Hs.201591	ESTs	0.11	0.60
15	315745	AI821759	Hs.191856	ESTs	3.50	7.25
	315791	AA678177		gb:z15a05.s1 Soares_fetal_liver_spleen_	1.78	2.63
	315801	AA827752	Hs.266134	ESTs	4.31	6.23
	316820	AI652022	Hs.258785	ESTs	2.35	3.01
20	315878	AA683336	Hs.189046	ESTs	2.12	2.64
	315905	AI821911	Hs.209452	ESTs	1.03	1.97
	315923	AI052789	Hs.133263	ESTs	2.63	5.06
	315954	AW276810	Hs.254859	ESTs, Moderately similar to ALU5_HUMAN A	1.21	0.85
	315978	AA830893	Hs.119769	ESTs	3.09	3.41
25	316001	AI248584	Hs.190745	Homo sapiens cDNA: FLJ21326 fis, clone C	2.20	6.82
	316011	AW516953	Hs.201372	ESTs	0.35	1.63
	316012	AA764950	Hs.119898	ESTs	6.56	8.13
	316040	AI983409	Hs.189226	ESTs	5.69	10.69
	316048	AI720759	Hs.224971	ESTs	2.84	10.45
30	316076	AW297895	Hs.116424	ESTs	0.30	1.05
	316124	AI308862	Hs.167028	ESTs	1.00	1.43
	316151	AI806016	Hs.155520	ESTs	5.80	9.03
	316187	AW518299	Hs.192253	ESTs	1.20	3.96
	316204	AA731509	Hs.120257	ESTs	4.92	6.94
35	316232	AW297853	Hs.251203	ESTs	1.48	1.60
	316275	AI671041	Hs.292811	ESTs, Moderately similar to ALU1_HUMAN A	5.86	12.14
	316291	AW375974	Hs.156704	ESTs	2.73	2.69
	316303	AA740994	Hs.209609	ESTs	1.53	1.26
	316344	AA744518	Hs.120610	ESTs	3.66	8.34
40	316346	AI028478	Hs.157447	ESTs	3.51	6.69
	316365	AI627845	Hs.210776	ESTs	2.50	4.33
	316380	AI393378	Hs.164496	ESTs	1.16	2.16
	316470	AA809902	Hs.243813	ESTs	5.40	10.34
	316509	AA767310	Hs.291766	ESTs	2.46	2.89
45	316514	AA768037	Hs.291671	ESTs	4.70	6.04
	316519	AI929097		gb:od10c11.s1 NCI_CGAP_GCB1 Homo sapiens	4.41	9.70
	316609	AW292520	Hs.122082	ESTs	1.00	2.89
	316633	AI125586	Hs.127955	ESTs	2.61	3.72
	316700	AW172316	Hs.252961	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.46	4.64
50	316711	AI743721	Hs.285316	ESTs, Moderately similar to ALU7_HUMAN A	4.45	6.95
	316713	AI090671	Hs.134807	hypothetical protein FLJ12057	0.30	2.40
	316715	AI440266	Hs.170673	ESTs, Weakly similar to AF126780 1 retin	0.20	1.45
	316787	AW389770	Hs.130351	ESTs	4.05	5.53
	316809	AA825839	Hs.202238	ESTs	2.25	3.82
55	316811	AA922060	Hs.132471	ESTs	1.00	1.32
	316812	AW135045	Hs.232001	ESTs	3.28	4.70
	316818	AA827176	Hs.124316	ESTs	0.67	1.81
	316824	AA837416	Hs.124299	ESTs	3.53	6.00
	316827	AI380429	Hs.172445	ESTs	0.72	1.56
60	316891	AW298119	Hs.202536	ESTs	1.64	2.97
	316951	AA134365	Hs.57548	ESTs	1.45	1.08
	316970	AA860172	Hs.132406	ESTs	1.00	1.53
	316971	AA860212	Hs.170991	ESTs	1.08	1.96
	316990	AA861611	Hs.130643	ESTs	5.44	10.04
65	317001	AI627917	Hs.233694	hypothetical protein FLJ11350	3.56	4.37
	317008	AW051597	Hs.143707	ESTs	0.69	1.37
	317051	AA873253	Hs.126233	ESTs	6.18	12.72
	317128	AA971374	Hs.125674	ESTs	1.87	2.66
	317129	H12523	Hs.78521	Homo sapiens cDNA: FLJ21193 fis, clone C	4.12	6.64
70	317137	AW341567	Hs.125710	ESTs	2.82	5.12
	317196	AI348258	Hs.153412	ESTs	1.98	2.51
	317212	AI866468	Hs.148294	ESTs	1.86	2.83
	317223	AW297920	Hs.130054	ESTs	0.83	1.57
	317224	D56760	Hs.93029	sparc/osteonectin, cwcw and kazal-like d	2.74	0.86
75	317266	AA906289	Hs.203614	ESTs	1.00	1.00
	317282	AI807444	Hs.176101	ESTs	2.60	4.21
	317285	AW370882	Hs.222080	ESTs	1.96	3.49
	317302	AA908709	Hs.135564	ESTs	7.16	8.32
	317304	AW449899	Hs.130184	ESTs	1.38	2.28
80	317320	AA927151	Hs.130452	ESTs	3.58	8.13
	317413	AW341701	Hs.126622	ESTs	2.08	4.92
	317417	AA918420	Hs.145378	ESTs	3.06	4.79
	317452	AA972965	Hs.135568	ESTs	4.22	9.21
	317519	AI859895	Hs.126860	ESTs	1.88	4.15
85	317521	AI824338	Hs.126891	ESTs	3.12	4.55
	317529	AI916517	Hs.126865	ESTs	2.73	3.34

	317570	AI733361	Hs.127122	ESTs	1.00	2.43
	317571	AA938663	Hs.199828	ESTs	5.20	11.95
	317598	AW206035	Hs.192123	ESTs	0.33	1.66
5	317627	AI346110	Hs.132553	ESTs	1.50	1.39
	317650	AI733310	Hs.127346	ESTs	0.48	1.46
	317659	AA961216	Hs.127785	ESTs	4.18	7.14
	317674	AW294909	Hs.132208	ESTs	2.92	3.20
	317686	AA969051	Hs.187319	ESTs	1.00	1.01
10	317692	AI307659	Hs.174794	ESTs	5.33	9.59
	317701	AI674774	Hs.128014	ESTs	1.00	1.00
	317711	AI733015	Hs.272189	ESTs	5.13	7.81
	317722	AI733373	Hs.128119	ESTs	2.50	6.03
	317756	AA973667	Hs.128320	ESTs	1.59	1.30
15	317777	AI143525	Hs.47313	KIAA0258 gene product	1.00	2.48
	317799	AI498273	Hs.128808	ESTs	1.78	2.11
	317803	AA983251	Hs.128899	ESTs	0.80	1.06
	317821	AI368158	Hs.70983	PTPL1-associated RhoGAP 1	0.17	0.68
	317848	AI820575	Hs.129086	Homo sapiens cDNA FLJ12007 fis, clone HE	5.30	8.16
20	317850	N29974	Hs.152982	hypothetical protein FLJ13117	1.30	2.28
	317861	AW341064	Hs.129119	ESTs	2.18	5.93
	317865	AI298794	Hs.129130	ESTs	4.48	8.20
	317869	AW295184	Hs.129142	deoxyribonuclease II beta	0.44	0.99
	317881	AI827248	Hs.224398	Homo sapiens cDNA FLJ11469 fis, clone HE	4.06	2.23
25	317890	AI915599	Hs.129225	ESTs	4.68	7.48
	317899	AI952430	Hs.150614	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.14	3.37
	317986	AI005163	Hs.201378	ESTs, Weakly similar to T12545 hypotheti	0.28	1.66
	318001	AW235697	Hs.130980	ESTs	5.12	9.97
	318016	AI016694	Hs.256921	ESTs	1.86	4.50
30	318023	AW243058	Hs.131155	ESTs	2.92	5.22
	318054	AW449270	Hs.232140	ESTs	3.92	6.37
	318068	AI024540	Hs.131574	ESTs	1.21	1.27
	318117	AI208304	Hs.250114	ESTs	0.86	1.17
	318187	AI792585	Hs.133272	ESTs, Weakly similar to ALUC_HUMAN IIII	5.90	6.98
35	318223	AI077540	Hs.134090	ESTs	1.05	0.90
	318240	AI085377	Hs.143610	ESTs	3.10	2.40
	318255	AI082692	Hs.134662	ESTs	0.02	1.05
	318268	AI554341	Hs.271443	ESTs	6.12	10.55
	318330	AI093840	Hs.143758	ESTs	4.98	7.90
40	318369	AI493501	Hs.170974	ESTs	2.48	5.62
	318428	AI949409	Hs.194591	ESTs	0.77	0.45
	318458	AI149783	Hs.158438	ESTs	3.54	4.92
	318467	AI151395	Hs.144834	ESTs	4.56	5.62
	318473	AI939339	Hs.146883	ESTs	2.08	4.05
45	318476	AI693927	Hs.265165	ESTs	4.22	8.07
	318487	AI167877	Hs.143716	ESTs	1.47	1.05
	318488	AI217431	Hs.144709	ESTs	1.40	4.14
	318491	T26477	Hs.22883	ESTs, Weakly similar to ALU8_HUMAN ALU S	1.84	1.90
	318499	T25451		gb:PTH188 HTCCL1 Homo sapiens cDNA 5/3	2.58	5.20
50	318537	AA377908	Hs.13254	ESTs	3.26	4.18
	318538	N28625	Hs.74034	Homo sapiens clone 24651 mRNA sequence	0.35	1.07
	318547	R20578	Hs.90431	ESTs	3.22	4.60
	318552	R18364	Hs.90363	ESTs	4.87	9.06
	318575	R55102	Hs.107761	ESTs, Weakly similar to unnamed protein	1.91	1.98
55	318580	T34571	Hs.49007	poly(A) polymerase alpha	2.74	6.22
	318587	AA779704	Hs.168830	Homo sapiens cDNA FLJ12136 fis, clone MA	0.85	2.46
	318596	AI470235	Hs.172698	EST	4.88	4.93
	318622	T48325	Hs.237658	apolipoprotein A-II	4.80	12.51
	318629	N25163	Hs.8861	ESTs	0.39	1.04
60	318637	AA243539	Hs.9196	hypothetical protein	1.72	3.57
	318648	T77141	Hs.184411	albumin	6.27	9.91
	318650	AA393302	Hs.176626	hypothetical protein EDAG-1	3.96	8.84
	318671	AA188823	Hs.299254	Homo sapiens cDNA: FLJ23597 fis, clone L	1.53	0.81
	318679	T58115	Hs.10336	ESTs	1.00	2.19
65	318711	AI936475	Hs.101282	Homo sapiens cDNA: FLJ21238 fis, clone C	3.05	3.18
	318725	AI962487	Hs.242990	ESTs	1.08	2.46
	318728	Z30201	Hs.291289	ESTs, Weakly similar to ALU1_HUMAN ALU S	0.77	1.33
	318740	NM_002543	Hs.77729	oxidised low density lipoprotein (lectin	0.25	1.49
	318776	R24963	Hs.23766	ESTs	1.00	3.01
70	318784	H00148	Hs.5181	proliferation-associated 2G4, 38kD	2.70	3.86
	318816	F07873	Hs.21273	ESTs	3.90	7.13
	318865	H10818		gb:ym04f10.r1 Soares infant brain 1N1B H	2.25	3.56
	318879	R56332	Hs.18268	adenylate kinase 5	1.78	5.00
	318881	Z43224	Hs.124952	ESTs	4.79	14.13
75	318894	F08138	Hs.7387	DKFZP564B116 protein	5.31	7.00
	318901	AW368520	Hs.301528	L-kynurenine/alpha-aminoadipate aminotra	1.03	0.91
	318925	Z43577	Hs.21470	ESTs	2.23	3.80
	318936	AI219221	Hs.308298	ESTs	1.86	7.16
	318982	Z44140	Hs.268622	ESTs	5.84	9.79
80	318986	Z44186	Hs.169161	ESTs, Highly similar to MAON_HUMAN NADP-	1.00	1.00
	319041	Z44720	Hs.98365	ESTs, Weakly similar to weak similarity	3.38	6.11
	319103	H05896	Hs.4993	KIAA1313 protein	1.00	1.07
	319170	R13678	Hs.285306	putative selenocysteine lyase	3.79	5.03
	319196	F07953	Hs.16085	putative G-protein coupled receptor	1.00	2.98
85	319199	F07361	Hs.13306	ESTs	3.53	5.66
	319242	F11472	Hs.12839	ESTs	5.87	7.26

	319263	T65331	Hs.81360	Homo sapiens cDNA: FLJ21927 fis, clone H	1.81	1.57
	319267	F11802	Hs.6818	ESTs	1.10	4.72
	319270	R13474	Hs.290263	ESTs	4.80	10.40
5	319279	T65094	Hs.12677	CGI-147 protein	1.50	2.11
	319282	AA461358	Hs.12876	ESTs	1.00	1.00
	319289	W07304	Hs.79059	transforming growth factor, beta recepto	0.18	0.68
	319291	W86578	Hs.285243	hypothetical protein FLJ22029	0.26	0.62
	319293	F12119	Hs.12583	ESTs	3.13	4.50
10	319312	Z45481		gb:HSC2QE041 normalized Infant brain cDN	1.10	1.00
	319370	H54254	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	0.16	0.73
	319391	R06304	Hs.13911	ESTs	1.26	2.43
	319396	H67130	Hs.301743	ESTs	0.70	0.76
	319398	AA359754	Hs.191196	ESTs	2.45	3.59
15	319407	R05329		gb:ye91b04.r1 Soares fetal liver spleen	2.00	3.54
	319425	T82930		gb:yd39f07.r1 Soares fetal liver spleen	4.28	8.81
	319433	R06050	Hs.191198	ESTs	6.15	14.13
	319437	AA282420	Hs.111991	ESTs, Weakly similar to Y48A5A.1 [C.eleg	3.26	5.68
	319466	AI809937	Hs.116417	ESTs	1.76	5.65
20	319471	R06546	Hs.19717	ESTs	4.29	4.84
	319480	R06933	Hs.184221	ESTs	1.00	1.00
	319484	T91772		gb:yd52a10.s1 Soares fetal liver spleen	2.81	4.88
	319486	AI382429	Hs.250799	ESTs	2.08	2.82
	319508	T99898	Hs.270104	ESTs, Moderately similar to ALU8_HUMAN A	2.80	4.39
25	319523	T69499	Hs.191184	ESTs	1.55	3.25
	319545	R83716	Hs.14355	Homo sapiens cDNA FLJ13207 fis, clone NT	1.65	1.19
	319546	R09692		gb:yr23b12.r1 Soares fetal liver spleen	5.11	8.54
	319552	AA086106	Hs.20403	ESTs	1.89	3.36
	319582	T82998	Hs.250154	hypothetical protein FLJ12973	3.48	4.82
30	319586	D78808	Hs.283683	chromosome 8 open reading frame 4	0.26	0.82
	319604	R11679	Hs.297753	vimentin	1.68	3.41
	319609	AW247514	Hs.12293	hypothetical protein FLJ21103	3.06	4.24
	319611	H14957		gb:ym19c10.r1 Soares infant brain 1N1B H	2.76	4.24
	319653	AA770183	Hs.173515	uncharacterized hypothalamus protein HTO	2.51	3.55
35	319657	R19897	Hs.106604	ESTs	5.32	7.68
	319658	R13432	Hs.167481	syntrophin, gamma 1	3.35	5.00
	319661	H08035	Hs.21398	ESTs, Moderately similar to A Chain A, H	5.18	12.55
	319682	H06382	Hs.21400	ESTs	1.58	1.56
	319708	R15372	Hs.22664	ESTs	1.00	1.22
40	319742	T77668	Hs.21162	ESTs	2.48	3.13
	319748	R18178	Hs.295866	Homo sapiens mRNA; cDNA DKFZp434N1923 (f	3.02	4.85
	319772	R76633	Hs.22646	ESTs	4.36	11.61
	319788	AA321932	Hs.117414	KIAA1320 protein	2.56	3.68
	319805	R92857	Hs.271350	likely ortholog of mouse polydom	4.63	6.56
45	319812	N74880	Hs.264330	N-acylsphingosine amidohydrolase (acid c	0.63	1.32
	319834	AA071267		gb:zm61g01.r1 Stratagene fibroblast (937	0.30	0.94
	319878	T78517	Hs.13941	ESTs	3.99	6.44
	319882	AA258981	Hs.291392	ESTs	5.09	7.36
	319912	T77559	Hs.84109	Homo sapiens cDNA FLJ13634 fis, clone PL	3.24	3.21
50	319935	H79460	Hs.271722	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.40	9.42
	319944	T79248	Hs.133510	ESTs	3.31	5.39
	319947	AA160967	Hs.14479	Homo sapiens cDNA FLJ14199 fis, clone NT	2.90	4.95
	319962	H06350	Hs.135056	Human DNA sequence from clone RP5-850E9	1.81	1.57
	320007	AA336314		gb:EST40943 Endometrial tumor Homo sapie	3.42	6.29
55	320018	T83263		gb:yd40h09.r1 Soares fetal liver spleen	2.77	5.14
	320030	H63789	Hs.296288	ESTs, Weakly similar to KIAA0638 protein	4.10	6.69
	320032	AI699772	Hs.292664	ESTs, Weakly similar to A46010 X-linked	3.27	3.27
	320040	AA233871	Hs.87164	hypothetical protein FLJ14001	1.81	1.64
	320047	T86564	Hs.302256	EST	3.38	7.36
60	320063	AA074108	Hs.120844	FOXJ2 forkhead factor	5.90	16.73
	320096	H58138	Hs.117915	ESTs	2.08	4.47
	320099	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	1.00	1.00
	320112	T92107	Hs.188489	ESTs	2.27	2.06
	320140	H94179	Hs.119023	SMC2 (structural maintenance of chromoso	1.00	1.00
65	320188	AW419200	Hs.172318	ESTs	1.26	1.00
	320193	AA831259	Hs.17132	ESTs	2.58	6.23
	320195	R62203	Hs.24321	Homo sapiens cDNA FLJ12028 fis, clone HE	2.85	4.53
	320199	R78659	Hs.29792	ESTs	0.40	0.94
	320203	AL049227	Hs.124776	Homo sapiens mRNA; cDNA DKFZp564N116 (f	0.84	1.18
70	320219	AA327564	Hs.127011	tubulointerstitial nephritis antigen	1.00	1.17
	320220	AF054910	Hs.127111	tektin 2 (testicular)	0.18	1.09
	320225	AF058989	Hs.128231	G antigen, family B, 1 (prostate associa	5.26	13.75
	320231	H03139	Hs.24683	ESTs	1.59	1.93
	320260	NM_003608	Hs.131924	G protein-coupled receptor 65	1.38	4.56
75	320267	AL049337	Hs.132571	Homo sapiens mRNA; cDNA DKFZp564P016 (fr	1.00	1.92
	320268	H06019	Hs.151293	Homo sapiens cDNA FLJ10664 fis, clone NT	5.58	5.70
	320322	AF077374	Hs.139322	small proline-rich protein 3	1.41	1.01
	320325	AI167978	Hs.139851	caveolin 2	0.05	0.67
	320330	AF026004	Hs.141660	chloride channel 2	2.17	1.26
80	320339	H10807	Hs.281434	Homo sapiens cDNA FLJ14028 fis, clone HE	1.81	2.32
	320388	H16065	Hs.31286	ESTs	1.00	3.22
	320402	R22291	Hs.23368	Homo sapiens clone FLC0578 PRO2852 mRNA,	1.41	1.36
	320413	AA203711	Hs.173269	ESTs	2.31	3.61
	320432	R62786	Hs.124136	ESTs	11.25	20.78
85	320436	AA253352	Hs.293663	ESTs	2.22	3.49
	320438	W24548	Hs.5669	ESTs	3.53	8.14

	320448	AI240233	Hs.80887	v-yes-1 Yamaguchi sarcoma viral related	1.42	3.46
	320451	R26944	Hs.180777	Homo sapiens mRNA; cDNA DKFZp564M0264 (f	0.87	0.81
	320484	AA094436	Hs.298267	folliculin-like 1	0.65	1.18
5	320499	R32555	Hs.24321	Homo sapiens cDNA FLJ12028 fis, clone HE	3.44	7.15
	320514	AB007978	Hs.158278	KIAA0509 protein	6.44	13.62
	320521	N31464	Hs.24743	hypothetical protein FLJ20171	1.48	1.04
	320526	AW374205	Hs.111314	ESTs	3.66	7.87
	320527	R34672	Hs.324522	ESTs	3.16	5.63
10	320536	AA331732	Hs.137224	ESTs	2.83	5.83
	320556	AF054177	Hs.14570	hypothetical protein FLJ22530	1.28	1.00
	320564	AF056209	Hs.159396	peptidylglycine alpha-amidating monooxyg	1.22	0.81
	320587	Z44524	Hs.167456	Homo sapiens mRNA full length insert cDN	1.84	2.44
	320635	R54159	Hs.80508	small nuclear ribonucleoprotein polypept	1.00	6.25
	320639	AA243258	Hs.7395	hypothetical protein FLJ23182	2.60	2.30
15	320648	N48521	Hs.26549	Homo sapiens mRNA for KIAA1708 protein,	1.00	1.53
	320651	AA489268	Hs.111334	ferritin, light polypeptide	0.14	0.79
	320664	AI904216	Hs.91251	hypothetical protein FLJ11198	5.02	8.84
	320676	AA132650	Hs.300511	ESTs	3.63	5.37
	320683	R59291	Hs.26638	ESTs, Weakly similar to unnamed protein	0.37	1.31
20	320689	AA334609	Hs.171929	ESTs, Weakly similar to A54849 collagen	1.27	1.02
	320696	AW135016	Hs.172780	ESTs	3.53	4.60
	320714	AI445591		gb:yc04a10.r1 Soares fetal liver spleen	1.06	0.85
	320727	U96044	Hs.181125	immunoglobulin lambda locus	1.35	1.49
25	320771	AI793266	Hs.117176	poly(A)-binding protein, nuclear 1	0.04	0.82
	320794	AA281993	Hs.91226	ESTs	2.96	4.33
	320822	AF100780	Hs.194679	WNT1 Inducible signaling pathway protein	0.10	0.79
	320824	AF120274	Hs.194689	arlemiln	1.16	1.11
	320830	AJ132445	Hs.266416	claudin 14	1.06	1.75
30	320843	AA317372	Hs.34744	Homo sapiens mRNA; cDNA DKFZp547C136 (fr	1.36	1.47
	320849	D60031	Hs.34771	ESTs	5.30	7.49
	320853	AI473796	Hs.135904	ESTs	1.00	1.00
	320896	AB002155	Hs.271580	uropalakin 1B	5.90	2.55
	320921	R94038	Hs.199538	Inhibin, beta C	2.20	1.17
35	320927	AI205786	Hs.213923	ESTs	0.18	1.46
	320957	AI878933	Hs.92023	core histone macroH2A.2	1.67	2.18
	320997	H22544		gb:yn69f11.r1 Soares adult brain N2b5HB5	3.26	3.62
	321045	W88483	Hs.293650	ESTs	2.25	4.55
	321046	H27794	Hs.269055	ESTs	2.69	4.25
40	321052	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	2.14	2.66
	321059	AI092824	Hs.126465	ESTs	1.69	0.53
	321062	R87955	Hs.241411	Homo sapiens mRNA full length insert cDN	2.76	5.20
	321067	AF131782	Hs.241438	Homo sapiens clone 24941 mRNA sequence	4.79	7.41
	321102	AA018306		gb:ze40d08.r1 Soares retina N2b4HR Homo	1.79	4.27
45	321130	H43750	Hs.125494	ESTs	1.00	3.14
	321142	AI817933	Hs.298351	ASPL protein	8.73	15.36
	321155	AA336635	Hs.99598	hypothetical protein MGC5338	3.04	5.03
	321158	AA700289		gb:yu76f11.r1 Soares fetal liver spleen	4.62	8.39
	321170	N53742	Hs.172982	ESTs	2.21	4.46
50	321199	AW385512		gb:yy56d10.s1 Soares_multiple_sclerosis_	5.69	8.01
	321206	H54178	Hs.226469	Homo sapiens cDNA FLJ12417 fis, clone MA	4.00	7.32
	321225	AL080073	Hs.251414	Homo sapiens mRNA; cDNA DKFZp564B1462 (f	4.17	4.63
	321236	AW371941	Hs.18192	Ser/Arg-related nuclear matrix protein (1.00	1.00
	321244	AF058654		gb:Homo sapiens isolate AN.1 Immunoglobu	2.18	9.13
55	321270	R83560		gb:yv76c06.s1 Soares fetal liver spleen	3.80	5.26
	321317	AI937060	Hs.6298	KIAA1151 protein	1.81	1.65
	321318	AB033041	Hs.137507	KIAA1215 protein	1.00	1.00
	321325	AB033100	Hs.300646	KIAA protein (similar to mouse paladin)	0.44	0.93
	321342	AA127984	Hs.222024	transcription factor BMAL2	4.94	4.93
60	321356	R93443	Hs.271770	ESTs	3.10	4.66
	321418	AI739161	Hs.161075	ESTs	2.28	2.54
	321420	AI368667	Hs.132743	ESTs	1.13	0.97
	321430	U05890		gb:H.sapiens (DIG3) mRNA for immunoglobu	2.42	3.35
	321453	N50080	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H	1.60	3.11
65	321467	X13075		gb:Human 2a12 mRNA for kappa-immunoglobu	0.42	0.72
	321468	AA514198	Hs.38540	ESTs	2.46	6.50
	321491	H70865	Hs.292549	ESTs	1.00	1.25
	321498	AW295517	Hs.255436	ESTs	3.19	6.24
	321504	W02356	Hs.268980	ESTs	2.28	3.86
70	321510	AA703650	Hs.255748	ESTs	2.14	3.94
	321513	H84972	Hs.108651	ESTs	2.78	5.37
	321516	AI382803	Hs.159235	ESTs	3.06	7.19
	321565	AI525773	Hs.268514	hypothetical protein FLJ11342	4.89	7.82
	321577	H84260		gb:ys90g04.r1 Soares retina N2b5HR Homo	1.00	1.73
75	321581	AA019984	Hs.28803	ESTs	4.88	6.73
	321582	AA143755	Hs.21858	trinucleotide repeat containing 3	1.00	2.08
	321587	H95531		gb:ys76e02.r1 Soares retina N2b4HR Homo	2.26	4.52
	321626	AA295430	Hs.96322	hypothetical protein FLJ23560	1.95	3.83
	321628	H87064	Hs.161051	ESTs, Moderately similar to ALU6_HUMAN A	0.47	1.02
80	321642	AW085917	Hs.247084	ESTs	1.52	1.38
	321669	H95404	Hs.294110	ESTs	2.17	2.45
	321687	AA625149		gb:af70c12.r1 Soares_NhHMPu_S1 Homo sapi	4.31	6.95
	321688	H97646	Hs.123158	Homo sapiens cDNA FLJ12830 fis, clone NT	2.82	3.28
	321693	AA700017	Hs.173737	ras-related C3 botulinum toxin substrate	0.51	1.08
85	321700	N55160	Hs.167260	ESTs	4.57	7.46
	321701	AW390923	Hs.42568	ESTs	1.00	1.00

	321709	N25847	Hs.108923	RAB38, member RAS oncogene family	1.00	1.00
	321710	N35682	Hs.259743	ESTs	2.97	5.26
	321775	AI694875	Hs.202312	Homo sapiens clone N11 NTera2D1 teratoca	1.00	1.00
5	321777	AI637993	Hs.202312	Homo sapiens clone N11 NTera2D1 teratoca	1.68	0.45
	321779	N42729	Hs.163835	ESTs	0.90	0.90
	321829	D81993	Hs.8966	tumor endothelial marker 8	2.69	3.89
	321846	AA281594	Hs.87902	ESTs	5.11	7.64
	321879	AL109670	Hs.302809	ESTs	6.49	9.58
10	321883	AA426494	Hs.46901	KIAA1462 protein	0.28	0.95
	321899	N55158	Hs.29468	ESTs	0.39	0.95
	321911	AF026944	Hs.293797	ESTs	6.20	10.76
	321949	R49202	Hs.181694	EST	4.62	10.51
	321955	AI651866	Hs.195689	ESTs	2.89	5.47
	321956	AL110177	Hs.132882	ESTs	0.32	1.25
15	321987	AL133612	Hs.272759	KIAA1457 protein	1.00	1.83
	321991	AL133627	Hs.158923	Homo sapiens mRNA; cDNA DKFZp434K0722 (f	4.00	6.47
	322002	AA328801	Hs.84522	ESTs	2.10	3.48
	322035	AL137517	Hs.306201	hypothetical protein DKFZp564O1278	1.00	1.90
20	322044	AW340926		gb:xy51b10.x1 NCI_CGAP_Lu34.1 Homo sapie	3.20	9.67
	322057	N92197	Hs.154679	synaptotagmin 1	1.55	1.07
	322060	AI341937		gb:qt10e03.x1 NCI_CGAP_GC4 Homo sapiens	4.59	7.68
	322070	U80769	Hs.210322	Homo sapiens mRNA for KIAA1766 protein,	2.78	4.52
	322083	AF074982	Hs.226031	ESTs, Highly similar to KIAA0535 protein	3.10	5.52
	322091	AI819863	Hs.108243	ESTs	1.59	1.75
25	322125	R93901		gb:yq16c12.r1 Soares fetal liver spleen	2.06	5.27
	322130	R98978	Hs.117767	ESTs	10.12	16.49
	322147	AF085919	Hs.114176	ESTs	0.94	0.64
	322166	AF085958		gb:yr88b03.r1 Soares fetal liver spleen	4.09	6.67
30	322173	H52587		gb:y185d04.r1 Soares_pineal_gland_N3HPG	3.46	4.85
	322178	H56535		gb:y188g03.r1 Soares_pineal_gland_N3HPG	0.44	2.54
	322179	H92891		gb:y194c02.s1 Soares_pineal_gland_N3HPG	4.52	7.50
	322186	H67346	Hs.269187	ESTs	0.15	0.98
	322196	W87895	Hs.211516	ESTs	2.20	5.04
35	322212	AF087995	Hs.134877	ESTs	3.42	4.84
	322221	AI890619	Hs.179562	nucleosome assembly protein 1-like 1	0.82	2.14
	322277	AI640193	Hs.226389	ESTs	3.62	3.98
	322278	AF086283		gb:zd46f01.r1 Soares_fetal_heart_NbHH19W	1.00	1.00
	322284	AI792140	Hs.49265	ESTs	0.66	2.76
	322288	AL037273	Hs.7886	pellino (Drosophila) homolog 1	0.71	0.70
40	322320	AF086419		gb:zd78d03.r1 Soares_fetal_heart_NbHH19W	2.02	2.76
	322336	AA308526	Hs.76152	decorin	2.92	4.44
	322339	W17348		gb:zb18c07.x5 Soares_fetal_lung_NbHL19W	8.50	11.56
	322366	AW404274	Hs.122492	hypothetical protein	0.61	1.34
45	322372	W25624	Hs.153943	ESTs	7.37	12.07
	322374	AI394663	Hs.122116	ESTs, Moderately similar to Osf2 [M.musc	4.78	10.50
	322378	AF054819	Hs.201877	DESC1 protein	1.00	1.00
	322388	AI815730	Hs.247474	hypothetical protein FLJ21032	7.09	8.49
	322416	AA223183	Hs.298442	adaptor-related protein complex 3, mu 1	3.20	5.80
50	322419	AA248987	Hs.14084	ring finger protein 7	1.64	1.57
	322425	W37943	Hs.34892	KIAA1323 protein	0.83	1.00
	322431	AA069222	Hs.141892	ESTs	3.96	5.22
	322450	AA040131	Hs.25144	ESTs	5.18	12.67
	322465	AA137152	Hs.286049	phosphoserine aminotransferase	3.41	2.23
55	322467	AF116826	Hs.180340	putative protein-tyrosine kinase	1.00	1.30
	322473	AA744286	Hs.266935	tRNA selenocysteine associated protein	1.75	2.03
	322509	T52172	Hs.302213	ESTs	1.00	2.27
	322523	W80398	Hs.193197	ESTs	2.75	5.49
	322527	AF147359		gb:Homo sapiens full length insert cDNA	1.25	1.27
60	322560	AI916847	Hs.270947	ESTs	4.57	8.81
	322566	W87285	Hs.269587	ESTs	1.00	1.42
	322585	AA837622		gb:zh69c01.r1 Soares_fetal_liver_spleen_	4.18	6.94
	322635	AA679084		gb:zh90h08.r1 Soares_fetal_liver_spleen_	2.40	4.85
	322641	AA007352	Hs.256042	ESTs	2.94	4.64
65	322653	AI828854	Hs.258538	striatin, calmodulin-binding protein	0.48	0.38
	322664	AA011522		gb:zi03g07.r1 Soares_fetal_liver_spleen_	1.92	2.18
	322687	AI110759		gb:AF074668 Human fetal liver cDNA libra	4.14	6.75
	322692	AA018117	Hs.60843	potassium voltage-gated channel, shaker-	3.50	5.00
	322694	AI110872	Hs.279812	PRO0327 protein	1.80	1.72
70	322708	AF113674	Hs.283773	clone FLB1727	1.00	3.43
	322712	AA021328	Hs.23607	hypothetical protein FLJ11109	3.28	3.86
	322766	AW068805	Hs.288467	Homo sapiens cDNA FLJ12280 fis, clone MA	1.63	1.53
	322770	AA045796	Hs.122682	ESTs	1.53	1.06
	322794	AI808591	Hs.38991	S100 calcium-binding protein A2	12.05	1.94
75	322810	AI962276	Hs.127444	ESTs	4.09	6.90
	322818	AW043782	Hs.293616	ESTs	1.20	1.63
	322820	AI377755	Hs.120895	ESTs	0.21	1.93
	322872	AA827228	Hs.126943	ESTs	2.04	1.63
	322882	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE	5.26	1.22
80	322887	AI986306	Hs.86149	phosphoinositol 3-phosphate-binding prot	2.80	2.24
	322913	AI733737	Hs.68837	ESTs	2.38	6.61
	322926	AI825940	Hs.211192	ESTs	4.02	5.79
	322929	AI365585	Hs.146246	ESTs	0.30	1.14
	322958	AI905228	Hs.83484	SRY (sex determining region Y)-box 4	2.06	1.13
85	322971	C15953	Hs.212760	hypothetical protein FLJ13649	1.18	2.00
	322981	AA493252	Hs.159577	ESTs	2.28	2.61

	322988	C18727	Hs.171941	ESTs	0.39	2.00
	323003	AI733859	Hs.149089	ESTs	3.28	1.00
	323013	AA134042	Hs.191451	ESTs	3.38	5.68
5	323025	AL157565	Hs.315369	Homo sapiens cDNA: FLJ23075 fis, clone L	0.06	1.10
	323032	AW244073	Hs.145946	ESTs	10.18	21.27
	323052	R21124	Hs.85573	Homo sapiens DC29 mRNA, complete cds	1.46	1.90
	323064	AL119341	Hs.49359	Homo sapiens mRNA; cDNA DKFZp547E052 (fr	3.08	5.64
	323098	AI700025	Hs.270471	ESTs	2.31	4.49
10	323102	AL119913	Hs.163615	ESTs	5.38	11.64
	323155	AL135041		gb:DKFZp762K2310_r1 762 (synonym: hmel2)	2.38	5.56
	323176	AW071648	Hs.82101	pleckstrin homology-like domain, family	1.06	1.41
	323191	AA195600	Hs.301570	ESTs	0.73	1.24
	323225	AA205654	Hs.24790	KIAA1573 protein	5.25	11.95
15	323232	AA148722	Hs.224680	ESTs	0.45	1.35
	323266	AW003362	Hs.243885	nuclear autoantigenic sperm protein (his	1.71	1.83
	323281	AI697555	Hs.292659	ESTs	1.24	3.21
	323283	AA256014	Hs.86682	Homo sapiens cDNA: FLJ21578 fis, clone C	12.68	15.05
	323314	AA226310	Hs.191501	ESTs	4.42	9.61
20	323316	AL134620	Hs.280175	ESTs	2.98	5.93
	323334	AI336501	Hs.77273	ras homolog gene family, member A	1.98	3.30
	323338	R74219	Hs.23348	S-phase kinase-associated protein 2 (p45	1.62	1.00
	323348	AA233056	Hs.191518	ESTs	1.00	1.07
	323351	AA704103	Hs.24049	ESTs	1.43	1.68
25	323359	AA234172	Hs.137418	ESTs	0.34	1.18
	323360	AA716061	Hs.161719	ESTs	3.01	3.71
	323405	AW139550	Hs.115173	ESTs	1.90	8.81
	323420	AI672386	Hs.263780	ESTs	0.29	1.01
	323434	AW081455	Hs.120219	ESTs	2.27	1.92
30	323445	AA253103	Hs.135569	ESTs, Weakly similar to NEUROD (H.sapien	0.43	0.80
	323449	AA262865	Hs.284153	Fanconi anemia, complementation group A	3.19	3.85
	323492	H00978	Hs.20887	hypothetical protein FLJ10392	2.70	3.20
	323501	AA182461	Hs.84520	ESTs	2.04	3.31
	323505	AI652287		gb:EST382593 MAGE resequences, MAGK Homo2.21	2.21	3.08
35	323515	AA282274	Hs.256083	ESTs	2.69	3.40
	323541	AI185116	Hs.104613	RP42 homolog	1.20	1.09
	323545	AI814405	Hs.224569	ESTs	1.25	1.55
	323635	R63117	Hs.9691	Homo sapiens cDNA: FLJ23249 fis, clone C	0.27	0.72
	323675	AA984759	Hs.272168	tumor differentially expressed 1	3.70	5.80
40	323678	AL042121	Hs.20880	ESTs	3.33	5.10
	323691	AA317561	Hs.145599	ESTs	1.00	1.00
	323693	AW297758	Hs.249721	ESTs	2.01	1.54
	323746	AW298611	Hs.12808	MARK	4.11	5.53
	323774	AA329806	Hs.321056	Homo sapiens mRNA; cDNA DKFZp586F1322 (f	2.06	3.70
45	323856	AA355264	Hs.267604	hypothetical protein FLJ10450	3.42	8.13
	323857	T18988	Hs.293668	ESTs	5.97	12.51
	323870	AA341774	Hs.129212	ESTs	3.17	4.52
	323876	AL042492	Hs.147313	ESTs	0.36	1.00
	323885	AA344308	Hs.128427	Homo sapiens BAC clone RP11-335J18 from	2.31	3.33
50	323911	AL043212	Hs.92550	ESTs	4.38	5.41
	323919	AA862973	Hs.220704	ESTs	5.80	10.20
	323972	AI869964	Hs.182906	ESTs	3.10	6.14
	324005	AA610011	Hs.208021	ESTs	5.34	10.07
	324036	AI472078	Hs.303662	ESTs	1.00	5.03
55	324055	AA528794	Hs.128644	ESTs	0.86	1.00
	324063	AW292740	Hs.272813	dual oxidase 1	0.45	0.91
	324072	AA381829		gb:EST94855 Activated T-cells I Homo sap	2.82	5.12
	324092	AW269931	Hs.202473	Homo sapiens cDNA: FLJ22278 fis, clone H	2.40	2.52
	324095	AW377983	Hs.298140	Homo sapiens cDNA: FLJ22502 fis, clone H	1.32	4.30
60	324129	AI381918	Hs.285833	Homo sapiens cDNA: FLJ22135 fis, clone H	1.40	1.77
	324132	AW504860	Hs.288836	hypothetical protein FLJ12673	4.24	6.21
	324214	AA412395	Hs.225740	ESTs	6.96	10.69
	324227	AA295552	Hs.28631	Homo sapiens cDNA: FLJ22141 fis, clone H	0.81	0.53
	324266	AL047634	Hs.231913	ESTs	2.42	4.05
65	324275	AA429088	Hs.98523	ESTs	3.62	5.38
	324281	AL048026	Hs.124675	ESTs, Weakly similar to T14742 hypotheti	0.14	0.70
	324290	AA432032	Hs.304420	ESTs	3.71	4.34
	324303	AL118754		gb:DKFZp761P1910_r1 761 (synonym: hamy2)	0.95	0.91
	324312	AI198841	Hs.128173	ESTs	4.08	5.91
70	324325	AL138153	Hs.300410	ESTs	5.88	8.25
	324338	AL138357	Hs.145078	regulator of differentiation (in S. pomb	0.87	1.25
	324341	AW197734	Hs.99807	ESTs, Weakly similar to unnamed protein	1.28	1.00
	324343	AW452016	Hs.293232	ESTs	2.54	3.46
	324371	AA452305	Hs.270319	ESTs	5.85	8.36
75	324382	AW502749	Hs.24724	MFH-amplified sequences with leucine-ric	0.76	1.64
	324384	AA453395	Hs.127656	KIAA1349 protein	2.88	5.69
	324385	F28212	Hs.284247	KIAA1491 protein	1.81	1.99
	324388	AI924963	Hs.306206	hypothetical protein FLJ11215	1.00	1.00
	324432	AA464510	Hs.152812	ESTs	2.73	2.17
	324497	AW152624	Hs.136340	ESTs, Weakly similar to unnamed protein	0.71	1.90
80	324510	AI148353	Hs.287425	Homo sapiens cDNA FLJ11569 fis, clone HE	1.00	1.00
	324580	AA492588		gb:ng99c08.s1 NCI_CGAP_Thy1 Homo sapiens	2.18	3.50
	324582	AA506935	Hs.132036	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.98	11.36
	324633	AA572994	Hs.325489	ESTs	2.92	4.22
	324640	AW295832	Hs.134798	ESTs, Moderately similar to TTL MOUSE TU	5.48	11.74
85	324675	AW014734	Hs.157969	ESTs	0.39	0.73

	324699	AW504732	Hs.21275	hypothetical protein FLJ11011	0.93	0.93
	324747	AA603532	Hs.130807	ESTs	1.57	1.81
	324748	AA657457	Hs.292385	ESTs	1.55	1.34
5	324801	AI819924	Hs.14553	sterol O-acyltransferase (acyl-Coenzyme	1.00	6.56
	324804	AI692552		gb:wd73f12.x1 NCI_CGAP_Lu24 Homo sapiens	1.00	7.53
	324828	AA843926	Hs.124434	ESTs	2.00	3.25
	324855	AW152305	Hs.122364	ESTs	2.74	3.43
	324866	AI541214	Hs.46320	Small proline-rich protein SPRK (human,	1.07	0.95
10	324871	AW297755	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	1.68	1.21
	324886	AA808794	Hs.131511	ESTs	2.56	5.61
	324889	D31010		gb:HUML12147 Human fetal lung Homo sapie	2.20	4.65
	324948	AW383618	Hs.265459	ESTs, Moderately similar to ALU2_HUMAN A	5.28	7.05
	324953	AI264628	Hs.125428	ESTs	3.37	5.51
15	324958	AA625076	Hs.132892	protocadherin 20	5.12	9.81
	324988	T06997	Hs.121028	hypothetical protein FLJ10549	2.52	1.08
	325024	F13254	Hs.78672	laminin, alpha 4	5.24	10.22
	325105	H97109	Hs.105421	ESTs	1.00	1.00
	325108	AA401863	Hs.22380	ESTs	1.99	2.14
20	325114	D83901	Hs.315562	ESTs	2.73	3.17
	325146	AI064690	Hs.171176	ESTs	1.86	3.41
	325149	D61117	Hs.187646	ESTs	0.42	0.93
	325187	AI653882	Hs.197812	ESTs	6.50	11.31
	325228				6.18	15.76
25	325235				2.64	4.12
	325328				2.87	4.42
	325340				0.29	0.33
	325367				16.56	24.29
	325373				0.63	1.22
30	325389				0.88	1.05
	325436				5.75	14.14
	325471				8.46	17.82
	325498				3.32	6.42
	325557				5.51	8.28
35	325559				7.48	21.40
	325560				4.08	6.25
	325569				4.20	5.24
	325585				1.10	1.13
	325587				1.00	1.00
40	325597				2.98	13.40
	325639				0.78	0.78
	325685				0.46	0.66
	325686				0.95	1.55
	325735				4.48	9.20
45	325739				0.69	0.88
	325740				2.42	6.61
	325792				7.88	9.83
	325819				4.74	7.18
	325883				2.02	2.64
50	325895				7.78	15.98
	325925				2.04	10.60
	325932				4.18	7.36
	325941				3.66	9.03
	325969				0.61	0.80
55	325971				4.88	7.42
	326025				0.55	1.07
	326046				7.21	14.72
	326099				3.60	5.98
	326108				1.27	1.08
60	326163				3.27	6.70
	326165				0.45	1.11
	326189				0.13	0.45
	326204				5.60	9.00
	326230				7.00	12.01
65	326274				1.00	8.09
	326360				9.86	15.35
	326393				0.52	0.77
	326505				1.00	1.42
	326515				1.24	5.84
70	326589				9.20	13.49
	326592				2.77	4.01
	326605				2.01	2.53
	326692				1.00	1.00
	326693				1.00	1.31
75	326720				0.19	0.65
	326742				2.34	7.20
	326770				0.25	0.83
	326818				3.09	4.56
	326936				2.08	3.45
80	326964				0.41	1.70
	326983				2.02	3.80
	326991				1.09	1.20
	327036				1.00	8.04
	327040				3.05	4.22
85	327053				3.55	6.31
	327075				1.59	1.40

	327085	2.50	12.57
	327130	5.38	8.04
	327156	3.74	6.58
5	327220	1.28	1.54
	327224	6.56	12.91
	327288	2.61	5.40
	327321	2.42	3.11
	327332	6.62	10.58
10	327361	2.69	4.41
	327377	2.04	6.72
	327396	2.61	4.50
	327414	1.00	8.01
	327442	5.91	9.65
15	327467	6.58	18.01
	327473	3.79	7.48
	327483	4.08	8.87
	327562	0.68	2.86
	327568	1.00	2.00
20	327608	2.06	3.61
	327611	5.90	14.26
	327642	4.06	8.74
	327654	1.05	2.08
	327734	1.00	1.00
25	327776	1.46	11.79
	327796	3.47	5.65
	327840	3.28	6.64
	327940	6.84	15.58
	327984	0.36	1.50
30	328004	1.87	1.42
	328021	0.42	0.69
	328068	2.83	4.68
	328100	3.04	5.39
	328101	3.54	5.20
35	328113	0.72	0.91
	328157	5.58	5.16
	328196	5.76	11.13
	328197	5.98	10.58
	328264	3.11	4.88
40	328299	2.20	3.06
	328342	1.49	1.94
	328365	1.00	1.00
	328369	4.40	7.36
	328381	1.86	4.93
45	328451	5.51	7.56
	328481	0.13	0.72
	328500	2.71	3.97
	328530	5.41	7.62
	328600	3.14	10.68
50	328608	4.56	8.17
	328616	2.24	11.91
	328623	3.04	5.46
	328632	0.70	1.19
	328664	3.48	6.80
55	328666	10.42	26.47
	328698	9.68	14.56
	328700	2.74	10.22
	328708	0.15	0.57
	328735	6.23	8.91
60	328743	3.62	6.54
	328808	0.22	0.78
	328861	3.68	10.54
	328908	5.42	16.36
	328933	2.02	5.29
65	328934	1.73	4.45
	328949	3.34	5.41
	329005	2.88	7.26
	329011	2.52	3.72
	329033	1.00	1.03
70	329037	5.07	8.16
	329067	1.98	2.41
	329134	2.24	3.25
	329157	2.30	11.04
	329178	2.64	5.02
75	329192	6.41	15.27
	329194	0.31	0.79
	329204	1.60	3.75
	329224	2.99	8.11
	329228	0.83	0.83
80	329288	0.63	1.01
	329337	1.00	1.00
	329541	0.76	1.68
	329560	1.34	2.02
	329588	1.68	2.22
85	329643	4.18	11.77
	329703	1.00	1.00

	329764			5.78	15.50	
	329816			2.09	5.44	
	329860			3.13	10.77	
	329993			7.83	14.21	
5	330020			5.58	13.12	
	330036			3.32	5.57	
	330052			4.31	7.97	
	330085			1.34	1.76	
	330088			4.70	12.46	
10	330093			0.44	1.06	
	330100			3.47	4.83	
	330106			2.14	3.61	
	330107			3.17	6.87	
	330120			5.61	11.89	
15	330123			4.50	12.74	
	330208			1.55	7.62	
	330283			13.10	23.38	
	330300			2.81	4.98	
	330313			3.00	4.41	
20	330366			0.67	0.76	
	330372			4.76	11.82	
	330385	AA449749	Hs.182971	karyopherin alpha 5 (Importin alpha 6)	2.14	2.15
	330397	D14659	Hs.154387	KIAA0103 gene product	0.40	1.15
	330468	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	1.11	0.94
25	330472	L24203	Hs.82237	ataxia-telangiectasia group D-associated	1.67	1.17
	330478	L38486	Hs.295049	microfibrillar-associated protein 4	0.46	1.07
	330493	M27826	Hs.267319	endogenous retroviral protease	1.07	0.95
	330495	M31328	Hs.71642	guanine nucleotide binding protein (G pr	0.97	0.96
	330506	M61906	Hs.6241	phosphoinositide-3-kinase, regulatory su	0.17	3.66
30	330512	M80563	Hs.81256	S100 calcium-binding protein A4 (calcium	0.60	1.06
	330537	U19765	Hs.2110	zinc finger protein 9 (a cellular retrov	2.81	2.07
	330547	U32989	Hs.183671	tryptophan 2,3-dioxygenase	3.91	1.49
	330551	U39840	Hs.299867	hepatocyte nuclear factor 3, alpha	1.15	1.03
	330568	U56244		(NONE)	2.83	4.79
35	330599	U90437		gb:Human RP1 homolog mRNA, 3'UTR region	2.08	1.54
	330601	U90916	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H	0.89	1.35
	330605	X02419	Hs.77274	plasminogen activator, urokinase	1.87	1.55
	330609	X04741	Hs.76118	ubiquitin carboxyl-terminal esterase L1	1.83	1.30
40	330617	X53587	Hs.85266	integrin, beta 4	1.54	1.15
	330630	X78669	Hs.79088	reticulocalbin 2, EF-hand calcium bindin	1.39	1.19
	330644	Y07755	Hs.38991	S100 calcium-binding protein A2	3.83	1.13
	330650	Z68228	Hs.2340	junction plakoglobin	1.25	0.95
	330660	AA347868	Hs.139293	ESTs, Weakly similar to ALU7_HUMAN ALU S	15.50	29.07
	330692	AA017045	Hs.6702	ESTs	1.00	1.00
45	330707	AA133891	Hs.293690	ESTs	0.20	1.35
	330715	AA233707	Hs.11571	Homo sapiens cDNA FLJ11570 fis, clone HE	0.12	1.40
	330717	AA233926	Hs.52620	Integrin, beta 8	6.62	5.42
	330722	AA243560	Hs.34382	ESTs	1.40	1.65
50	330740	AA297746	Hs.22854	Homo sapiens voltage-gated sodium channe	0.27	2.04
	330742	AA400979	Hs.25691	receptor (calcitonin) activity modifying	0.44	0.90
	330744	AA408142	Hs.12393	dTDP-D-glucose 4,6-dehydratase	0.71	3.23
	330751	AA428286	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT	1.66	1.52
	330760	AA448663	Hs.30469	ESTs	0.52	0.90
55	330763	AA450200	Hs.274337	hypothetical protein FLJ20666	0.37	0.97
	330786	D60374	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN A	0.78	0.84
	330790	T48536	Hs.105807	ESTs	0.23	3.17
	330814	AA015730	Hs.266398	ESTs, Weakly similar to transformation-r	0.37	2.07
	330827	AA040332	Hs.12744	ESTs	1.60	1.00
60	330844	AA063037	Hs.66803	ESTs	0.93	1.16
	330901	AA157818	Hs.267319	endogenous retroviral protease	1.02	1.03
	330931	F01443	Hs.284256	hypothetical protein FLJ14033 similar to	0.24	0.88
	330952	H02855	Hs.29567	ESTs	0.08	1.31
	330961	H10998	Hs.7164	a disintegrin and metalloproteinase doma	1.29	1.26
65	330968	H16568	Hs.23748	ESTs	0.48	0.96
	331014	H98597	Hs.30340	hypothetical protein KIAA1165	0.29	0.74
	331046	N66563	Hs.191358	ESTs	0.99	8.56
	331060	N75081	Hs.157148	Homo sapiens cDNA FLJ11883 fis, clone HE	1.24	1.00
	331099	R36671	Hs.83937	hypothetical protein	0.75	1.03
70	331108	R41408	Hs.21983	ESTs	1.00	2.75
	331131	R54797		gb:yg87b07.s1 Soares infant brain 1N1B H	6.04	10.68
	331135	R61398	Hs.4197	ESTs	0.80	0.96
	331170	T23461	Hs.159293	ESTs	2.63	4.29
	331180	T32446	Hs.6640	Human DNA sequence from PAC 75N13 on chr	1.78	2.71
75	331183	T40769	Hs.8469	ESTs	1.00	3.01
	331203	T82310		(NONE)	1.70	3.80
	331271	AA059347	Hs.82226	glycoprotein (transmembrane) nmb	1.20	3.19
	331306	AA252079	Hs.63931	dachshund (Drosophila) homolog	0.31	1.30
	331327	AA281076	Hs.109221	ESTs	2.09	2.41
80	331341	AA303125	Hs.23240	Homo sapiens cDNA FLJ13496 fis, clone PL	0.72	2.43
	331359	AA416979	Hs.46901	KIAA1462 protein	0.09	0.91
	331363	AA421562	Hs.91011	anterior gradient 2 (Xenopus laevis) hom	1.02	0.87
	331378	AA448881	Hs.49282	hypothetical protein FLJ11088	1.03	1.23
	331384	AA456001	Hs.93847	NADPH oxidase 4	1.40	1.00
	331402	AA505135	Hs.44037	ESTs	1.80	3.93
85	331422	F10802	Hs.163628	ESTs, Moderately similar to ALU7_HUMAN	1.65	1.89

	331490	N32912	Hs.26813	CDA14	2.48	1.73
	331531	N51343		gb:yz15g04.s1 Soares_multiple_sclerosis_	0.98	1.68
	331547	N54811		gb:od74f04.s1 NCI_CGAP_Ov2 Homo sapiens	3.80	5.75
5	331578	N67960	Hs.248989	ESTs	0.11	0.67
	331589	N71027	Hs.152618	ESTs	1.09	1.38
	331608	N89861	Hs.112110	PTD007 protein	0.93	0.76
	331614	N92293	Hs.240272	EST	0.17	1.34
	331668	W69707	Hs.58030	EST	2.24	3.82
10	331671	W72033	Hs.194695	ras homolog gene family, member I	1.00	1.24
	331676	W79834	Hs.58559	ESTs, Weakly similar to rhotekin [M.musc	0.08	1.07
	331681	W85712	Hs.119571	collagen, type III, alpha 1 (Ehlers-Danl	8.72	4.27
	331692	W93592	Hs.152213	wingless-type MMTV Integration site fami	0.94	0.54
	331717	AA190888	Hs.153881	Homo sapiens NY-REN-62 antigen mRNA, par	1.57	1.34
15	331718	AA191404	Hs.104072	ESTs	6.80	11.77
	331811	AA404500	Hs.301570	ESTs	1.10	1.00
	331820	AA405970	Hs.97996	transcription termination factor, mitoc	0.73	0.59
	331831	AA412031	Hs.97901	EST	2.77	4.08
	331852	AA418988	Hs.98314	Homo sapiens mRNA; cDNA DKFZp586L0120 (f	0.23	0.93
20	331943	AA453418	Hs.21275	hypothetical protein FLJ11011	0.36	1.88
	331969	AA460702	Hs.82772	collagen, type XI, alpha 1	1.00	1.00
	331990	AA478102	Hs.139631	ESTs	3.04	3.87
	332002	AA482009	Hs.105104	ESTs	1.19	0.78
	332027	AA489671	Hs.65641	hypothetical protein FLJ20073	1.27	1.03
25	332029	AA489697	Hs.145053	ESTs	0.30	1.62
	332033	AA489840	Hs.251014	EST	2.30	3.70
	332048	AA496019	Hs.201591	ESTs	0.17	0.52
	332071	AA598594	Hs.205293	KIAA1211 protein	1.35	1.23
30	332074	AA599012		gb:ae41e11.s1 Gessler Wilms tumor Homo s	0.19	2.00
	332083	AA600200	Hs.155546	KIAA1080 protein; Golgi-associated, gamm	0.31	1.18
	332085	AA600353	Hs.173933	nuclear factor IIA	0.30	1.50
	332125	AA609861	Hs.312447	ESTs	0.22	0.62
	332177	F10812	Hs.101433	ESTs	8.21	18.03
35	332180	H03348	Hs.7327	claudin 1	2.27	1.57
	332185	H10356	Hs.101689	ESTs	0.09	1.18
	332203	H49388	Hs.317769	EST	8.05	5.02
	332232	N48891	Hs.101915	Stargardt disease 3 (autosomal dominant)	0.78	0.85
	332240	N54803	Hs.324267	ESTs, Weakly similar to putative p150 (0.96	1.23
	332261	N70294	Hs.269137	ESTs	2.40	3.74
40	332275	R08838	Hs.26530	serum deprivation response (phosphatidyl	0.27	0.75
	332280	R38100	Hs.148381	RNA binding motif protein, X chromosome	0.39	1.88
	332299	R69250	Hs.21201	nectin 3; DKFZP566B0846 protein	5.24	12.76
	332304	R74041	Hs.101539	ESTs	1.44	3.18
	332314	T25862	Hs.101774	hypothetical protein FLJ23045	0.68	1.32
45	332384	M11433	Hs.101850	retinol-binding protein 1, cellular	1.71	0.88
	332434	N75542	Hs.289068	Homo sapiens cDNA FLJ11918 fis, clone HE	0.43	0.86
	332445	T63781	Hs.111112	ESTs	0.68	1.00
	332453	L00205	Hs.111758	keratin 6A	31.54	1.00
	332458	M33493	Hs.250700	trypsin beta 1	0.51	1.00
50	332504	AA053917	Hs.15108	chromosome 14 open reading frame 1	0.79	1.24
	332525	M17252	Hs.278430	cytochrome P450, subfamily XXIA (steroid	0.98	1.70
	332530	M31682	Hs.1735	Inhibin, beta B (activin AB beta polypep	0.88	0.66
	332535	N20284	Hs.19280	cysteine-rich motor neuron 1	0.22	1.46
	332539	AA412528	Hs.20183	ESTs, Weakly similar to AF164793 1 prote	0.93	1.49
55	332559	M13955	Hs.166189	cytokeratin 2	0.35	1.13
	332563	N92924	Hs.274407	protease, serine, 16 (thymus)	1.00	1.00
	332565	AA234896	Hs.25272	E1A binding protein p300	0.36	1.05
	332594	AA279313	Hs.3239	methyl CpG binding protein 2 (Rett syndr	0.53	0.59
	332634	S38953	Hs.283750	tenascin XA	0.38	1.16
60	332638	AA283034	Hs.50640	JAK binding protein	1.00	1.70
	332640	AA417152	Hs.5101	protein regulator of cytokinesis 1	6.15	1.16
	332654	AA001296	Hs.288217	hypothetical protein MGC2941	1.50	2.73
	332665	AA223335	Hs.63788	propionyl Coenzyme A carboxylase, beta p	1.20	0.91
	332692	AA496035	Hs.247926	gap junction protein, alpha 5, 40kD (con	0.17	1.12
65	332716	L00058	Hs.79070	v-myc avian myelocytomatosis viral oncog	1.00	1.44
	332736	L13773	Hs.114765	myeloid/lymphoid or mixed-lineage leukem	1.00	1.81
	332758	X93921	Hs.296938	dual specificity phosphatase 7	0.53	0.78
	332781	AA233258	Hs.247112	hypothetical protein FLJ10902	1.44	1.56
	332792				1.70	1.19
70	332816				1.85	2.47
	332858				1.04	1.57
	332906				3.48	8.04
	332911				1.00	1.00
	332912				1.06	4.40
75	332922				1.00	1.00
	332956				0.42	0.88
	332959				1.96	6.34
	332982				0.56	0.99
	332984				0.30	0.78
80	332998				1.47	2.01
	333058				0.47	1.38
	333097				2.14	3.19
	333121				2.76	3.70
	333122				1.92	1.21
85	333123				1.85	1.39
	333138				0.47	0.52

	333139	1.88	0.84
	333140	0.21	0.64
	333221	1.51	1.11
5	333260	0.75	1.01
	333380	6.68	15.75
	333387	4.56	12.61
	333512	5.05	8.01
	333524	2.28	3.98
10	333585	2.31	1.53
	333603	2.23	1.17
	333604	2.51	1.58
	333618	0.52	0.98
	333627	1.44	1.36
15	333628	1.90	1.90
	333650	1.85	2.10
	333678	1.85	2.35
	333750	2.18	5.67
	333763	1.99	2.60
20	333767	1.02	0.98
	333768	1.78	1.65
	333769	2.15	2.13
	333772	1.46	2.53
	333777	1.00	1.42
25	333846	2.99	4.50
	333884	0.47	0.94
	333887	0.50	1.00
	333891	0.43	0.89
	333892	0.51	0.91
30	333904	0.26	1.13
	333906	0.55	0.98
	333948	1.70	2.15
	333954	0.37	1.09
	333966	8.10	14.30
35	333968	0.63	1.38
	334061	4.24	12.30
	334094	1.30	12.03
	334113	4.55	8.63
	334161	0.82	1.59
40	334183	0.47	0.76
	334187	1.36	3.70
	334219	0.69	1.04
	334222	1.88	1.70
	334223	4.72	3.14
45	334239	0.79	0.62
	334255	0.45	1.10
	334333	1.00	3.56
	334378	3.98	5.76
	334382	1.50	1.31
50	334492	3.59	4.75
	334562	5.94	15.40
	334588	8.14	19.53
	334616	1.55	1.56
	334633	5.16	8.07
55	334648	0.59	2.13
	334787	3.70	7.15
	334866	8.13	10.60
	334891	0.32	1.14
	334933	1.00	3.84
60	334934	4.01	7.43
	334945	1.04	2.98
	334967	0.29	1.14
	334990	1.50	1.39
	335015	5.88	18.65
65	335093	0.55	1.75
	335120	4.31	8.01
	335125	0.38	1.97
	335179	1.24	1.98
	335188	0.46	1.47
70	335211	1.61	1.42
	335288	0.73	0.97
	335289	0.20	0.26
	335361	2.18	1.58
	335379	0.50	0.71
75	335414	3.64	14.94
	335416	2.93	3.98
	335496	0.98	0.91
	335497	1.71	1.92
	335548	1.15	2.40
80	335551	3.22	10.54
	335558	3.42	4.89
	335586	5.50	12.75
	335619	2.99	3.07
	335620	3.80	8.29
85	335621	0.28	0.57
	335682	0.46	1.17

	335686	2.55	3.81
	335755	2.24	1.07
	335784	0.20	0.97
5	335814	1.13	1.48
	335815	2.45	3.51
	335823	1.00	4.16
	335835	0.49	1.70
	335851	1.66	1.39
10	335868	2.98	6.43
	335896	0.98	0.99
	335936	12.10	21.93
	335948	1.00	1.64
	335983	1.00	4.21
	335995	0.37	1.17
15	336021	1.04	0.84
	336034	11.40	23.54
	336038	1.19	1.21
	336066	0.54	1.63
20	336107	0.95	0.70
	336205	3.13	6.29
	336275	3.20	10.10
	336292	2.34	3.09
	336331	1.00	1.00
25	336419	0.65	0.79
	336632	2.33	2.16
	336633	2.55	2.23
	336634	2.19	2.03
	336635	2.69	2.48
30	336636	2.13	1.83
	336637	2.43	2.24
	336638	2.31	2.03
	336659	0.60	1.31
	336675	0.31	1.18
35	336684	1.50	1.14
	336694	4.74	7.10
	336716	4.43	6.37
	336721	2.20	0.74
	336798	1.64	2.14
40	336900	6.14	12.73
	336948	1.00	1.00
	337028	1.30	2.09
	337043	4.01	11.53
	337046	1.67	1.84
45	337054	2.78	7.35
	337128	7.20	16.14
	337162	3.45	6.34
	337183	5.72	11.41
	337184	3.72	5.90
50	337192	1.27	1.06
	337194	1.88	1.68
	337229	0.22	1.03
	337268	1.00	3.31
	337299	3.23	5.14
55	337325	2.76	3.72
	337389	5.80	10.42
	337493	2.06	6.30
	337497	7.88	20.29
	337500	3.80	4.48
60	337549	1.66	2.31
	337603	1.27	8.54
	337605	5.76	7.16
	337671	0.73	0.97
	337755	1.54	0.92
65	337786	5.07	9.73
	337809	6.18	12.87
	337862	3.78	12.97
	337871	2.66	8.16
	337958	0.26	1.34
70	338008	1.48	1.12
	338033	2.38	14.59
	338083	0.65	2.16
	338110	1.00	1.61
	338112	5.86	8.25
75	338145	1.70	1.97
	338148	8.07	18.19
	338158	1.30	4.55
	338161	2.58	3.57
	338179	1.00	1.00
80	338182	3.32	4.63
	338189	1.00	3.34
	338197	0.99	1.69
	338199	4.58	7.62
	338215	6.01	15.85
85	338279	0.53	0.95
	338316	20.58	38.66

	338322	3.23	7.39
	338357	4.10	11.39
	338359	10.12	21.59
5	338366	0.69	1.02
	338374	0.40	1.18
	338414	0.47	1.06
	338418	6.12	13.86
	338469	3.09	5.11
10	338501	6.28	10.32
	338506	6.97	12.41
	338523	3.10	5.84
	338549	1.70	2.70
	338561	0.79	0.81
15	338662	1.72	1.46
	338671	0.17	0.91
	338676	2.10	15.86
	338726	1.20	1.09
	338779	0.12	0.57
20	338804	0.99	1.67
	338836	1.00	1.00
	338871	4.30	9.81
	338872	5.02	12.81
	338879	0.23	1.12
25	338937	6.55	12.26
	338966	1.76	5.42
	338993	1.00	2.40
	339047	5.26	10.81
	339100	5.10	6.88
30	339114	1.00	1.70
	339121	1.00	3.75
	339170	10.36	19.67
	339229	4.08	13.48
	339264	2.64	3.83
35	339293	1.73	1.94

TABLE 8B shows the accession numbers for those Pkeys in Table 8A lacking unigenelD's. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

	Pkey	CAT number	Accessions
	322044	187363_1	AW340926 AA249063 N86075
	322060	44320_1	AI341937 AW003063 U34725 AA904742
50	321430	42705_1	X57414 X57415
	321467	43034_1	X13075 X13076
	322125	46779_1	R93901 AF075073 R93902
	322166	46861_1	H69434 AF085958 H69846
55	322173	46873_1	H52567 H52567 AF085970 H52164
	322178	46882_1	H56535 AF085980 H56712
	322179	46885_1	H92891 AF085982 H92777
	321577	1615102_1	H84849 H84252 H84260 H86664 H85320
	321587	1615333_1	H95531 H95521 H84529
60	313723	111953_1	AA070412 AA102346 AA081885
	320997	627492_1	H22544 H46842 AI204929
	322278	47271_1	W69304 AF086283 W69200
	321687	218439_1	AA625149 AA313030 AA313052 H97463
65	313883	129439_1	AA665089 AA135130 AA484059 AA102419 AW877765
	322320	47422_1	W79150 AF086419
	322339	814584_1	AI668646 AI734214 W17348
	314648	293660_1	AW979268 AA878419 AA431342 AA431628
	300201	682222_1	AI308300 AI308296
	306897	25196_2	AI093967
70	323155	979809_1	AL120701 AL135041 AL121624
	322527	38927_1	AF147359 T58511 T58560
	322585	473768_2	W88919 W89125
	300362	1574395_1	Z42308 H23514
	322635	82296_1	AA005129 AA679084 AA694399
75	322664	85042_1	AA011522 AA702841 AA011691 AA330797
	315454	380580_1	AI239464 AI239473 AA625812 AI208703
	322687	37372_1	AF074666 AI110759 AF090902
	314852	327472_1	AI903735 AA491283 AI694953 AW976903 AA761362
	307783	697809_1	AI347274 AW844024
80	324072	269032_1	AA381722 AA381829 AW983906 AW983902 AA381242
	300627	221345_1	AA488472 W27363 AA317053 BE082689 AW967036 BE079872
	323505	196389_1	AW970512 AA280251 AI652287 BE466438 AI650725 AA551854 AA281574 AW571481
	316791	403558_1	AA678177 AA677034
	324303	233842_1	AL118754 AA333202 H38001
85	316519	442885_1	AA847835 AA768376
	300926	333127_1	AA504860 AA504911

	324580	328264_1	AA492588 AA492498 AA492571
	301882	275087_1	T78054 T79888 AA398185
	324804	398093_1	AI692552 AI393343 AI800510 AI377711 F24263 AA661876
5	324889	1515978_1	D31010 D30991 D31168 D31166 D31465
	302697	43219_1	AJ001409 AJ001410
	302711	45419_1	LD8442 D51348
	302742	458_39	L12081
	318499	364430_1	T25451 AA585295 AA585305
10	310624	34624_4	U88896 U88898 AA916056 T03285 AI341594 AI359534 AI634031 U88897
	302847	458_105	X98941 X98942 X98943 X98953 X98949
	304122	77271_5	H28966
	303598	270283_1	AA382814 AA402411 AA412355
	311409	837264_1	AI698839 AI909260 AI909259
	312094	797889_1	Z78390 T97427
15	319312	1540116_1	Z45481 F12393 T74437
	319407	1688823_1	R05329 R01555 R08276
	319425	1689571_1	T82930 R02424 T85145
	320007	229683_1	AA336314 T82938 AA327744 AW967388 AA639967 T10753
20	320018	1815987_1	T83263 T85731 T85730
	319484	1691553_1	T91772 R07257 R07098
	318865	1535937_1	H10818 F07831 Z43072
	312220	1671607_1	N74613 T98756 T98589
	319546	243305_1	R09692 R09414 AA346353
25	312389	902067_1	AI863140 W80703 R43474
	319611	1566863_1	H14957 R55522 R11908
	312437	291472_1	BE080180 AW827313 AW231970 AA995028 AA428584 AW872716 AW892508 AW854593 AA578441 AW975234 AA664937 AA984131 AA528743 AA552874 AA564758 AW063245 AI267534 AW070190 AW893483 AA770330 AA906928 AA906582 AA758746 AA551717 AW063311 AA429538
30	311896	579192_1	AW206447 AI248530 AI084433 AI400976 R16653
	319834	112523_1	AA071267 T65940 T64515 AA071334
	321102	80531_1	AA018306 H38925 AA001221
	321158	410938_1	H79670 H47798 AA700289
	321199	212379_1	N34524 AA305071 AW954803 AA502335 AI433430 AI203597 AW026670 AW265323 AW850787 AA317554 AW993643 AW835572 AW385512 AI334966 W32951 H62656 H53902 R88904 AW835732
35	305528	28832_3	AA769156
	321270	1662057_1	N59537 N78278 R83560
	314126	177666_1	AA226431 AA226569 AA488748
	320714	743644_1	R91883 AI445591
40	306442	AA976899	
	306446	AA977348	
	306458	AA978186	
	306510	AA988546	
	306557	AA994530	
45	306572	AA995686	
	306582	AA996248	
	306656	AI004024	
	306686	AI015815	
	306751	AI032589	
50	308011	AI439473	
	306892	AI092465	
	308106	AI476803	
	308154	AI500600	
	306956	AI125111	
55	306958	AI125152	
	308213	AI557041	
	308216	AI557135	
	308219	AI557246	
	308588	AI718299	
60	308599	AI719893	
	308643	AI745040	
	308673	AI760864	
	308697	AI767143	
	308778	AI811109	
65	308808	AI818289	
	308875	AI832332	
	308886	AI833240	
	308898	AI858845	
	308966	AI870704	
70	308979	AI873111	
	303011	41689_1	AF090405 AF090407 AF090406
	303077	44060_1	AF163305 AF163307 AF163303
	305016	AA626876	
	305034	AA630128	
75	305072	AA641012	
	305148	AA654070	
	305190	AA665955	
	303978	AW513315	
	303990	AW515465	
80	303998	AW516449	
	303999	AW516611	
	305235	AA670480	
	305312	AA700201	
	305413	AA724659	
85	305447	AA737856	
	321244	29327_1	AF088654 AF088656 AF088655

WO 02/086443

PCT/US02/12476

	305614	AA782866	
	305637	AA806124	
	305639	AA806138	
5	305650	AA807709	
	305690	AA813477	
	305728	AA828209	
	305759	AA835353	
	305792	AA845256	
10	307041	AI144243	
	307091	AI167439	
	307181	AI189251	
	305901	AA872968	
	305910	AA875981	
15	307415	AI242118	
	307426	AI243364	
	307517	AI275055	
	307551	AI281556	
	307581	AI282207	
20	307608	AI290295	
	307691	AI318285	
	307730	AI336092	
	307760	AI342387	
	307764	AI342731	
25	307796	AI350556	
	309045	AI910902	
	309051	AI911975	
	307807	AI351799	
	307808	AI351826	
30	307820	AI355761	
	307852	AI365541	
	309122	AI928178	
	309164	AI937761	
	309177	AI951118	
35	307902	AI380462	
	309299	AW003478	
	309303	AW004823	
	309476	AW129368	
	309532	AW151119	
40	309747	AW264889	
	309769	AW272346	
	309799	AW276964	
	309866	AW299916	
	302679	311853_1	H65022 AA186889
45	309923	AW340684	
	309928	AW341418	
	309931	AW341683	
	309933	AW341936	
	302705	31765_1	U09060 U09061
50	302789	34161_1	AJ245067 AJ245070
	304006	AW517947	
	304024	T03036	
	304026	T03160	
	304028	T03266	
55	304046	T54803	
	304061	T61521	
	304063	T62536	
	302802	34487_1	Y08250 Y08245
	304114	R78946	
60	304155	H68696	
	304203	N56929	
	304234	W81609	
	304348	AA179868	
	304430	AA347682	
	304456	AA411240	
65	304521	AA464716	
	304526	AA476427	
	304607	AA513322	
	304735	AA576453	
	304760	AA580401	
70	306015	AA897116	
	306063	AA906316	
	306065	AA906725	
	306104	AA910956	
	306109	AA911881	
75	306242	AA932805	
	306288	AA936900	
	306396	AA970223	
	330568	NOT_FOUND_entrez	U56244
80	330599	15323_-12	U90437
	331131	genbank_R54797	R54797
	331203	NOT_FOUND_entrez	T82310
	331531	genbank_N51343	N51343
	331547	467396_1	AA828597 N54811
85	332074	genbank_AA599012	AA599012

TABLE 8C shows the genomic position for those Pkeys in Table 8A lacking unigene ID's and accession numbers. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

5	Pkey:	Unique number corresponding to an Eos probeset		
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.		
	Strand:	Indicates DNA strand from which exons were predicted.		
10	Nt_position:	Indicates nucleotide positions of predicted exons.		
	Pkey	Ref	Strand	Nt_position
	332792	Dunham, I. et al.	Plus	73381-73768
	332816	Dunham, I. et al.	Plus	359844-360030
15	332906	Dunham, I. et al.	Plus	1923101-1923205
	332911	Dunham, I. et al.	Plus	1961767-1961858
	332912	Dunham, I. et al.	Plus	1962120-1962246
	332922	Dunham, I. et al.	Plus	2009620-2009738
20	332956	Dunham, I. et al.	Plus	2510528-2510558
	332959	Dunham, I. et al.	Plus	2518145-2518213
	333138	Dunham, I. et al.	Plus	3369205-3369323
	333139	Dunham, I. et al.	Plus	3369495-3369571
	333221	Dunham, I. et al.	Plus	3978070-3978187
	333380	Dunham, I. et al.	Plus	4904775-4904846
25	333387	Dunham, I. et al.	Plus	4910935-4910997
	333512	Dunham, I. et al.	Plus	5560510-5560564
	333524	Dunham, I. et al.	Plus	5612620-5612780
	333585	Dunham, I. et al.	Plus	6234778-6234894
30	333618	Dunham, I. et al.	Plus	6562391-6562566
	333627	Dunham, I. et al.	Plus	6620584-6620903
	333628	Dunham, I. et al.	Plus	6629004-6629233
	333650	Dunham, I. et al.	Plus	6796852-6797128
	333678	Dunham, I. et al.	Plus	7068223-7068288
35	333750	Dunham, I. et al.	Plus	7608165-7608234
	333763	Dunham, I. et al.	Plus	7692491-7692630
	333767	Dunham, I. et al.	Plus	7694407-7694623
	333768	Dunham, I. et al.	Plus	7695440-7695697
	333769	Dunham, I. et al.	Plus	7696625-7696707
40	333772	Dunham, I. et al.	Plus	7706773-7706902
	333777	Dunham, I. et al.	Plus	7746805-7746916
	333846	Dunham, I. et al.	Plus	8008623-8008757
	333884	Dunham, I. et al.	Plus	8153960-8154161
	333887	Dunham, I. et al.	Plus	8154882-8155025
45	333891	Dunham, I. et al.	Plus	8156437-8156709
	333892	Dunham, I. et al.	Plus	8156825-8157001
	333948	Dunham, I. et al.	Plus	8583497-8583627
	333954	Dunham, I. et al.	Plus	8563186-8563335
	333966	Dunham, I. et al.	Plus	8655643-8655826
50	333968	Dunham, I. et al.	Plus	8681004-8681241
	334061	Dunham, I. et al.	Plus	9686941-9687077
	334094	Dunham, I. et al.	Plus	9889953-9890105
	334113	Dunham, I. et al.	Plus	10282459-10282597
	334161	Dunham, I. et al.	Plus	10599033-10599180
55	334219	Dunham, I. et al.	Plus	12716160-12716384
	334239	Dunham, I. et al.	Plus	13056569-13056693
	334333	Dunham, I. et al.	Plus	13603544-13603657
	334378	Dunham, I. et al.	Plus	13907239-13907370
	334382	Dunham, I. et al.	Plus	13915866-13916036
60	334562	Dunham, I. et al.	Plus	14987847-14987940
	334588	Dunham, I. et al.	Plus	15032740-15032817
	334616	Dunham, I. et al.	Plus	15176123-15176470
	334633	Dunham, I. et al.	Plus	15333206-15333305
	334866	Dunham, I. et al.	Plus	18872214-18872317
65	334891	Dunham, I. et al.	Plus	19299770-19299944
	334934	Dunham, I. et al.	Plus	20103970-20104058
	335015	Dunham, I. et al.	Plus	20682792-20682945
	335120	Dunham, I. et al.	Plus	21436286-21436384
	335125	Dunham, I. et al.	Plus	21441390-21441471
70	335179	Dunham, I. et al.	Plus	21634405-21634526
	335188	Dunham, I. et al.	Plus	21669118-21669328
	335211	Dunham, I. et al.	Plus	21774611-21774680
	335361	Dunham, I. et al.	Plus	22807292-22807445
	335379	Dunham, I. et al.	Plus	22899306-22899420
75	335414	Dunham, I. et al.	Plus	23235546-23235684
	335416	Dunham, I. et al.	Plus	23237354-23237465
	335496	Dunham, I. et al.	Plus	24164386-24164545
	335497	Dunham, I. et al.	Plus	24167666-24167869
	335558	Dunham, I. et al.	Plus	24740167-24740347
80	335586	Dunham, I. et al.	Plus	24990333-24990497
	335686	Dunham, I. et al.	Plus	25439839-25439920
	335784	Dunham, I. et al.	Plus	25942710-25942792
	335823	Dunham, I. et al.	Plus	26365925-26366004
	335983	Dunham, I. et al.	Plus	27938968-27939070
85	335995	Dunham, I. et al.	Plus	28009044-28009184
	336021	Dunham, I. et al.	Plus	28686482-28686559

WO 02/086443

PCT/US02/12476

	336034	Dunham, I. et al.	Plus	29014404-29014590
	336038	Dunham, I. et al.	Plus	29022953-29023165
	336107	Dunham, I. et al.	Plus	29987731-29987869
5	336632	Dunham, I. et al.	Plus	983890-985529
	336633	Dunham, I. et al.	Plus	985591-986221
	336634	Dunham, I. et al.	Plus	986296-986670
	336635	Dunham, I. et al.	Plus	987908-988364
	336636	Dunham, I. et al.	Plus	988418-989185
10	336637	Dunham, I. et al.	Plus	989276-990813
	336638	Dunham, I. et al.	Plus	991906-993240
	336659	Dunham, I. et al.	Plus	1896402-1896478
	336694	Dunham, I. et al.	Plus	2420546-2420616
	336721	Dunham, I. et al.	Plus	3371522-3371586
15	336900	Dunham, I. et al.	Plus	10236423-10236523
	336948	Dunham, I. et al.	Plus	12692290-12692381
	337028	Dunham, I. et al.	Plus	16644817-16644942
	337054	Dunham, I. et al.	Plus	17821742-17821922
	337162	Dunham, I. et al.	Plus	23478943-23479145
20	337183	Dunham, I. et al.	Plus	23943606-23943696
	337184	Dunham, I. et al.	Plus	23973949-23974016
	337268	Dunham, I. et al.	Plus	28011979-28012034
	337299	Dunham, I. et al.	Plus	29022656-29022775
	337389	Dunham, I. et al.	Plus	31401509-31401579
25	337493	Dunham, I. et al.	Plus	33330760-33330981
	337549	Dunham, I. et al.	Plus	34474472-34474531
	337755	Dunham, I. et al.	Plus	3971764-3971900
	337809	Dunham, I. et al.	Plus	4449069-4449193
	337871	Dunham, I. et al.	Plus	5443027-5443101
30	337958	Dunham, I. et al.	Plus	6969162-6969270
	338008	Dunham, I. et al.	Plus	7697068-7697236
	338033	Dunham, I. et al.	Plus	8092128-8092271
	338110	Dunham, I. et al.	Plus	10384481-10384621
	338112	Dunham, I. et al.	Plus	10391398-10391600
35	338145	Dunham, I. et al.	Plus	11386629-11386692
	338148	Dunham, I. et al.	Plus	11448985-11449085
	338179	Dunham, I. et al.	Plus	12808775-12808833
	338197	Dunham, I. et al.	Plus	13638107-13638181
	338279	Dunham, I. et al.	Plus	16168944-16169091
40	338316	Dunham, I. et al.	Plus	17089711-17089988
	338322	Dunham, I. et al.	Plus	17132477-17132547
	338357	Dunham, I. et al.	Plus	18062184-18062402
	338359	Dunham, I. et al.	Plus	18074402-18074501
	338366	Dunham, I. et al.	Plus	18262026-18262189
45	338374	Dunham, I. et al.	Plus	18371200-18371282
	338414	Dunham, I. et al.	Plus	19345573-19345660
	338418	Dunham, I. et al.	Plus	19435506-19435596
	338501	Dunham, I. et al.	Plus	21244713-21244828
	338506	Dunham, I. et al.	Plus	21221871-21221953
50	338523	Dunham, I. et al.	Plus	21509763-21509864
	338652	Dunham, I. et al.	Plus	24404720-24404899
	338804	Dunham, I. et al.	Plus	27236005-27236108
	338836	Dunham, I. et al.	Plus	27792166-27792272
	338879	Dunham, I. et al.	Plus	28410653-28410734
55	338937	Dunham, I. et al.	Plus	29160655-29160725
	338993	Dunham, I. et al.	Plus	30077787-30078184
	339047	Dunham, I. et al.	Plus	30760793-30760968
	339100	Dunham, I. et al.	Plus	31141580-31141765
	339114	Dunham, I. et al.	Plus	31456454-31456519
60	339121	Dunham, I. et al.	Plus	31583467-31583536
	339170	Dunham, I. et al.	Plus	32216399-32216527
	339293	Dunham, I. et al.	Plus	33223671-33223819
	332858	Dunham, I. et al.	Minus	1339607-1339397
	332982	Dunham, I. et al.	Minus	2628296-2628109
65	332984	Dunham, I. et al.	Minus	2632606-2632457
	332998	Dunham, I. et al.	Minus	2711704-2711565
	333058	Dunham, I. et al.	Minus	3028925-3028811
	333097	Dunham, I. et al.	Minus	3204124-3204036
	333121	Dunham, I. et al.	Minus	3308446-3308358
70	333122	Dunham, I. et al.	Minus	3309596-3309531
	333123	Dunham, I. et al.	Minus	3310817-3310749
	333140	Dunham, I. et al.	Minus	3377220-3376309
	333260	Dunham, I. et al.	Minus	4308400-4308304
	333603	Dunham, I. et al.	Minus	6466335-6466727
75	333604	Dunham, I. et al.	Minus	6467090-6466768
	333904	Dunham, I. et al.	Minus	8217374-8217261
	333906	Dunham, I. et al.	Minus	8218238-8218063
	334183	Dunham, I. et al.	Minus	11832582-11832508
	334187	Dunham, I. et al.	Minus	11921456-11921205
80	334222	Dunham, I. et al.	Minus	12732417-12732289
	334223	Dunham, I. et al.	Minus	12734365-12734269
	334255	Dunham, I. et al.	Minus	13200776-13200692
	334492	Dunham, I. et al.	Minus	14478333-14478172
	334648	Dunham, I. et al.	Minus	15363301-15363222
85	334787	Dunham, I. et al.	Minus	16299093-16298937
	334933	Dunham, I. et al.	Minus	20078117-20077991

WO 02/086443

	334945	Dunham, I. et.al.	Minus	20138885-20138637
	334967	Dunham, I. et.al.	Minus	20173311-20173218
	334990	Dunham, I. et.al.	Minus	20341159-20341087
5	335093	Dunham, I. et.al.	Minus	21297367-21297214
	335288	Dunham, I. et.al.	Minus	22304275-22303770
	335289	Dunham, I. et.al.	Minus	22305950-22305708
	335548	Dunham, I. et.al.	Minus	24662773-24662673
	335551	Dunham, I. et.al.	Minus	24679828-24678961
10	335619	Dunham, I. et.al.	Minus	25082677-25082498
	335620	Dunham, I. et.al.	Minus	25092561-25092434
	335621	Dunham, I. et.al.	Minus	25098878-25098767
	335682	Dunham, I. et.al.	Minus	25421215-25421093
	335755	Dunham, I. et.al.	Minus	25763806-25763747
15	335814	Dunham, I. et.al.	Minus	26320043-26319845
	335815	Dunham, I. et.al.	Minus	26320518-26320421
	335835	Dunham, I. et.al.	Minus	26393311-26393245
	335851	Dunham, I. et.al.	Minus	26604863-26604742
	335868	Dunham, I. et.al.	Minus	26711437-26711300
20	335896	Dunham, I. et.al.	Minus	26977639-26977558
	335936	Dunham, I. et.al.	Minus	27360474-27360400
	335948	Dunham, I. et.al.	Minus	27555924-27555788
	336066	Dunham, I. et.al.	Minus	29241080-29240842
	336205	Dunham, I. et.al.	Minus	30477456-30477311
25	336275	Dunham, I. et.al.	Minus	32086675-32086536
	336292	Dunham, I. et.al.	Minus	32818035-32817927
	336331	Dunham, I. et.al.	Minus	33594527-33594371
	336419	Dunham, I. et.al.	Minus	34052568-34052445
	336675	Dunham, I. et.al.	Minus	2020758-2020664
30	336684	Dunham, I. et.al.	Minus	2158060-2157993
	336716	Dunham, I. et.al.	Minus	3259952-3259862
	336798	Dunham, I. et.al.	Minus	5888954-5888757
	337043	Dunham, I. et.al.	Minus	17407330-17407251
	337046	Dunham, I. et.al.	Minus	17610892-17610821
35	337128	Dunham, I. et.al.	Minus	22215251-22216034
	337192	Dunham, I. et.al.	Minus	24591853-24591771
	337194	Dunham, I. et.al.	Minus	24610510-24610359
	337229	Dunham, I. et.al.	Minus	26716579-26716481
	337325	Dunham, I. et.al.	Minus	30015948-30015800
40	337497	Dunham, I. et.al.	Minus	33371317-33371258
	337500	Dunham, I. et.al.	Minus	33376212-33376158
	337603	Dunham, I. et.al.	Minus	1299296-1299194
	337605	Dunham, I. et.al.	Minus	1346555-1346397
	337671	Dunham, I. et.al.	Minus	3260634-3260547
45	337786	Dunham, I. et.al.	Minus	4133203-4133081
	337862	Dunham, I. et.al.	Minus	5347658-5347550
	338083	Dunham, I. et.al.	Minus	9318439-9318301
	338158	Dunham, I. et.al.	Minus	11794465-11794343
	338181	Dunham, I. et.al.	Minus	12124716-12124658
50	338182	Dunham, I. et.al.	Minus	12824919-12824827
	338189	Dunham, I. et.al.	Minus	12878594-12878478
	338199	Dunham, I. et.al.	Minus	13760865-13760780
	338215	Dunham, I. et.al.	Minus	14055447-14055355
	338469	Dunham, I. et.al.	Minus	20520387-20520242
55	338549	Dunham, I. et.al.	Minus	22049171-22049081
	338561	Dunham, I. et.al.	Minus	22311966-22311856
	338671	Dunham, I. et.al.	Minus	24508421-24508346
	338676	Dunham, I. et.al.	Minus	24637427-24637369
	338726	Dunham, I. et.al.	Minus	25926206-25925618
50	338779	Dunham, I. et.al.	Minus	27030151-27029795
	338871	Dunham, I. et.al.	Minus	28301708-28301611
	338872	Dunham, I. et.al.	Minus	28300921-28300790
	338968	Dunham, I. et.al.	Minus	29614876-29614749
	339229	Dunham, I. et.al.	Minus	32722330-32722199
55	339264	Dunham, I. et.al.	Minus	32975145-32975053
	325228	6381940	Plus	2630-2694
	325235	6381943	Minus	162154-162264
	329588	3962484	Plus	1169-1819
	329560	3962491	Plus	2095-2990
70	329541	3983503	Minus	2765-3059
	325328	5866875	Plus	86780-86854
	325340	6017033	Minus	166656-166819
	325373	5866920	Minus	1136686-1136777
	325367	5866920	Minus	922881-922958
	325389	5866921	Plus	239672-239759
75	325436	5866939	Minus	29778-29907
	325498	5866967	Plus	173372-173930
	325471	6017034	Minus	289268-289342
	325557	6056302	Plus	50921-51050
30	325559	6249595	Minus	118590-119172
	325560	6249595	Minus	133794-133981
	325569	6249599	Plus	79927-80217
	325587	6682462	Plus	126724-126967
	325585	6682462	Plus	73476-73574
35	325597	5866992	Plus	1065020-1065089
	325639	5867002	Plus	253525-253608

WO 02/086443

	325739	5867038	Minus	205138-205269
	325740	5867038	Minus	207533-207690
	325792	6469828	Minus	1018-1176
5	325735	6552447	Minus	269122-269190
	325685	6682468	Plus	117397-117483
	325686	6682468	Plus	118337-118439
	325819	6682490	Minus	130314-130370
	329764	6048195	Minus	109733-109968
10	329703	6065793	Minus	139994-140138
	328643	6448539	Plus	53403-53537
	329816	6624888	Minus	70296-70423
	329860	6687260	Minus	163474-163605
	325883	5867087	Plus	22498-22663
15	325895	5867097	Plus	358317-358476
	325925	5867124	Plus	115749-115962
	325932	5867127	Plus	7369-7441
	325941	5867133	Minus	64228-64402
	325969	5867153	Plus	101911-102081
20	325971	5867153	Plus	105841-106035
	329993	4567166	Minus	101307-101434
	330020	6671887	Plus	172397-172491
	326163	5867168	Minus	7831-8035
	326274	5867171	Minus	410289-410404
25	326025	5867176	Plus	70854-70915
	326046	5867182	Minus	62668-62825
	326099	5867186	Minus	661381-661510
	326108	5867187	Minus	23784-23903
	326165	5867208	Minus	62787-62929
30	326189	5867212	Plus	69288-69413
	326204	5867218	Minus	148088-148200
	326230	5867230	Minus	301868-301972
	330052	4567182	Plus	352560-352963
	330036	6042048	Plus	117120-117216
35	326360	5867293	Plus	13627-13844
	326589	5867320	Plus	22760-22919
	326393	5867341	Plus	41702-41841
	326505	5867435	Minus	8818-8949
	326515	5867439	Plus	36683-36809
40	326592	6138928	Plus	23689-23828
	330107	6015249	Minus	100091-100282
	330106	6015249	Minus	99443-99778
	330100	6015253	Plus	21166-21301
	330093	6015278	Plus	1043-1199
45	330088	6015293	Plus	37517-37638
	330085	6015302	Minus	59613-59770
	330120	6671864	Minus	127553-127656
	330123	6671869	Minus	35311-35406
	326742	5867611	Minus	95187-95248
50	326605	5867637	Plus	24656-24749
	326818	6117831	Minus	15199-15309
	326720	6552456	Plus	84525-84677
	326770	6598307	Minus	513603-513668
	326692	6682502	Plus	117697-117899
55	326693	6682502	Minus	335002-335096
	326983	5867657	Minus	16023-16581
	326991	5867660	Plus	18147-18339
	326936	6004446	Minus	10217-10357
	326964	6469836	Plus	75340-75456
60	327040	6531965	Plus	783670-783817
	327053	6531965	Plus	2247267-2247437
	327075	6531965	Plus	4041318-4041431
	327085	6531965	Plus	4734947-4735069
	327036	6531965	Plus	319951-320040
	327130	6531976	Plus	20247-22343
65	327156	5866841	Minus	2462-2620
	327288	5867481	Plus	48583-48773
	327332	5867516	Minus	56361-56532
	327220	5867525	Minus	65701-65781
	327224	5867534	Plus	188468-188544
70	327321	6249562	Minus	99745-99836
	327381	6552412	Minus	61013-62130
	327396	5867743	Plus	8702-8820
	327414	5867750	Plus	102461-102586
75	327442	5867759	Plus	111483-111618
	327467	5867772	Plus	88030-88151
	327473	5867775	Plus	75101-75181
	327483	5867783	Plus	181573-181662
	327377	5867793	Minus	37610-37676
80	327562	5867804	Minus	343989-344474
	327568	5867811	Minus	46152-46287
	327606	6004463	Plus	200262-200495
	327611	5867868	Minus	175063-175392
	327642	5867891	Minus	2513-2743
85	327654	5867910	Minus	97584-97710
	327734	5867940	Minus	31003-31583

WO 02/086443

PCT/US02/12476

	327775	5867964	Minus	130791-130871
	327796	5867982	Plus	85267-85405
	327840	6249578	Minus	73065-73206
5	330208	6013599	Plus	66517-66931
	330263	6671884	Minus	101503-101634
	328004	5867993	Minus	157407-157887
	328101	5868020	Plus	289920-290014
	328100	5868020	Minus	263545-263635
10	328113	5868024	Minus	80378-80491
	328157	5868064	Plus	73326-73615
	328196	5868080	Minus	16551-16729
	328197	5868081	Minus	42133-42438
	327940	5868197	Minus	95240-95428
15	327984	5868216	Plus	66611-66677
	328021	5902482	Plus	713478-714590
	328068	6117819	Plus	253903-254022
	328264	6381912	Plus	55086-55404
	330300	2905862	Minus	3246-3302
20	328608	5868222	Minus	87770-87953
	328600	5868229	Minus	38889-40010
	328616	5868239	Plus	293920-294224
	328623	5868246	Minus	120020-120126
	328632	5868247	Plus	76734-76853
25	328666	5868254	Minus	778-901
	328698	5868264	Minus	625555-625633
	328700	5868264	Plus	764089-764203
	328708	5868271	Minus	68114-68854
	328735	5868289	Plus	89389-89455
30	328743	5868289	Plus	274638-274726
	328806	5868324	Plus	29408-29684
	328299	5868366	Minus	149708-149889
	328342	5868383	Plus	59955-60094
	328365	5868387	Minus	270724-270798
35	328369	5868388	Plus	75371-75583
	328381	5868392	Plus	662758-662848
	328451	5868425	Minus	217275-217336
	328481	5868449	Minus	8987-9180
	328500	5868464	Plus	59098-59481
40	328530	5868482	Plus	334973-335408
	328664	6004473	Plus	1193739-1193866
	328861	6381928	Minus	108317-108403
	328908	5868493	Plus	117002-117059
	328933	5868500	Plus	771765-771889
45	328934	5868500	Plus	846342-846448
	328949	6456765	Minus	43552-43619
	330313	6042030	Minus	33642-33775
	329005	5868542	Plus	85470-85673
	330366	2944106	Plus	151837-151914
50	330372	6580495	Minus	317461-317688
	329033	5868561	Minus	5390-5479
	329037	5868562	Minus	32466-32582
	329067	5868591	Minus	146417-147652
	329134	5868679	Plus	29959-30018
55	329157	5868687	Minus	145940-146155
	329178	5868704	Plus	179177-179463
	329192	5868716	Plus	166936-167020
	329194	5868716	Minus	304450-304559
	329204	5868720	Minus	3050-3190
60	329224	5868728	Plus	27422-27664
	329228	5868728	Minus	50118-50287
	329288	5868771	Plus	25554-26299
	329337	5868806	Minus	467155-467222
	329011	6682532	Plus	48658-48741

TABLE 9A: Potential Therapeutic, Diagnostic and Prognostic targets for Therapy of Lung Cancer

Table 9A shows about 1312 genes up-regulated in lung tumors (including squamous cell carcinomas, adenocarcinomas, small cell carcinomas, granulomatous and carcinoid tumors) relative to normal body tissues. These genes were selected from about 59680 probesets on the Eos/Arraymetrix Hu03 Genechip array.

Table 9B show the accession numbers for those Pkey's lacking UnigeneID's for table 9A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Table 9C show the genomic positioning for those Pkey's lacking UnigeneID's and accession numbers in table 9A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 R1: Average of lung tumors (including squamous cell carcinomas, adenocarcinomas, small cell carcinomas, granulomatous and carcinoid tumors) divided by the average of normal lung samples
 R2: Average of non-malignant lung disease samples (including bronchitis, emphysema, fibrosis, atelectasis, asthma) divided by the average of normal lung samples

Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2
400195			NM_007057*:Homo sapiens ZW10 interactor	1.00	1.00
400205			NM_006265*:Homo sapiens RAD21 (S. pombe)	15.80	396.00
400220			Eos Control	2.28	2.84
400277			Eos Control	7.68	9.72
400285			Eos Control	1.00	1.00
400288	X06256	Hs.149609	integrin, alpha 5 (fibronectin receptor,	1.04	2.24
400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	132.45	4.00
400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	43.86	74.00
400301	X03835	Hs.1657	estrogen receptor 1	1.00	1.00
400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	1.75	1.65
400328	X87344	Hs.180062	transporter 2, ATP-binding cassette, sub	0.87	1.80
400419	AF084545		Target	156.55	253.00
400512			NM_030878*:Homo sapiens cytochrome P450,	1.00	2.00
400517	AF242388		lengsin	3.67	87.00
400560			NM_030878*:Homo sapiens cytochrome P450,	1.00	1.00
400684			NM_002425*:Homo sapiens matrix metallopro	20.26	45.00
400665			NM_002425*:Homo sapiens matrix metallopro	1.36	1.07
400666			NM_002425*:Homo sapiens matrix metallopro	3.26	3.22
400749			NM_003105*:Homo sapiens sortilin-related	1.00	91.00
400763			Target Exon	7.63	24.00
401027			Target Exon	1.00	1.00
401093			C12000586*:g 6330167 dbj BAA86477.1 (A	1.00	155.00
401203			Target Exon	1.00	86.00
401212			C12000457*:g 7512178 pir T30337 polypr	1.00	400.00
401411			ENSP00000247172*:HYPOTHETICAL 126.2 kDa	1.00	72.00
401435			C14000397*:g 7499898 pir T33295 hypoth	1.00	64.00
401464	AF039241		histone deacetylase 5	3.82	49.00
401714			ENSP00000241802*:CDNA FLJ11007 FIS, CLON	2.02	40.00
401747			Homo sapiens keratin 17 (KRT17)	128.43	68.00
401760			Target Exon	1.74	35.00
401780			NM_005557*:Homo sapiens keratin 16 (foca	26.47	10.50
401781			Target Exon	10.33	4.61
401785			NM_002275*:Homo sapiens keratin 15 (KRT1	4.13	2.70
401797			Target Exon	1.44	2.10
401961			NM_021626*:Homo sapiens serine carboxypep	1.41	1.86
401985	AF053004		class I cytokine receptor	1.00	177.00
401994			Target Exon	61.84	47.00
402075			ENSP00000251056*:Plasma membrane calcium	1.00	1.00
402260			NM_001436*:Homo sapiens fibrillarin (FBL	1.58	1.39
402265			Target Exon	2.09	35.00
402297			Target Exon	1.00	92.00
402408			NM_030920*:Homo sapiens hypothetical pro	28.87	13.00
402420			C1000823*:g 10432400 emb CAC10290.1 (A	1.00	1.44
402674			Target Exon	7.44	243.00
402802			NM_001397*:Homo sapiens endothelin conver	1.00	70.00
402994			NM_002463*:Homo sapiens myxovirus (influ	1.37	1.43
403137			NM_005381*:Homo sapiens nucleolin (NCL),	1.00	19.00
403306	NM_006825		transmembrane protein (63kD), endoplasmic	1.00	43.00
403329			Target Exon	1.00	61.00
403381			ENSP00000231844*:Ecotropic virus integra	1.00	119.00
403478			NM_022342*:Homo sapiens kinesin protein 9	28.13	136.00
403485			C3001813*:g 12737279 ref XP_012163.1 k	20.23	76.00
403627			Target Exon	6.30	29.33
403715			Target Exon	1.30	35.00
404044			ENSP00000237855*:DJ398G3.2 (NOVEL PROTEI	1.00	54.00
404076			NM_016020*:Homo sapiens CGI-75 protein (14.29	91.00
404101			C8000950*:g 423560 pir A47318 RNA-bind	1.00	1.00
404140			NM_006510*:Homo sapiens ret finger protei	1.42	1.44
404165			ENSP00000244562*:NRH dehydrogenase [quino	1.00	54.00
404185			Target Exon	1.00	117.00
404210			NM_005936*:Homo sapiens myeloid/lymphoid	5.93	13.77
404253			NM_021058*:Homo sapiens H2B histone fami	1.00	1.00

	404287		C6001909:gi 704441 dbj BAA18908.1 (D298	29.71	42.00
	404298		C6001238*:gi 121715 sp P26697 GTA3_CHICK	1.30	1.00
	404347		Target Exon	1.00	1.00
5	404440		NM_021048:Homo sapiens melanoma antigen,	1.00	15.00
	404721		NM_005596*:Homo sapiens nuclear factor I	1.00	60.00
	404794	NM_000078	cholesterol ester transfer protein, plas	1.07	1.38
	404854		Target Exon	1.61	2.01
	404877		NM_005365:Homo sapiens melanoma antigen,	1.00	1.00
10	404927		Target Exon	1.00	1.00
	404996		Target Exon	1.00	1.00
	405449		CY000047*:gi 11427234 ref XP_009399.1 z	1.00	1.00
	405568		NM_031413*:Homo sapiens cat eye syndrome	1.00	78.00
	405572		Target Exon	0.76	1.14
15	405646		C12000200:gi 4557225 ref NP_000005.1 al	1.01	1.28
	405676	BE336714	cytochrome c-1	1.13	2.89
	405770		NM_002362:Homo sapiens melanoma antigen,	45.52	37.00
	405932		C15000305:gi 3806122 gb AAC69198.1 (AF0	1.99	1.99
	406137		NM_000179*:Homo sapiens mutS (E. coli) h	2.77	2.38
20	406360		Target Exon	1.00	35.00
	406399		NM_003122*:Homo sapiens serine protease	1.00	39.00
	406467		Target Exon	1.00	1.00
	406621	X57809	Immunoglobulin lambda locus	1.41	1.74
	406642	AJ245210	gb:Homo sapiens mRNA for immunoglobulin	2.16	3.91
25	406663	U24683	immunoglobulin heavy constant mu	2.07	2.93
	406671	AA129547	met proto-oncogene (hepatocyte growth fa	15.00	51.00
	406673	M34996	major histocompatibility complex, class	0.98	3.09
	406676	X58399	Human L2-9 transcript of unrearranged Im,	1.30	1.53
	406678	U77534	gb:Human clone 1A11 immunoglobulin varia	1.33	1.45
30	406685	M18728	gb:Human nonspecific crossreacting antig	1.46	2.85
	406687	M31126	pregnancy specific beta-1-glycoprotein 9	8.61	8.50
	406690	M29540	carcinoembryonic antigen-related cell ad	226.37	350.00
	406698	X03068	major histocompatibility complex, class	1.01	2.52
	406815	AA833930	tRNA isopentenylpyrophosphate transferas	20.25	32.00
35	406851	AA609784	major histocompatibility complex, class	0.76	1.91
	406964	M21305	gb:Human alpha satellite and satellite 3	38.15	1114.00
	406967	M24349	gb:Human parathyroid hormone-like protei	1.00	1.00
	406974	M57293	gb:Human parathyroid hormone-related pep	1.00	1.00
	407103	AA424881	hypothetical protein MGC13170	1.77	1.10
40	407128	R83312	EST	1.00	1.00
	407137	T97307	gb:ye53h05.s1 Soares fetal liver spleen	142.70	135.00
	407168	R45175	ESTs	2.16	18.00
	407239	AA076350	leukocyte immunoglobulin-like receptor,	1.10	1.57
	407242	M18728	gb:Human nonspecific crossreacting antig	1.12	2.85
45	407244	M10014	fibrinogen, gamma polypeptide	3.24	15.38
	407289	AA135159	Homo sapiens cDNA FLJ12149 fis, clone MA	3.53	3.68
	407300	AA102616	gb:zn43e07.s1 Stratagene HeLa cell s3 93	19.74	73.00
	407366	AF026942	gb:Homo sapiens cig33 mRNA, partial sequ	0.06	8.25
	407378	AA299264	ESTs, Moderately similar to i38022 hypot	1.00	26.00
50	407430	AF169351	gb:Homo sapiens protein tyrosine phospho	1.00	25.00
	407453	AJ132087	gb:Homo sapiens mRNA for axonemal dynein	1.00	75.00
	407577	AW131324	hypothetical protein MGC12538	1.00	1.00
	407634	AW016569	UDP-GlcNAc:betaGal beta-1,3-N-acetylgluc	111.20	228.00
	407710	AW022727	ESTs	1.00	28.00
55	407720	AB037776	KIAA1355 protein	1.89	1.31
	407746	AK001962	hypothetical protein FLJ11100	1.00	1.00
	407756	AA116021	ubiquitin specific protease 18	4.51	5.00
	407758	D50915	KIAA0125 gene product	1.00	28.00
	407782	AA608956	ESTs, Moderately similar to PURKINJE CEL	0.97	1.14
60	407788	BE514982	S100 calcium-binding protein A2	7.88	3.83
	407790	AI027274	Homo sapiens cDNA FLJ14866 fis, clone PL	3.63	42.00
	407811	AW190902	cysteine knot superfamily 1, BMP antagon	89.96	109.00
	407839	AA045144	ESTs	173.91	108.00
	407944	R34008	desmocollin 2	111.30	70.00
65	408000	L11690	bulbos pemphigoid antigen 1 (230/240kD)	151.17	8.00
	408031	AA081395	Homo sapiens cDNA FLJ10366 fis, clone NT	9.91	93.00
	408063	BE086548	calcineurin-binding protein calcisarcin-1	195.78	231.00
	408070	AW148852	gb:xf05d05.x1 NCI_CGAP_Bm35 Homo sapien	1.00	1.00
	408101	AW968504	CDC2-related protein kinase 7	37.84	61.00
70	408122	AI432652	hypothetical protein FLJ10718	0.85	1.71
	408212	AA297567	hypothetical protein	5.88	7.91
	408243	Y00787	interleukin 8	4.27	9.98
	408349	BE546947	homeo box C10	3.79	3.46
	408353	BE439838	mitochondrial ribosomal protein S17	1.88	1.65
75	408354	AI382803	ESTs	1.00	73.00
	408369	R38438	solute carrier family 15 (H777) transport	1.41	16.50
	408380	AF123050	diubiquitin	15.19	37.22
	408482	NM_000676	adenosine A2b receptor	1.65	1.19
	408522	AI541214	Small proline-rich protein SPRK (human,	1.98	1.24
80	408538	AW381532	ESTs	1.55	1.50
	408545	AW235405	ESTs	1.00	1.00
	408572	AA055611	ESTs, Moderately similar to ALU4_HUMAN A	1.00	44.00
	408633	AW963372	PRO2000 protein	107.16	56.00
	408660	AA525775	ESTs, Moderately similar to PC4259 ferri	1.00	1.00
85	408761	AA057264	ESTs, Weakly similar to (define not ava	52.24	141.00
	408771	AW732573	potassium voltage-gated channel, delayed	3.05	109.00

	408783	AF192522	Hs.47701	NPC1 (Niemann-Pick disease, type C1, gen	1.02	1.07
	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	41.19	61.00
	408805	H69912	Hs.48269	vaccinia related kinase 1	24.67	45.00
5	408841	AW438865	Hs.256862	ESTs	1.00	58.00
	408873	AL046017	Hs.182278	calmodulin 2 (phosphorylase kinase, delt	1.00	89.00
	408908	BE286227	Hs.250822	serine/threonine kinase 15	7.76	1.00
	408992	AA059325	Hs.71642	guanine nucleotide binding protein (G pr	1.00	1.00
	408996	AI979168	Hs.344096	glycoprotein (transmembrane) nmb	3.71	5.50
10	409015	BE389387	Hs.49767	NM_004553:Homo sapiens NADH dehydrogenas	1.44	1.24
	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	4.28	5.32
	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	112.42	195.00
	409077	AA401369	Hs.190721	ESTs	1.00	17.00
	409093	BE243834	Hs.50441	CGI-04 protein	2.02	1.93
15	409103	AF251237	Hs.112208	XAGE-1 protein	80.44	40.00
	409142	AL136877	Hs.50758	SMC4 (structural maintenance of chromoso	14.87	6.00
	409187	AF154830	Hs.50966	carbamoyl-phosphate synthetase 1, mitocho	1.00	1.00
	409228	AI654298	Hs.271695	ESTs, Weakly similar to 2109260A B cell	1.22	1.00
	409234	AI879419	Hs.27206	ESTs	1.00	1.00
20	409268	AA625304	Hs.187579	ESTs	11.90	23.00
	409269	AA576953	Hs.22972	hypothetical protein FLJ13352	1.00	1.00
	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	168.91	35.00
	409404	BE220053	Hs.129056	ESTs	1.00	1.00
	409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini	79.74	96.00
25	409430	R21945	Hs.346735	splicing factor, arginine/serine-rich 5	1.45	2.10
	409446	AI561173	Hs.87688	ESTs	1.00	4.00
	409506	NM_006153	Hs.54589	NCK adaptor protein 1	3.97	28.00
	409522	AA075382		gb:zm87b03.s1 Stratagene ovarian cancer	15.98	141.00
	409582	AA401369	Hs.190721	ESTs	1.00	17.00
30	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibit	292.12	79.00
	409705	M37762	Hs.56023	brain-derived neurotrophic factor	1.00	82.00
	409719	AI769160	Hs.108681	Homo sapiens brain tumor associated prot	1.00	1.00
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	0.12	18.12
	409744	AW675258	Hs.56265	Homo sapiens mRNA; cDNA DKFZp586P2321 (f	20.75	51.00
35	409757	NM_001898	Hs.123114	cystatin SN	22.46	15.80
	409866	AW502152		gb:UL-HF-BR0p-ajr-f-11-0-UL.r1 NIH_MGC_5	1.00	1.00
	409893	AW247090	Hs.57101	minichromosome maintenance deficient (S.	1.50	1.09
	409902	AI337658	Hs.156351	ESTs	25.92	50.00
	409935	AW511413	Hs.278025	ESTs	2.63	2.11
40	409956	AW103364	Hs.727	inhibin, beta A (activin A, activin AB a	2.17	4.01
	409958	NM_001523	Hs.57697	hyaluronan synthase 1	0.91	2.07
	410001	AB041036	Hs.57771	kallikrein 11	1.04	2.28
	410032	BE065985		gb:RC3-BT0319-120200-014-a09 BT0319 Homo	1.00	58.00
	410037	AB020725	Hs.58009	KIAA0918 protein	1.00	34.00
45	410044	BE566742	Hs.58169	highly expressed in cancer, rich in leuc	1.00	1.00
	410048	W76467	Hs.58218	proline oxidase homolog	1.03	1.44
	410076	T05387	Hs.7991	ESTs	1.12	1.50
	410102	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE	9.89	1.00
	410153	BE311926	Hs.15830	hypothetical protein FLJ12691	1.00	1.00
50	410166	AK001376	Hs.59346	hypothetical protein FLJ10514	1.00	1.00
	410193	AJ132592	Hs.59757	zinc finger protein 281	42.01	51.00
	410274	AA381807	Hs.61762	hypoxia-inducible protein 2	1.72	1.32
	410309	BE043077	Hs.278153	ESTs	1.00	2.00
	410340	AW182833	Hs.112188	hypothetical protein FLJ13149	32.08	75.00
55	410348	AW182663	Hs.95469	ESTs	1.00	1.00
	410407	X66839	Hs.63287	carbonic anhydrase IX	1.40	1.11
	410418	D31382	Hs.63325	transmembrane protease, serine 4	4.30	2.03
	410438	AB037756	Hs.45207	hypothetical protein KIAA1335	1.00	18.00
	410553	AW016824	Hs.255527	hypothetical protein MGC14128	1.34	1.04
60	410555	W27235	Hs.64311	a disintegrin and metalloproteinase doma	23.99	1.41
	410561	BES40255	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	10.04	1.00
	410681	AW246890	Hs.65425	calbindin 1, (28kD)	10.88	18.92
	410781	AI375672	Hs.165028	ESTs	1.00	57.00
	411027	AF072099	Hs.67846	leukocyte immunoglobulin-like receptor,	1.62	3.78
65	411074	X60435	Hs.68137	adenylate cyclase activating polypeptide	1.00	1.15
	411089	AA456454		cell division cycle 2-like 1 (PITSLRE pr	1.58	1.58
	411152	BE069199		gb:QV3-BT0379-010300-105-g03 BT0379 Homo	1.00	84.00
	411248	AA551538	Hs.334605	Homo sapiens cDNA FLJ14408 fis, clone HE	1.82	1.45
	411252	AB018549	Hs.69328	MD-2 protein	7.32	12.74
70	411263	BE297802	Hs.69360	kinesin-like 6 (mitotic centromere-assoc	3.44	2.55
	411365	M76477	Hs.289082	GM2 ganglioside activator protein	1.35	2.02
	411402	BE297855	Hs.69855	NRAS-related gene	1.00	46.00
	411573	AB029000	Hs.70823	KIAA1077 protein	11.40	11.35
	411579	AC005258	Hs.70830	U8 snRNA-associated Sm-like protein LSm7	1.08	1.90
75	411617	AA247994	Hs.90063	neurocalcin delta	1.74	2.57
	411732	AA059325	Hs.71642	guanine nucleotide binding protein (G pr	1.02	1.00
	411773	NM_006799	Hs.72026	protease, serine, 21 (testisin)	1.34	2.19
	411789	AF245505	Hs.72157	Adlcan	2.19	2.79
	411800	N39342	Hs.103042	microtubule-associated protein 1B	23.34	34.00
80	411945	AL033527	Hs.92137	v-myc avian myelocytomatosis viral oncog	1.00	8.00
	412115	AK001763	Hs.73239	hypothetical protein FLJ10901	2.07	1.64
	412140	AA219691	Hs.73825	RAB6 interacting, kinesin-like (rabkines	118.48	92.00
	412276	BE262621	Hs.73798	macrophage migration inhibitory factor (1.98	1.49
	412464	T78141	Hs.22826	ESTs, Weakly similar to I55214 salivary	1.16	1.34
85	412530	AA766268	Hs.266273	hypothetical protein FLJ13346	41.52	84.00
	412537	AL031778		nuclear transcription factor Y, alpha	17.90	55.00

	412659	AW753865	Hs.74376	olfactomedin related ER localized protel	14.65	47.00
	412719	AW016610	Hs.816	ESTs	382.46	128.00
	412723	AA648459	Hs.335951	hypothetical protein AF301222	54.90	1.00
5	412811	H06382		ESTs	1.00	11.00
	412817	AL037159	Hs.74619	proteasome (prosome, macropain) 26S subu	1.63	1.42
	412863	AA121673	Hs.59757	zinc finger protein 281	17.63	56.00
	412924	BE018422	Hs.75258	H2A histone family, member Y	1.00	22.00
	413004	T35901	Hs.75117	interleukin enhancer binding factor 2, 4	2.19	2.05
10	413011	AW068115	Hs.821	biglycan	1.22	1.88
	413048	M93221	Hs.75182	mannose receptor, C type 1	0.30	6.23
	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	3.43	8.71
	413129	AF292100	Hs.104613	RP42 homolog	4.67	4.77
	413142	M81740	Hs.75212	ornithine decarboxylase 1	1.92	2.59
	413223	A1732182	Hs.191866	ESTs	5.73	27.00
15	413248	T64858	Hs.21433	hypothetical protein DKFZp547J036	0.99	1.06
	413273	U75679	Hs.75257	stem-loop (histone) binding protein	1.00	18.00
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	1.10	1.09
	413281	AA861271	Hs.222024	transcription factor BMAL2	95.94	69.00
	413364	BE536218	Hs.137516	ridgetin-like 1	1.00	1.00
20	413385	M34455	Hs.840	indoleamine-pyrrole 2,3 dioxygenase	0.95	2.09
	413409	AI638418	Hs.1440	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	1.00	1.00
	413453	AA129640	Hs.128065	ESTs	1.00	31.00
	413527	BE250788	Hs.179882	hypothetical protein FLJ12443	1.08	1.46
	413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	79.15	114.00
25	413573	A1733859	Hs.149089	ESTs	1.00	1.00
	413582	AW295647	Hs.71331	hypothetical protein MGC5350	8.80	10.00
	413597	AW302885	Hs.117183	ESTs	1.00	1.00
	413690	BE157489		gb:RC1-HT0375-120200-011-e06 HT0375 Homo	1.00	1.00
30	413691	AB023173	Hs.75478	ATPase, Class VI, type 11B	3.16	2.32
	413719	BE439580	Hs.75498	small inducible cytokine subfamily A (Cy	2.88	9.52
	413753	U17760	Hs.75517	laminin, beta 3 (nicotin (125kD), kallinin	144.10	108.00
	413801	M62246	Hs.35406	ESTs, Highly similar to unnamed protein	1.00	17.00
	413833	Z15005	Hs.75573	centromere protein E (312kD)	1.00	1.00
35	413882	AA132973	Hs.184492	ESTs	64.24	148.00
	413926	AA133338	Hs.54310	ESTs	1.00	67.00
	413943	AW294416	Hs.144687	Homo sapiens cDNA FLJ12981 fis, clone NT	43.42	42.00
	413995	BE048146	Hs.75671	syntaxin 1A (brain)	1.23	1.11
	414035	Y00630	Hs.75716	serine (or cysteine) proteinase inhibito	2.02	2.51
40	414142	AW368397	Hs.334485	Homo sapiens cDNA FLJ14438 fis, clone HE	1.00	102.00
	414180	AI863304	Hs.120905	Homo sapiens cDNA FLJ11448 fis, clone HE	6.92	77.00
	414245	BE148072	Hs.75850	WAS protein family, member 1	1.00	1.00
	414275	AW970254	Hs.889	Charot-Leyden crystal protein	1.00	59.00
	414317	BE263280	Hs.75888	phosphogluconate dehydrogenase	1.52	1.73
45	414334	AA824298	Hs.21331	hypothetical protein FLJ10036	1.78	1.72
	414341	D80004	Hs.75909	KIAA0182 protein	33.90	151.00
	414368	W70171	Hs.75939	uridine monophosphate kinase	171.60	97.00
	414416	AW409985	Hs.76084	hypothetical protein MGC2721	2.32	1.85
	414430	AI346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1	226.15	66.00
50	414570	Y00285	Hs.76473	insulin-like growth factor 2 receptor	1.64	1.98
	414618	AI204600	Hs.96978	hypothetical protein MGC10764	1.87	72.00
	414675	R79015	Hs.296281	interleukin enhancer binding factor 1	1.51	1.39
	414683	S78296	Hs.76888	hypothetical protein MGC12702	43.61	64.00
	414696	AF002020	Hs.76918	Niemann-Pick disease, type C1	28.63	71.00
55	414711	AI310440	Hs.288735	Homo sapiens cDNA FLJ13522 fis, clone PL	14.86	42.00
	414718	H95348	Hs.107987	ESTs	1.00	5.00
	414732	AW410976	Hs.77152	minichromosome maintenance deficient (S.	1.64	1.44
	414747	U30872	Hs.77204	centromere protein F (350/400kD, mitotin	65.01	74.00
	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	130.35	121.00
60	414774	X02419	Hs.77274	plasminogen activator, urokinase	2.24	2.19
	414806	D14694	Hs.77329	phosphatidylserine synthase 1	1.63	1.53
	414809	AI346699	Hs.77358	transferrin receptor (p90, CD71)	1.97	2.60
	414812	X72755	Hs.77367	monokine induced by gamma interferon	3.48	10.60
	414825	X06370	Hs.77432	epidermal growth factor receptor (avian	103.22	143.00
65	414839	X63692	Hs.77462	DNA (cytosine-5)-methyltransferase 1	1.80	1.69
	414883	AA926960		CDC28 protein kinase 1	14.29	10.06
	414907	X90725	Hs.77597	polo (Drosophila)-like kinase	1.95	2.20
	414914	U49844	Hs.77613	ataxia telangiectasia and Rad3 related	3.00	2.90
	414945	BE076358	Hs.77667	lymphocyte antigen 6 complex, locus E	1.02	1.21
70	414972	BE263782	Hs.77695	KIAA0008 gene product	1.00	1.00
	415014	AW954064	Hs.24951	ESTs	1.42	2.84
	415091	AL044872	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A sy	1.00	30.00
	415138	C18356	Hs.295944	tissue factor pathway inhibitor 2	34.72	107.00
	415227	AW821113	Hs.72402	ESTs	1.87	49.00
75	415238	R37780	Hs.21422	ESTs	1.00	1.00
	415263	AA948033	Hs.130853	ESTs	1.00	1.00
	415295	R41450	Hs.6546	ESTs	1.00	1.00
	415339	NM_015156	Hs.78398	KIAA0071 protein	51.18	166.00
	415669	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibito	30.84	63.00
80	415674	BE394784	Hs.78596	proteasome (prosome, macropain) subunit,	1.48	1.39
	415709	AA649850	Hs.278558	ESTs	1.00	1.00
	415735	AA704162	Hs.120811	ESTs, Weakly similar to I38022 hypotheti	1.00	72.00
	415799	AA653718	Hs.225841	DKFZP434D193 protein	6.23	31.00
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	24.30	1.00
85	415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	32.51	35.00
	415989	AI267700		ESTs	78.89	1.00

	416018	AW138239	Hs.78977	proprotein convertase subtilisin/kexin 1	1.00	1.00
	416065	BE267931	Hs.78996	proliferating cell nuclear antigen	3.35	2.32
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (39.03	3.00
5	416177	AA174069	Hs.187607	ESTs	1.00	9.00
	416178	AI808527	Hs.192822	serologically defined breast cancer anti	3.83	3.76
	416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	3.67	1.00
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	9.70	1.00
	416239	AL038450	Hs.48948	ESTs	83.87	129.00
10	416250	AA581386	Hs.73452	hypothetical protein MGC10791	1.96	2.12
	416322	BE019494	Hs.79217	pyrroline-5-carboxylate reductase 1	2.08	1.73
	416423	H54375	Hs.268921	ESTs	1.00	89.00
	416448	L13210	Hs.79339	lectin, galactoside-binding, soluble, 3	1.28	1.54
	416498	U33632	Hs.79351	potassium channel, subfamily K, member 1	27.29	67.00
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	53.29	51.00
15	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	9.96	5.00
	416722	AA354604	Hs.122546	hypothetical protein FLJ23017	3.68	33.00
	416819	U77735	Hs.80205	pim-2 oncogene	1.59	1.84
	416936	N21352	Hs.42987	ESTs, Weakly similar to S21348 probable	1.00	1.00
20	417034	NM_006183	Hs.80962	neurotensin	1.00	1.00
	417061	AI875944	Hs.188691	Homo sapiens cDNA FLJ12033 fs, clone HE	32.95	156.00
	417079	U65590	Hs.81134	interleukin 1 receptor antagonist	3.91	4.93
	417218	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth fa	1.00	51.00
	417233	W25005	Hs.24395	small inducible cytokine subfamily B (Cy	3.38	2.05
25	417308	H60720	Hs.81892	KIAA0101 gene product	82.94	25.36
	417315	AI080042	Hs.180450	ribosomal protein S24	106.61	121.00
	417324	AW265494		ESTs	1.20	1.28
	417366	BE185289	Hs.1076	small proline-rich protein 1B (cornifin)	8.97	3.27
	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor	2.59	1.82
30	417428	N87579	Hs.278871	gb:LL2030F Human fetal heart, Lambda ZAP	1.00	52.00
	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	304.75	173.00
	417466	AI681547	Hs.59457	hypothetical protein FLJ22127	1.24	1.34
	417512	AI979168	Hs.344096	glycoprotein (transmembrane) nmb	2.14	5.50
	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated	2.66	1.68
35	417542	J04129	Hs.82269	progesterone-associated endometrial prote	1.28	1.35
	417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	42.76	51.00
	417715	AW969587	Hs.86366	ESTs	6.35	2.75
	417720	AA205625	Hs.208067	ESTs	113.31	58.00
	417791	AW965339	Hs.111471	ESTs	39.98	16.00
40	417830	AW504786	Hs.122579	hypothetical protein FLJ10461	2.61	31.00
	417866	AW067903	Hs.82772	collagen, type XI, alpha 1	2.35	2.44
	417900	BE250127	Hs.82906	CDC20 (cell division cycle 20, S. cerevi	1.52	1.11
	417933	X02308	Hs.82962	thymidylate synthetase	4.74	2.55
	417944	AU077196	Hs.82985	collagen, type V, alpha 2	3.61	5.21
45	417975	AA641836	Hs.30085	hypothetical protein FLJ23186	12.49	38.00
	417991	AA731452	Hs.190008	ESTs	1.00	26.00
	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	3.02	2.12
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	187.59	1.00
	418054	NM_002318	Hs.83354	lysyl oxidase-like 2	2.85	2.63
50	418057	NM_012151	Hs.83363	coagulation factor VIII-associated (intr	1.54	1.69
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	6.82	5.22
	418140	BE613836	Hs.83551	microfibrillar-associated protein 2	1.26	1.46
	418203	X54942	Hs.83758	CDC28 protein kinase 2	134.19	144.00
	418207	C14685	Hs.34772	ESTs	1.00	1.00
55	418216	AA662240	Hs.283099	AF15q14 protein	64.66	61.00
	418236	AW994005	Hs.337534	ESTs	18.53	147.00
	418249	H89226	Hs.34892	KIAA1323 protein	30.53	105.00
	418281	U09550	Hs.1154	oviductal glycoprotein 1, 120kD (mucin 9	1.00	3.00
	418283	S79895	Hs.83942	cathepsin K (pycnodysostosis)	3.96	5.16
60	418300	AI433074	Hs.86582	Homo sapiens cDNA: FLJ21578 fs, clone C	3.18	2.91
	418322	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	11.96	6.68
	418327	U70370	Hs.84136	paired-like homeodomain transcription fa	9.23	2.22
	418345	AJ001696	Hs.241407	serine (or cysteine) proteinase inhibito	1.00	1.00
	418379	AA218940	Hs.137516	fidgetin-like 1	21.68	44.00
65	418397	NM_001269	Hs.84746	chromosome condensation 1	1.00	8.00
	418403	D86978	Hs.84790	KIAA0225 protein	16.91	18.98
	418462	BE001596	Hs.85266	integrin, beta 4	1.56	1.16
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	3.22	2.38
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	2.66	2.22
70	418526	BE019020	Hs.85838	solute carrier family 16 (monocarboxylic	2.04	2.21
	418538	BE244323	Hs.85951	exportin, tRNA (nuclear export receptor	1.33	37.00
	418543	NM_005329	Hs.85962	hyaluronan synthase 3	1.04	1.23
	418574	N28754		M-phase phosphoprotein 9	48.60	85.00
	418592	X99226	Hs.284153	Fanconi anemia, complementation group A	18.24	26.00
75	418641	BE243136	Hs.86947	a disintegrin and metalloproteinase doma	1.19	1.41
	418661	NM_001949	Hs.1189	E2F transcription factor 3	29.05	43.00
	418663	AK001100	Hs.41690	desmocollin 3	112.17	19.00
	418678	NM_001327	Hs.87225	cancer/testis antigen	1.18	1.10
	418686	Z36830	Hs.87268	annexin A8	1.54	1.98
80	418689	AI360883	Hs.274448	hypothetical protein FLJ11029	1.19	1.04
	418712	Z42183		gb:HSC0BF041 normalized infant brain cDN	1.00	12.00
	418727	AA227609	Hs.94834	ESTs	1.00	49.00
	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	49.85	1.00
	418819	AA228776	Hs.191721	ESTs	1.00	140.00
	418830	BE513731	Hs.88959	hypothetical protein MGC4816	20.97	23.00
85	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	57.09	35.00

	418971	AA360392	Hs.87113	ESTs	1.00	12.00
	418973	AA233056	Hs.191518	ESTs	4.89	28.00
	419078	M93119	Hs.89584	insulinoma-associated 1	1.00	10.00
5	419079	AW014836	Hs.18844	ESTs	1.09	1.98
	419080	AW150835	Hs.18878	hypothetical protein FLJ21620	2.06	1.68
	419088	AI538323	Hs.52620	integrin, beta 8	15.60	51.00
	419092	J05581	Hs.89603	mucin 1, transmembrane	1.11	1.83
	419121	AA374372	Hs.89626	parathyroid hormone-like hormone	1.00	1.00
10	419171	NM_002846	Hs.89655	protein tyrosine phosphatase, receptor t	1.10	1.14
	419183	U60669	Hs.89663	cytochrome P450, subfamily XXIV (vitamin	1.00	1.00
	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	3.18	2.43
	419288	AA256106	Hs.87507	ESTs	1.00	34.00
	419335	AW960146	Hs.284137	hypothetical protein FLJ12888	1.00	8.00
15	419354	M62839	Hs.1252	apolipoprotein H (beta-2-glycoprotein I)	22.63	54.00
	419359	AL043202	Hs.90073	chromosome segregation 1 (yeast homolog)	2.50	1.98
	419423	D26488	Hs.90315	KIAA0007 protein	1.00	7.00
	419443	D62703		gb:HUM316G10B Clontech human aorta polyA	1.00	12.00
	419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	1.84	1.84
20	419474	AW968619	Hs.155849	ESTs	13.63	62.00
	419485	AA489023	Hs.99807	ESTs, Weakly similar to unnamed protein	4.27	2.26
	419488	AA316241	Hs.90691	nucleophosmin/nucleoplasm 3	3.65	3.63
	419502	AU076704		fibrinogen, A alpha polypeptide	13.05	115.00
	419539	AF070590	Hs.90869	Homo sapiens clones 24622 and 24623 mRNA	74.60	117.00
25	419558	U29615	Hs.91093	chitinase 1 (chitotriosidase)	1.47	4.98
	419569	AI971651	Hs.91143	Jagged 1 (Alagille syndrome)	1.00	4.00
	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	94.30	94.00
	419703	AI793257	Hs.128151	ESTs	15.26	50.00
	419721	NM_001650	Hs.288650	aquaporin 4	1.00	191.00
30	419729	AA586442	Hs.21411	gb:nc53a03.s1 NCI_CGAP_SS1 Homo sapiens	1.00	59.00
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	2.02	1.08
	419745	AF042001	Hs.93005	slug (chicken homolog), zinc finger prot	1.00	1.00
	419752	AA249573	Hs.152618	ESTs, Moderately similar to ZN91_HUMAN Z	29.87	77.00
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	50.99	214.00
35	419938	AI792788		gb:cl91d05.y5 NCI_CGAP_Kd5 Homo sapiens	1.00	1.00
	419937	AB040959	Hs.93836	DKFZP434N014 protein	1.64	2.47
	419983	W55956	Hs.94030	Homo sapiens mRNA; cDNA DKFZp586E1624 (f	15.72	94.00
	420005	AW271108	Hs.133294	ESTs	3.15	1.43
	420047	AI478658	Hs.94631	brefeldin A-inhibited guanine nucleotide	12.45	39.00
40	420058	AK001423	Hs.94694	Homo sapiens cDNA FLJ10561 fis, clone NT	1.00	117.00
	420162	BE378432	Hs.95577	cyclin-dependent kinase 4	1.43	1.21
	420251	AW374968	Hs.348112	Human DNA sequence from clone RP5-1103G7	2.35	3.23
	420259	AF004884	Hs.96253	calcium channel, voltage-dependent, P/Q	0.77	1.15
	420281	AI623693	Hs.323494	ESTs	45.04	54.00
45	420309	AW043637	Hs.21766	ESTs, Weakly similar to ALU5_HUMAN ALU S	49.22	31.00
	420332	NM_001756	Hs.1305	serine (or cysteine) proteinase inhibito	0.05	2.82
	420380	AA640891	Hs.102406	ESTs	0.99	2.74
	420462	AF050147	Hs.97932	chondromodulin I precursor	1.00	1.00
	420520	AK001978	Hs.98510	similar to rab11-binding protein	49.74	133.00
50	420552	AK000492	Hs.98808	hypothetical protein	94.65	88.00
	420560	AW207748	Hs.59115	ESTs	1.00	17.00
	420610	AI683183	Hs.99348	distal-less homeo box 5	1.00	13.00
	420689	H79979	Hs.88678	ESTs	50.09	95.00
	420721	AA927802	Hs.159471	ZAP3 protein	1.00	31.00
55	420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	1.00	48.00
	420783	AI659838	Hs.99923	lectin, galactoside-binding, soluble, 7	3.04	1.25
	420900	AL045633	Hs.44269	ESTs	2.24	7.00
	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	1.00	8.00
	421002	AF116030	Hs.100932	transcription factor 17	1.00	27.00
60	421027	AA761198	Hs.55254	ESTs	2.87	38.00
	421037	AI684808	Hs.197653	ESTs	1.00	46.00
	421041	N36914	Hs.14691	ESTs, Moderately similar to I38022 hypot	1.00	98.00
	421073	NM_004689	Hs.101448	metastasis associated 1	1.34	1.46
	421110	AJ250717	Hs.1355	cathepsin E	119.47	427.00
65	421133	AA401369	Hs.190721	ESTs	1.10	17.00
	421150	AI913562	Hs.189902	ESTs	1.45	1.63
	421155	H87879	Hs.102287	lysyl oxidase	1.00	15.00
	421307	BE539976	Hs.103305	Homo sapiens mRNA; cDNA DKFZp434B0425 (f	1.37	1.10
	421316	AA287203	Hs.324728	SMA5	1.00	21.00
70	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	1.92	3.94
	421451	AA291377	Hs.50831	ESTs	5.89	14.00
	421474	U76362	Hs.104637	solute carrier family 1 (glutamate trans	1.46	1.78
	421506	BE302796	Hs.105097	thymidine kinase 1, soluble	1.58	1.08
	421508	NM_004833	Hs.105115	absent in melanoma 2	5.11	5.23
75	421515	Y11339	Hs.105352	GaINAc alpha-2, 6-sialyltransferase I, I	1.00	3.00
	421524	AA312082	Hs.105445	GDNF family receptor alpha 1	2.63	10.58
	421526	AL080121	Hs.105460	DKFZP564O0823 protein	1.46	1.88
	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	30.21	50.32
	421574	AJ000152	Hs.105924	defensin, beta 2	1.67	1.74
80	421582	AI910275		trefoil factor 1 (breast cancer, estroge	1.23	1.00
	421633	AF121860	Hs.106260	sorting nexin 10	1.00	116.00
	421659	NM_014459	Hs.106511	protocadherin 17	0.05	6.33
	421677	H64092	Hs.38282	ESTs	1.31	1.42
	421753	BE314828	Hs.107911	ATP-binding cassette, sub-family B (MDR/	1.41	1.20
85	421773	W69233	Hs.112457	ESTs	1.12	1.14
	421777	BE562088	Hs.108196	HSPC037 protein	1.97	1.29

	421800	AA298151	Hs.222969	ESTs	1.03	1.30
	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	1.88	1.59
	421896	N62293	Hs.45107	ESTs	11.84	22.80
5	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	45.89	90.00
	421931	NM_000814	Hs.1440	gamma-aminobutyric acid (GABA) A recepto	1.13	1.49
	421948	L42583	Hs.334309	keratin 6A	51.83	20.25
	421975	AW961017	Hs.6459	hypothetical protein FLJ11856	1.17	1.15
	422026	U80736	Hs.110826	trinucleotide repeat containing 9	1.00	52.00
10	422094	AF129535	Hs.272027	F-box only protein 5	67.61	62.00
	422095	AI868872	Hs.282804	hypothetical protein FLJ22704	4.37	2.34
	422109	S73265	Hs.1473	gastrin-releasing peptide	4.18	95.50
	422128	AW881145		gb:QV0-OT0033-010400-182-a07 OT0033 Homo	40.89	71.00
	422129	AU076635	Hs.1478	serine (or cysteine) proteinase inhibito	1.13	1.38
15	422134	AW179019	Hs.112110	mitochondrial ribosomal protein L42	41.59	96.00
	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	2.37	1.10
	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias	3.29	1.68
	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	4.93	5.73
	422282	AF019225	Hs.114309	apolipoprotein L	1.49	1.71
20	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	25.99	10.91
	422310	AA316622	Hs.98370	cytochrome P450, subfamily IIS, polypept	1.54	1.41
	422311	AF073515	Hs.114948	cytokine receptor-like factor 1	1.15	1.78
	422330	D30783	Hs.115263	epiregulin	1.00	112.00
	422364	AF067800	Hs.115515	C-type (calcium dependent, carbohydrate-	9.39	60.00
25	422406	AF025441	Hs.116206	Opa-interacting protein 5	18.33	63.00
	422424	AI186431	Hs.296638	prostate differentiation factor	1.71	3.21
	422440	NM_004812	Hs.116724	aldo-keto reductase family 1, member B10	47.53	32.00
	422487	AJ010901	Hs.198287	mucin 4, tracheobronchial	73.68	35.54
	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	173.97	28.00
30	422515	AW500470	Hs.117950	multifunctional polypeptide similar to S	4.68	2.92
	422656	AI870435	Hs.1569	LIM homeobox protein 2	1.00	1.00
	422737	M26939	Hs.119571	collagen, type III, alpha 1 (Ehlers-Danl	3.89	4.55
	422756	AA441787	Hs.119689	glycoprotein hormones, alpha polypeptide	1.05	1.46
	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	3.88	1.53
35	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	99.56	63.00
	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	1.69	3.17
	422938	NM_001809	Hs.1594	centromere protein A (17kD)	70.46	61.00
	422956	BE545072	Hs.122579	ECT2 protein (Epithelial cell transformi	77.74	3.00
	422960	AW890487	Hs.63984	cadherin 13, H-cadherin (heart)	5.88	8.55
40	422963	AA401369	Hs.190721	ESTs	171.41	17.00
	422976	AU076657	Hs.1600	chaperonin containing TCP1, subunit 5 (e	2.12	1.62
	422981	AF026445	Hs.122752	TATA box binding protein (TBP)-associate	10.49	35.00
	422986	AA318777	Hs.221974	ESTs	12.40	32.47
	423034	AL119930		gb:DKFZp761A092_r1 761 (synonym: hamy2)	16.41	60.00
45	423049	X59373	Hs.188023	ESTs, Moderately similar to HXDA_HUMAN H	1.00	1.00
	423081	AF262992	Hs.123159	sperm associated antigen 4	1.82	2.96
	423184	NM_004428	Hs.1624	ephrin-A1	1.14	1.53
	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	2.14	1.69
	423248	AA380177	Hs.125845	ribulose-5-phosphate-3-epimerase	7.18	14.00
50	423309	BE006775	Hs.126782	sushi-repeat protein	21.90	64.00
	423361	AW170055	Hs.47628	ESTs	1.00	1.00
	423453	AW450737	Hs.128791	CGI-09 protein	55.52	66.00
	423511	AF036329	Hs.129715	gonadotropin-releasing hormone 2	0.88	1.17
	423516	AB007933	Hs.129729	ligand of neuronal nitric oxide synthase	1.76	5.40
55	423551	AA327598	Hs.233785	ESTs	3.54	4.33
	423554	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	1.00	50.00
	423575	C18863	Hs.163443	Homo sapiens cDNA FLJ11576 fis, clone HE	38.88	70.00
	423624	AI807408	Hs.166368	ESTs	1.00	67.00
	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	76.02	1.00
60	423642	AW452650	Hs.157148	hypothetical protein MGC13204	19.14	58.00
	423662	AA642452	Hs.130881	B-cell CLL/lymphoma 11A (zinc finger pro	3.61	13.57
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	240.73	40.00
	423698	AA329796	Hs.1098	DKFZp434J1813 protein	1.00	59.00
	423725	AJ403108	Hs.132127	hypothetical protein LOC57822	4.20	1.00
65	423761	NM_006194	Hs.132576	paired box gene 9	1.00	1.00
	423787	AJ295745	Hs.236204	nuclear pore complex protein	7.18	6.64
	423816	AF151084		hypothetical protein	1.00	44.00
	423826	U20325	Hs.1707	cocaine- and amphetamine-regulated trans	1.00	1.00
	423849	AL157425	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (f	1.00	1.00
70	423887	AL080207	Hs.134585	DKFZP434G232 protein	1.00	1.00
	423934	U89995	Hs.159234	forkhead box E1 (thyroid transcription f	31.33	31.00
	423954	AW753164	Hs.288604	KIAA1632 protein	5.81	10.87
	423961	D13666	Hs.136348	osteoblast specific factor 2 (fasciclin	3.55	3.30
	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	233.42	68.00
75	424016	AW163729	Hs.6140	hypothetical protein MGC15730	0.93	1.01
	424028	AF055084	Hs.153692	Homo sapiens cDNA FLJ14354 fis, clone Y7	21.30	52.00
	424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibito	1.00	1.00
	424086	AI351010	Hs.102267	lysyl oxidase	21.91	70.00
	424098	AF077374	Hs.139322	small proline-rich protein 3	137.82	54.00
80	424120	T80579	Hs.290270	ESTs	1.00	1.00
	424165	AW582904	Hs.142255	islet amyloid polypeptide	1.00	34.00
	424200	AA337221		gb:EST41944 Endometrial tumor Homo sapie	13.06	48.00
	424279	L29306	Hs.171814	tryptophan hydroxylase (tryptophan 5-mon	1.00	1.00
	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	164.58	87.00
85	424326	NM_014479	Hs.145296	disintegrin protease	53.72	302.00
	424340	AA339036	Hs.7033	ESTs	0.88	1.15

	424351	BE622117	Hs.145567	hypothetical protein	0.93	1.03
	424364	AW383226	Hs.201189	ESTs, Weakly similar to G01763 atrophin-	7.02	3.24
	424381	AA285249	Hs.146329	protein kinase Chk2	95.55	92.00
5	424411	NM_005209	Hs.146549	crystallin, beta A2	1.63	3.25
	424420	BE614743	Hs.146588	prostaglandin E synthase	1.63	1.33
	424441	X14850	Hs.147097	H2A histone family, member X	1.82	1.29
	424502	AF242388	Hs.149585	lensin	1.00	1.00
	424503	X06256	Hs.149509	Integrin, alpha 5 (fibronectin receptor,	1.02	2.24
10	424513	BE385864	Hs.149894	mitochondrial translational initiation f	1.00	17.00
	424539	L02911	Hs.150402	Activin A receptor, type 1 (ACVR1) (ALK	32.46	108.00
	424568	AF005418	Hs.150595	cytochrome P450, subfamily XXVIA, polype	3.40	2.58
	424602	AK002055	Hs.151046	hypothetical protein FLJ11193	31.87	25.00
	424629	M90656	Hs.151393	glutamate-cysteine ligase, catalytic sub	3.58	2.37
15	424645	NM_014682	Hs.151449	KIAA0535 gene product	1.00	1.00
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	2.12	2.23
	424717	AW992292	Hs.152213	wingless-type MMTV integration site fami	1.00	1.00
	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	56.19	12.00
	424840	D79987	Hs.153479	extra spindle poles, S. cerevisiae, homo	2.65	1.30
20	424867	A1024860	Hs.153591	Not56 (D. melanogaster)-like protein	1.23	1.05
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	21.35	1.00
	424979	D87989	Hs.154073	UDP-galactose transporter related	1.36	1.35
	424999	AW953120		gb:EST365190 MAGE resequences, MAGB Homo	1.24	1.41
	425048	H05468	Hs.164502	ESTs	1.00	11.00
25	425057	AA826434	Hs.1619	achaete-scute complex (Drosophila) homol	7.46	87.00
	425081	X74794	Hs.154443	minichromosome maintenance deficient (S.	2.52	3.82
	425118	AU076611	Hs.154672	methylene tetrahydrofolate dehydrogenase	4.84	4.03
	425159	NM_004341	Hs.154868	carbamoyl-phosphate synthetase 2, aspart	3.62	2.73
	425202	AW962282	Hs.152049	ESTs, Weakly similar to I38022 hypotheti	1.00	53.00
30	425234	AW152225	Hs.155909	ESTs, Weakly similar to I38022 hypotheti	100.77	44.00
	425236	AW067800	Hs.155223	stanniocalcin 2	3.30	2.90
	425245	A1751768	Hs.155314	KIAA0095 gene product	1.91	2.32
	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin	1.41	1.49
	425266	J00077	Hs.155421	alpha-fetoprotein	1.00	68.00
35	425274	BE281191	Hs.155462	minichromosome maintenance deficient (mi	1.97	1.63
	425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	141.49	123.00
	425349	AA425234	Hs.79886	ribose 5-phosphate isomerase A (ribose 5	1.00	84.00
	425371	D49441	Hs.155981	mesothelin	0.87	1.59
	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	14.90	5.76
40	425420	BE536911	Hs.234545	hypothetical protein NUF2R	1.00	1.00
	425424	NM_004954	Hs.157199	ELKL motif kinase	10.58	9.74
	425483	AF231022	Hs.158159	FAT tumor suppressor (Drosophila) homolo	1.74	1.40
	425566	AW162943	Hs.250618	UL16 binding protein 2	1.49	1.14
	425580	L11144	Hs.1907	galanin	53.29	233.00
45	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	33.45	1.00
	425692	D90041	Hs.155956	N-acetyltransferase 1 (arylamine N-acety	1.00	55.00
	425695	NM_005401	Hs.159238	protein tyrosine phosphatase, non-recept	1.00	10.00
	425734	AF056209	Hs.159396	peptidylglycine alpha-amidating monooxyg	1.00	41.00
	425776	U25128	Hs.159499	parathyroid hormone receptor 2	1.00	48.00
50	425810	A1923627	Hs.31903	ESTs	27.39	98.00
	425811	AL039104	Hs.159557	karyopherin alpha 2 (RAG cohort 1, impor	1.99	1.58
	425849	A1077288	Hs.296323	serum/glucocorticoid regulated kinase	71.16	3.42
	425852	AK001504	Hs.159651	death receptor 6, TNF superfamily member	1.35	1.34
	426067	AA401369	Hs.190721	ESTs	1.01	17.00
55	426088	AF038007	Hs.166196	ATPase, Class I, type 8B, member 1	26.26	47.00
	426215	AW067800	Hs.155223	stanniocalcin 2	1.91	2.90
	426227	U67058	Hs.154299	Human proteinase activated receptor-2 mR	22.40	25.00
	426269	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (f	1.00	1.00
	426283	NM_003937	Hs.169139	kynureninase (L-kynurenine hydrolase)	91.39	229.00
60	426329	AL389951	Hs.271623	nucleoporin 50kD	4.34	4.08
	426427	M85699	Hs.169840	TTK protein kinase	7.02	1.00
	426432	AF001601	Hs.169857	paraoxonase 2	1.16	1.68
	426440	BE382756	Hs.169902	solute carrier family 2 (facilitated glu	2.59	1.71
	426459	AF151812	Hs.169992	hypothetical 43.2 Kd protein	1.56	1.66
65	426471	M22440	Hs.170009	transforming growth factor, alpha	20.60	26.00
	426496	D31765	Hs.170114	KIAA0061 protein	9.81	22.00
	426501	AA401369	Hs.190721	ESTs	19.23	17.00
	426514	BE616633	Hs.170185	bone morphogenetic protein 7 (osteogenic	103.74	41.00
	426536	A1949749	Hs.44441	ESTs	4.65	23.00
70	426572	AB037783	Hs.170623	hypothetical protein FLJ11183	1.00	43.00
	426682	AV660038	Hs.2056	UDP glycosyltransferase 1 family, polype	160.08	8.00
	426691	NM_006201	Hs.171834	PCTAIRE protein kinase 1	1.51	1.35
	426746	J03626	Hs.2057	uridine monophosphate synthetase (crota	2.13	1.68
	426752	X69490	Hs.172004	titin	0.02	5.14
	426784	U03749	Hs.172216	chromogranin A (parathyroid secretory pr	1.72	1.71
75	426807	AA385315	Hs.156682	ESTs	1.30	1.64
	426812	AF105365	Hs.172613	solute carrier family 12 (potassium/chlo	1.47	1.53
	426814	AF036943	Hs.172619	myelin transcription factor 1-like	1.00	1.00
	426831	BE296216	Hs.172673	S-adenosylhomocysteine hydrolase	1.51	1.25
80	426897	AA401369	Hs.190721	ESTs	141.56	17.00
	426925	NM_001196	Hs.315689	Homo sapiens cDNA: FLJ22373 fis, clone H	32.61	38.00
	426935	NM_000088	Hs.172928	collagen, type I, alpha 1	2.65	3.16
	426964	AA393739	Hs.287416	Homo sapiens cDNA FLJ11439 fis, clone HE	1.97	3.49
	426966	A1493134		sclerostin	1.00	1.00
	426991	AK001536		Homo sapiens cDNA FLJ10674 fis, clone NT	3.39	2.28
85	427099	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	4.24	17.00

WO 02/086443

PCT/US02/12476

	427239	BE270447	Hs.174070	ubiquitin carrier protein	1.58	1.05
	427260	AA663848		gb:aa70b06.s1 Stratagene schizo brain S1	1.34	1.60
	427281	AA906147	Hs.102869	ESTs	1.00	66.00
5	427335	AA448542	Hs.251677	G antigen 7B	51.83	4.00
	427354	T57896	Hs.191095	ESTs	1.17	1.95
	427356	AW023482	Hs.97849	ESTs	7.31	41.00
	427376	AA401533	Hs.19440	ESTs	1.00	57.00
	427383	NM_005411	Hs.177582	surfactant, pulmonary-associated protein	0.42	1.32
10	427427	AF077345	Hs.177936	lectin, superfamily member 1 (cartilage-	1.00	20.00
	427441	AA412605	Hs.343879	SPANX family, member C	1.00	1.00
	427445	X80818	Hs.178078	glutamate receptor, metabotropic 4	0.97	1.03
	427505	AA361562	Hs.178761	26S proteasome-associated pad1 homolog	4.60	4.04
	427510	Z47542	Hs.179312	small nuclear RNA activating complex, po	22.00	45.00
	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	97.45	92.00
15	427546	AA188763	Hs.36793	hypothetical protein FLJ23188	1.50	3.24
	427562	R56424	Hs.26534	ESTs	6.81	40.00
	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	69.91	62.00
	427680	A1741320	Hs.114121	Homo sapiens cDNA: FLJ23228 fis, clone C	2.70	49.00
	427686	A1791495	Hs.180142	calmodulin-like skin protein	1.37	1.88
20	427688	AA298760	Hs.180191	hypothetical protein FLJ14904	29.55	67.00
	427677	NM_007045	Hs.180296	FGFR1 oncogene partner	3.52	2.63
	427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	7.41	34.00
	427711	M31659	Hs.180408	solute carrier family 25 (mitochondrial	15.84	70.00
	427719	A1393122	Hs.134726	ESTs	7.03	4.52
25	427722	AK000123	Hs.180479	hypothetical protein FLJ20116	2.92	1.74
	427747	AW411425	Hs.180655	serine/threonine kinase 12	1.76	1.26
	427912	AL022310	Hs.181097	tumor necrosis factor (ligand) superfam	9.63	59.00
	427961	AW293165	Hs.143134	ESTs	41.97	118.00
	428004	AA449563	Hs.151393	glutamate-cysteine ligase, catalytic sub	23.82	1.00
30	428023	AL038843		Homo sapiens cDNA: FLJ23602 fis, clone L	1.40	1.33
	428046	AW812795	Hs.337534	ESTs, Moderately similar to I38022 hypot	96.28	167.00
	428093	AW594506	Hs.104830	ESTs	1.25	1.29
	428098	AU077258	Hs.182429	protein disulfide isomerase-related prot	1.86	1.60
	428129	A1244311	Hs.26912	ESTs	1.00	42.00
35	428169	A1928984	Hs.182793	golgi phosphoprotein 2	2.76	2.11
	428182	BE386042	Hs.293317	ESTs, Weakly similar to GGC1_HUMAN G ANT	1.00	1.00
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	85.59	181.00
	428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	8.57	21.84
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	7.77	15.90
40	428434	A1909935	Hs.65551	Homo sapiens, Similar to DNA segment, Ch	0.58	1.43
	428450	NM_014791	Hs.184339	KIAA0175 gene product	237.53	204.00
	428471	X57348	Hs.184510	stratifin	6.00	4.60
	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to	58.54	16.00
	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	3.53	2.15
45	428505	AL035461	Hs.2281	chromogranin B (secretogranin 1)	1.00	1.00
	428532	AF157326	Hs.184786	TBP-interacting protein	1.00	58.00
	428645	AA431400	Hs.98729	ESTs, Weakly similar to 2017205A dihydro	1.00	16.00
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	1.00	1.00
	428698	AA852773	Hs.334838	KIAA1866 protein	187.37	255.00
50	428728	NM_016625	Hs.191381	hypothetical protein	47.24	80.00
	428748	AW593206	Hs.98785	Kap37 protein	1.00	87.00
	428758	AA433988	Hs.98502	hypothetical protein FLJ14303	1.06	1.13
	428771	AB028992	Hs.193143	KIAA1069 protein	1.98	92.00
	428801	AW277121	Hs.254881	ESTs	1.67	6.15
55	428810	AF068236	Hs.193788	nitric oxide synthase 2A (inducible, hep	1.03	1.27
	428839	A1767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	124.17	43.00
	428845	AL157579	Hs.153610	KIAA0751 gene product	1.00	1.00
	428959	AF100779	Hs.194680	WNT1 inducible signaling pathway protein	15.16	27.00
	428969	AF120274	Hs.194689	artemin	1.36	1.24
60	429038	AL023513	Hs.194766	seizure related gene 6 (mouse)-like	0.97	3.31
	429065	A1753247	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT	6.82	16.47
	429164	A1688663	Hs.116586	ESTs	19.08	67.00
	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	16.18	105.00
	429183	AB014604	Hs.197955	KIAA0704 protein	79.72	104.00
65	429201	X03178	Hs.198246	group-specific component (vitamin D bind	1.00	1.00
	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	1.33	1.09
	429220	AW207206		ESTs	1.00	7.00
	429228	A1553633	Hs.326447	ESTs	39.47	29.25
	429259	AA420450	Hs.292911	ESTs, Highly similar to S60712 band-6-pr	2.01	1.18
70	429263	AA019004	Hs.198396	ATP-binding cassette, sub-family A (ABC1	1.07	1.00
	429278	AF056085	Hs.198612	G protein-coupled receptor 51	3.70	142.00
	429359	W00482	Hs.2399	matrix metalloproteinase 14 (membrane-in	1.30	1.94
	429412	NM_006235	Hs.2407	POU domain, class 2, associating factor	94.09	86.00
	429413	NM_014058	Hs.201877	DESC1 protein	41.91	10.00
75	429486	AF155827	Hs.203963	hypothetical protein FLJ10339	12.19	1.00
	429504	X99133	Hs.204238	lipocalin 2 (oncogene 24p3)	1.61	1.08
	429538	BE182592	Hs.11261	small proline-rich protein 2A	4.43	2.90
	429547	AA401369	Hs.190721	ESTs	1.06	17.00
	429551	AW450624	Hs.220931	ESTs	2.89	65.00
80	429563	BE619413	Hs.2437	eukaryotic translation initiation factor	1.49	1.37
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	61.86	100.00
	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas	1.59	1.69
	429612	AF062649	Hs.252587	pituitary tumor-transforming 1	2.78	1.74
	429616	A1982722	Hs.120845	ESTs	1.00	1.00
85	429656	X05608	Hs.211584	neurofilament, light polypeptide (68kD)	1.00	4.00

	429663	M68874	Hs.211587	phospholipase A2, group IVA (cytosolic,	69.95	104.00
	429736	AF125304	Hs.212680	tumor necrosis factor receptor superfam	1.25	1.21
	429782	NM_005754	Hs.220689	Ras-GTPase-activating protein SH3-domain	1.00	7.00
5	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	11.80	1.00
	429918	AW873986	Hs.119383	ESTs	1.00	78.00
	429978	AA249027		ribosomal protein S6	1.98	3.09
	429986	AF092047	Hs.227277	sine oculis homeobox (Drosophila) homolo	1.00	48.00
	430044	AA464510	Hs.152812	ESTs	69.27	59.00
10	430114	AA847744	Hs.99640	ESTs	1.00	1.00
	430134	BE380149	Hs.105223	ESTs, Weakly similar to T33188 hypothe	1.00	51.00
	430147	R60704	Hs.234434	hairly/enhancer-of-split related with YRP	1.10	2.22
	430287	AW182459	Hs.125759	ESTs, Weakly similar to LEU5_HUMAN LEUKE	1.00	127.00
	430294	AI538226	Hs.32976	guanine nucleotide binding protein 4	3.80	1.47
	430300	U60805	Hs.238648	oncostatin M receptor	1.00	35.00
15	430315	NM_004293	Hs.239147	guanine deaminase	92.31	28.00
	430337	M36707	Hs.239600	calmodulin-like 3	1.18	1.08
	430378	Z29572	Hs.2556	tumor necrosis factor receptor superfam	5.28	66.00
	430388	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 2	16.76	38.00
	430393	BE185030	Hs.241305	estrogen-responsive B box protein	1.63	1.50
20	430439	AL133561		DKFZP434B061 protein	1.00	1.00
	430451	AA836472	Hs.297939	cathepsin B	1.64	2.12
	430454	AW469011	Hs.105635	ESTs	63.35	44.00
	430466	AF052573	Hs.241517	polymerase (DNA directed), theta	2.47	1.91
	430481	AA479678	Hs.203269	ESTs, Moderately similar to ALU8_HUMAN A	1.00	31.00
25	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	12.28	41.00
	430508	AI015435	Hs.104637	ESTs	4.75	7.27
	430533	AA480895	Hs.57749	ESTs, Weakly similar to T17288 hypothe	1.00	1.00
	430563	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	1.00	1.59
	430677	Z26317	Hs.94560	desmoglein 2	1.72	1.30
30	430678	AA401369	Hs.190721	ESTs	0.90	17.00
	430686	NM_001942	Hs.2633	desmoglein 1	1.00	1.00
	430788	AI742925	Hs.7179	ESTs, Weakly similar to 2004399A chromos	1.62	1.84
	430890	X54232	Hs.2699	glypican 1	1.58	1.40
35	430935	AW072916		zinc finger protein 131 (clone pHZ-10)	90.28	132.00
	430985	AA490232	Hs.27323	ESTs, Weakly similar to I78885 serine/th	0.94	1.28
	431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3	60.25	28.00
	431089	BE041395		ESTs, Weakly similar to unknown protein	23.32	941.00
	431092	AI332764	Hs.125757	ESTs	13.46	63.00
40	431124	AF284221	Hs.59506	doublesex and mab-3 related transcrip	49.43	62.00
	431164	AA493650	Hs.94367	Homo sapiens cDNA: FLJ23494 fis, clone L	0.44	2.20
	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	182.26	101.00
	431221	AW207837	Hs.286145	SRB7 (suppressor of RNA polymerase B, ye	4.15	13.97
	431277	AA501806	Hs.345824	ESTs	1.00	86.00
45	431322	AW970622		gb:EST382704 MAGE resequences, MAGK Homo	40.55	200.00
	431342	AW971018	Hs.21659	ESTs	1.00	53.00
	431384	BE158000	Hs.285026	gb:MR2-HT0377-150200-202-e03 HT0377 Homo	0.94	1.14
	431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precu	1.30	1.25
	431494	AA991355	Hs.298312	hypothetical protein DKFZp434A1315	3.90	25.00
50	431515	NM_012152	Hs.258583	endothelial differentiation, lysophospha	1.41	1.87
	431548	AI834273	Hs.9711	novel protein	5.68	15.00
	431630	NM_002204	Hs.265829	integrin, alpha 3 (antigen CD49C, alpha	0.99	1.44
	431745	AW972448	Hs.163425	ESTs	0.99	3.51
	431770	BE221880	Hs.268555	5'-3' exonuclease 2	67.12	91.00
55	431830	Y16645	Hs.271387	small inducible cytokine subfamily A (Cy	3.36	4.71
	431846	BE019924	Hs.271580	uroplakin 1B	4.49	2.51
	431890	X17033	Hs.271986	integrin, alpha 2 (CD49B, alpha 2 subuni	2.20	3.32
	431934	AB031481	Hs.272214	STG protein	1.01	1.04
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	51.17	46.35
60	432006	AL137382	Hs.272320	Homo sapiens mRNA; cDNA DKFZp434L1226 (f	0.94	1.65
	432023	R43020	Hs.236223	EST	0.94	47.00
	432201	AI538613	Hs.298241	Transmembrane protease, serine 3	1.10	2.24
	432210	AI567421	Hs.273330	Homo sapiens, clone IMAGE:3544662, mRNA,	1.42	1.45
	432226	AW182766	Hs.273558	phosphate cytidyltransferase 1, cholin	1.00	1.00
65	432239	X81334	Hs.2936	matrix metalloproteinase 13 (collagenase	18.67	1.00
	432265	BE382679	Hs.285753	SCG10-like-protein	1.09	1.21
	432281	AK001239	Hs.274263	hypothetical protein FLJ10377	40.98	58.00
	432365	AK001106	Hs.274419	hypothetical protein FLJ10244	1.00	214.00
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	157.34	37.00
70	432375	BE536069	Hs.2962	S100 calcium-binding protein P	1.65	1.06
	432407	AA221036		gb:zr03f12r1 Stratagene NT2 neuronal pr	73.71	75.00
	432441	AW292425	Hs.163484	ESTs	56.35	72.00
	432489	AI804855	Hs.207530	ESTs	1.00	24.00
	432543	AA552690	Hs.152423	Homo sapiens cDNA: FLJ21274 fis, clone C	137.72	98.00
75	432552	AI537170	Hs.173725	ESTs, Weakly similar to ALU8_HUMAN ALU S	1.00	31.00
	432583	AW023624	Hs.162282	potassium channel TASK-4; potassium chan	0.27	35.18
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	2.87	6.22
	432625	AI243596	Hs.94830	ESTs, Moderately similar to T03094 A-kin	26.63	56.00
	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci	1.92	5.29
80	432677	NM_004482	Hs.278611	UDP-N-acetyl-alpha-D-galactosamine:polyp	1.00	48.00
	432715	AA247152	Hs.200483	ESTs, Weakly similar to KIAA1074 protein	45.13	31.00
	432753	NM_014076	Hs.336938	Homo sapiens PRO0593 mRNA, complete cds	1.00	68.00
	432788	AA521091	Hs.178499	Homo sapiens cDNA: FLJ23117 fis, clone L	2.69	3.67
	432842	AW674093	Hs.334822	hypothetical protein MGC4485	1.22	1.34
85	432867	AW016936	Hs.233364	ESTs	1.00	1.00
	432917	NM_014125	Hs.241517	PRO0327 protein	10.25	6.62

	432920	U37689	Hs.3128	polymerase (RNA) II (DNA directed) polyp	1.44	1.30
	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	154.79	85.64
	433023	AW864793	Hs.87409	thrombospondin 1	20.96	100.00
5	433042	AW193534	Hs.281895	Homo sapiens cDNA FLJ11660 fis, clone HE	1.00	10.00
	433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	1.20	1.09
	433159	AB035898	Hs.150587	kinesin-like protein 2	13.82	39.00
	433183	AF231338	Hs.222024	transcription factor BMAL2	1.00	69.00
	433258	AA622788	Hs.203613	ESTs, Weakly similar to ALUB_HUMAN IIII	1.00	1.25
10	433409	AI278802	Hs.25661	ESTs	44.81	117.00
	433437	U20536	Hs.3280	caspase 6, apoptosis-related cysteine pr	70.39	105.00
	433485	AI493076	Hs.201967	aldo-keto reductase family 1, member C2	11.55	2.00
	433537	AI733692	Hs.112488	ESTs	8.66	65.00
	433547	W04978	Hs.303023	beta tubulin 1, class VI	25.16	83.00
	433556	W56321	Hs.111460	calcium/calmodulin-dependent protein kin	1.00	19.00
15	433647	AA603367	Hs.222294	ESTs	20.30	49.00
	433658	L03678	Hs.156110	immunoglobulin kappa constant	5.92	10.03
	433800	AI094221	Hs.135150	lung type-I cell membrane-associated gly	2.29	2.22
	433819	AW511097	Hs.112765	ESTs	3.71	8.00
	433862	D86960	Hs.3610	KIAA0205 gene product	62.08	104.00
20	433980	AA137152	Hs.286049	phosphoserine aminotransferase	108.91	47.00
	434088	AF116577	Hs.249270	hypothetical protein PRO1866	1.00	1.00
	434094	AA305599	Hs.238205	hypothetical protein PRO2013	121.27	87.00
	434105	AW952124	Hs.13094	presenilins associated rhomboid-like pro	1.22	1.23
	434217	AW014795	Hs.23349	ESTs	14.11	57.00
25	434340	AI193043	Hs.128685	ESTs, Weakly similar to T17226 hypotheti	2.10	2.56
	434360	AA401369	Hs.190721	ESTs	40.98	17.00
	434414	AI798376		gb:tr34b07.x1 NCI_CGAP_Ov23 Homo sapiens	1.48	1.56
	434424	AI811202	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	1.00	64.00
30	434467	BE552368	Hs.231853	Homo sapiens cDNA FLJ13445 fis, clone PL	54.91	85.00
	434551	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	2.46	2.00
	434627	AI221894	Hs.39311	ESTs	1.00	1.00
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	1.00	23.00
	434769	AA648884	Hs.134278	Homo sapiens cDNA FLJ12676 fis, clone NT	7.08	56.00
35	434792	AA649253	Hs.132458	ESTs	8.52	44.00
	434808	AF165108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810	11.33	1.00
	434828	D90070	Hs.96	phorbol-12-myristate-13-acetate-induced	1.00	1.00
	434876	AF160477	Hs.61460	lg superfamily receptor LNIR	1.25	1.29
	434891	AA814309	Hs.123583	ESTs	1.00	6.00
40	434928	AW015595	Hs.4267	Homo sapiens clones 24714 and 24715 mRNA	1.00	1.00
	435013	H91923	Hs.110024	Target CAT	1.26	1.10
	435066	BE261750	Hs.4747	dyskeratosis congenita 1, dyskerin	1.69	1.37
	435087	AW975241	Hs.23567	ESTs	1.00	1.00
	435099	AC004770	Hs.4756	flap structure-specific endonuclease 1	2.90	1.93
45	435159	AA668879	Hs.116649	ESTs	1.00	1.00
	435205	X54136	Hs.181125	immunoglobulin lambda locus	1.02	1.46
	435232	NM_001262	Hs.4854	cyclin-dependent kinase inhibitor 2C (p1	2.04	2.70
	435304	H10709	Hs.269524	ESTs	27.58	139.00
	435313	AI769400	Hs.189729	ESTs	1.00	14.00
50	435505	AF200492	Hs.211238	interleukin-1 homolog 1	1.00	38.00
	435509	AI458679	Hs.181915	ESTs	1.00	1.00
	435525	AI631297	Hs.123310	ESTs	1.00	66.00
	435532	AW291488	Hs.117305	Homo sapiens, clone IMAGE:3682908, mRNA	1.00	2.00
	435550	AI224456	Hs.324507	H.sapiens polyA site DNA	3.42	3.92
55	435602	AF217515	Hs.283532	uncharacterized bone marrow protein BM03	3.95	1.80
	435766	R11673	Hs.186498	ESTs	1.00	28.00
	435793	AB037734	Hs.4993	KIAA1313 protein	23.68	42.00
	436069	AI056879	Hs.263209	ESTs	1.00	58.00
	436170	AW450381	Hs.14529	ESTs	1.00	18.00
60	436211	AK001581	Hs.334828	hypothetical protein FLJ10719; KIAA1794	5.84	22.00
	436213	AA325512	Hs.71472	hypothetical protein FLJ10774; KIAA1709	1.42	1.27
	436217	T53925	Hs.107	fibrinogen-like 1	57.97	31.00
	436238	AK002163	Hs.301724	hypothetical protein FLJ11301	2.51	1.71
	436251	BE515065	Hs.296585	nucleolar protein (KKE/D repeat)	2.33	1.64
65	436291	BE568452	Hs.344037	protein regulator of cytokinesis 1	108.99	52.00
	436302	AL355841	Hs.99330	hypothetical protein FLJ23588	0.75	2.81
	436396	AW992292	Hs.152213	wingless-type MMTV integration site faml	60.01	1.00
	436414	BE264633	Hs.143638	WD repeat domain 4	2.50	2.19
	436419	AI948626	Hs.171356	ESTs	0.95	1.33
70	436443	AW138211	Hs.128746	ESTs	1.12	9.26
	436474	AJ270693	Hs.199887	ESTs	1.00	1.00
	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	3.28	1.56
	436486	AA742221	Hs.120633	ESTs	1.00	19.00
	436511	AA721252	Hs.291502	ESTs	16.76	14.00
75	436553	X57809	Hs.181125	immunoglobulin lambda locus	1.08	1.74
	436557	W15573	Hs.5027	ESTs, Weakly similar to A47582 B-cell gr	19.20	9.75
	436608	AA628980		down syndrome critical region protein DS	33.92	25.00
	436667	AW025183	Hs.127680	ESTs	0.89	1.19
	436771	AW975687	Hs.292979	ESTs	1.00	10.00
80	436839	AA401369	Hs.190721	ESTs	1.00	17.00
	436887	AW953157	Hs.193235	hypothetical protein DKFZp547D155	1.06	1.15
	436944	AW268614	Hs.5840	ESTs	1.00	1.00
	436961	AW375974	Hs.156704	ESTs	25.13	25.00
	436972	AA284679	Hs.25640	claudin 3	1.59	1.46
85	437016	AU076916	Hs.5388	guanine monophosphate synthetase	2.35	1.78
	437044	AL035864	Hs.69517	cDNA for differentially expressed CO16 g	1.34	1.13

5	437181	AI306615	Hs.125343	ESTs, Weakly similar to KIAA0758 protein	1.00	17.00
	437204	AL110216	Hs.22826	ESTs, Weakly similar to I55214 salivary	40.55	82.00
	437205	AL110232	Hs.279243	Homo sapiens mRNA; cDNA DKFZp564D2071 (f	1.00	112.00
	437259	AI377755	Hs.120695	ESTs	1.00	205.00
	437270	RI8087	Hs.323769	cisplatin resistance related protein CRR	1.56	1.54
10	437271	AL137445	Hs.28846	Homo sapiens mRNA; cDNA DKFZp566O134 (fr	113.25	125.00
	437370	AL359567	Hs.161962	Homo sapiens mRNA; cDNA DKFZp547D023 (fr	1.82	4.57
	437390	AI126859	Hs.112607	ESTs	1.35	1.75
	437412	BE069288	Hs.34744	Homo sapiens mRNA; cDNA DKFZp547C136 (fr	3.58	3.20
	437435	AI306152	Hs.27027	hypothetical protein DKFZp762H1311	3.03	1.08
15	437444	H46008	Hs.31518	ESTs	1.00	39.00
	437568	AI954795	Hs.156135	ESTs	1.00	19.00
	437623	D63880	Hs.5719	chromosome condensation-related SMC-asso	1.95	1.57
	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti	1.00	3.00
	437814	AI088192	Hs.135474	ESTs, Weakly similar to DDX9_HUMAN ATP-D	1.00	45.00
20	437840	AA884836	Hs.292014	ESTs	1.07	1.78
	437852	BE001836	Hs.256897	ESTs, Weakly similar to dJ365O12.1 [H.s	1.68	3.26
	437879	BE262082	Hs.5894	hypothetical protein FLJ10305	1.87	2.52
	437915	AI637993	Hs.202312	Homo sapiens clone N11 Ntera2D1 teratoca	74.05	35.00
	437916	BE566249	Hs.20999	hypothetical protein FLJ23142	23.15	89.00
25	437937	AI917222	Hs.121655	ESTs	1.00	1.00
	437942	AI888266	Hs.307526	ESTs	12.28	31.00
	438091	AW373062		nuclear receptor subfamily 1, group I, m	1.53	10.85
	438113	AI467908	Hs.8882	ESTs	1.80	2.39
	438119	AW963217	Hs.203961	ESTs, Moderately similar to AF116721 89	22.67	36.90
30	438274	AI918906	Hs.55080	ESTs	1.00	1.00
	438378	AW970529	Hs.86434	hypothetical protein FLJ21816	38.92	38.00
	438403	AA806607	Hs.292206	ESTs	1.00	1.00
	438494	AA908678	Hs.130183	ESTs	2.05	80.00
	438546	AW297204	Hs.125811	ESTs	1.00	131.00
35	438552	AJ245820	Hs.6314	type I transmembrane receptor (seizure-r	1.43	1.45
	438702	AI879064	Hs.54618	ESTs	1.00	34.00
	438724	AW612553	Hs.114670	Human DNA sequence from clone RP11-16L21	1.33	1.10
	438746	AI885815	Hs.184727	Human melanoma-associated antigen p97 (m	2.42	1.59
	438779	NM_003787	Hs.6414	nuclear protein 4	1.00	18.00
40	438821	AA826425	Hs.192375	ESTs	2.03	2.57
	438885	AI886558	Hs.184987	ESTs	6.42	88.00
	438898	AA401369	Hs.190721	ESTs	22.41	17.00
	438916	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	1.00	1.00
	438956	W00847	Hs.135056	Human DNA sequence from clone RP5-650E9	2.20	1.88
45	439000	AW979121		gb:EST391231 MAGE resequences, MAGP Homo	2.78	4.81
	439023	AA745978	Hs.28273	ESTs	1.17	1.31
	439024	R96596	Hs.35598	ESTs	1.00	28.00
	439128	AI949371	Hs.153089	ESTs	1.00	67.00
	439146	AW138909	Hs.156110	immunoglobulin kappa constant	1.38	1.41
50	439223	AW238299	Hs.250618	UL16 binding protein 2	1.93	1.64
	439286	AL133916		hypothetical protein FLJ20093	46.23	139.00
	439318	AW837046	Hs.6527	G protein-coupled receptor 56	2.00	2.20
	439343	AF086161	Hs.114611	hypothetical protein FLJ11808	6.10	7.37
	439394	AA401369	Hs.190721	ESTs	3.39	17.00
55	439410	AA632012	Hs.188746	ESTs	1.83	3.07
	439451	AF086270	Hs.278554	heterochromatin-like protein 1	23.28	52.00
	439452	AA918317	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	18.76	122.00
	439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13	2.78	1.58
	439477	W69813	Hs.58042	ESTs, Moderately similar to GFR3_HUMAN G	1.22	1.44
60	439492	AF086310	Hs.103159	ESTs	7.46	39.00
	439523	W72348	Hs.185029	ESTs	1.00	1.19
	439582	AF086413	Hs.58399	ESTs	1.00	1.00
	439606	W79123	Hs.58561	G protein-coupled receptor 87	33.61	1.00
	439670	AF088076	Hs.59507	ESTs, Weakly similar to AC004858 3 U1 sm	1.00	1.00
65	439702	AW085525	Hs.134182	ESTs	4.30	10.00
	439706	AW872527	Hs.59761	ESTs, Weakly similar to DAPI_HUMAN DEATH	86.55	11.00
	439738	BE246502	Hs.9598	sema domain, immunoglobulin domain (lg),	2.36	1.88
	439750	AL359053	Hs.57664	Homo sapiens mRNA full length insert cDN	2.02	6.08
	439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN	1.00	21.00
70	439780	AL109688		gb:Homo sapiens mRNA full length insert	7.27	25.00
	439840	AW449211	Hs.105445	GDNF family receptor alpha 1	1.00	1.00
	439926	AW014875	Hs.137007	ESTs	32.68	71.00
	439953	AW247529	Hs.6793	platelet-activating factor acetylhydrola	21.28	9.55
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	68.83	61.00
75	440006	AK000517	Hs.6844	hypothetical protein FLJ20510	1.83	4.02
	440028	AW473675	Hs.125843	ESTs, Weakly similar to T17227 hypotheti	1.42	2.54
	440106	AA864968	Hs.127699	KIAA1603 protein	1.00	54.00
	440138	AB033023	Hs.318127	hypothetical protein FLJ10201	24.18	52.00
	440273	AI805392	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	3.21	4.72
80	440289	AW450991	Hs.192071	ESTs	38.63	113.00
	440325	NM_003812	Hs.7164	a disintegrin and metalloproteinase doma	62.88	147.00
	440492	R39127	Hs.21433	hypothetical protein DKFZp547J036	2.35	3.62
	440527	AV657117	Hs.184164	ESTs, Moderately similar to S65657 alpha	10.84	57.00
	440659	AF134160	Hs.7327	claudin 1	3.18	2.37
85	440704	M69241	Hs.162	insulin-like growth factor binding prote	2.89	2.09
	440943	AW082298	Hs.146161	hypothetical protein MGC2408	2.02	1.41
	440994	AI160011	Hs.272068	ESTs	1.29	1.14
	441020	AA401369	Hs.190721	ESTs	142.99	17.00
	441031	AI110684	Hs.7645	fibrinogen, B beta polypeptide	1.41	99.00

	441128	AA570256	ESTs, Weakly similar to T23273 hypotheti	4.13	3.50
	441290	W27501	cholinergic receptor, nicotinic, alpha p	1.00	1.00
	441362	BE614410	RAD51 (S. carevisiae) homolog (E coli Re	130.23	43.00
5	441377	BE218239	ESTs	22.03	1.00
	441390	AI692560	ESTs	3.65	7.70
	441497	R51064	ESTs	1.00	1.00
	441525	AW241867	ESTs	1.53	1.42
	441553	AA281219	ESTs	1.89	1.57
	441607	NM_005010	neuronal cell adhesion molecule	1.47	2.11
10	441633	AW958544	normal mucosa of esophagus specific 1	216.22	363.00
	441636	AA081846	Homo sapiens mRNA; cDNA DKFZp566E183 (fr	2.31	2.05
	441737	X79449	adenosine deaminase, RNA-specific	1.30	1.49
	441790	AA401369	ESTs	44.15	17.00
	441801	AW242799	ESTs	1.00	1.00
15	441919	AI553802	ESTs	1.00	122.00
	441937	R41782	ESTs	0.86	1.37
	441954	AI744935	Fanconi anemia, complementation group G	1.48	1.39
	442025	AW887434	CDA11 protein	1.00	46.00
	442029	AW956698	neural precursor cell expressed, develop	9.92	45.00
20	442072	AI740832	Homo sapiens clone 23570 mRNA sequence	25.05	77.00
	442108	AW452649	Hs.166314	3.61	3.14
	442117	AW664964	ESTs	3.00	5.49
	442137	AA977235	ESTs, Weakly similar to Z192_HUMAN ZINC	1.00	1.00
	442159	AW163390	heterochromatin-like protein 1	1.92	1.66
25	442179	AA983842	chromosome 2 open reading frame 2	27.22	50.00
	442328	AI952430	ESTs, Weakly similar to ALU4_HUMAN ALU S	5.00	3.42
	442432	BE093589	hypothetical protein FLJ23468	181.59	76.00
	442530	AI580830	Homo sapiens cDNA FLJ14712 fis, clone NT	10.59	144.00
	442547	AA306997	ESTs, Weakly similar to ALU1_HUMAN ALU S	109.23	98.00
30	442566	AL137761	Homo sapiens mRNA; cDNA DKFZp586L2424 (f	1.00	53.00
	442619	AA447492	ESTs, Weakly similar to AF164793 1 prote	29.02	50.00
	442710	AI015631	ESTs	1.00	19.00
	442717	R88362	ESTs, Weakly similar to T23976 hypotheti	1.00	5.00
	442875	BE623003	Homo sapiens clone TCCCTA00142 mRNA sequ	22.85	50.00
35	442914	AW188551	hypothetical protein FLJ14007	25.33	82.00
	442932	AA457211	bromodomain adjacent to zinc finger doma	3.18	4.41
	442942	AW167087	ESTs	8.45	64.00
	443068	AI188710	ESTs	1.00	27.00
40	443204	AW205878	Homo sapiens cDNA FLJ13103 fis, clone NT	1.00	24.00
	443211	AI128388	ESTs	12.42	2.00
	443247	BE614387	c-Myc target JPO1	128.84	96.00
	443324	R44013	ESTs	0.02	4.59
	443383	AI792453	ESTs	1.00	47.00
45	443400	R28424	ESTs	18.52	61.00
	443426	AF098158	chromosome 20 open reading frame 1	4.02	1.75
	443572	AA025610	cleavage and polyadenylation specific fa	2.98	2.57
	443575	AI078022	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.00	29.00
	443614	AV655386	fibrinogen, B beta polypeptide	1.00	18.00
50	443633	AL031290	similar to pregnancy-associated plasma p	1.00	39.00
	443648	AI085377	ESTs	39.81	70.00
	443715	AI583187	cyclin E1	48.74	7.00
	443723	AI144442	syntaxin 6	1.29	1.30
	443802	AW504924	KIAA1291 protein	1.75	1.61
55	443859	NM_013409	folistatin	1.35	1.13
	443892	AA401369	ESTs	1.00	17.00
	443947	W24187	gb:zb47f09.r1 Soares_fetal_lung_NbHL19W	1.33	1.64
	443991	NM_002250	potassium intermediate/small conductance	5.71	6.87
	444006	BE395085	type I transmembrane protein Fn14	1.47	1.92
60	444009	AI380792	ESTs	1.00	77.00
	444017	U04840	neuro-oncological ventral antigen 1	1.00	1.00
	444127	N63620	ESTs	1.00	29.00
	444129	AW294292	ESTs	1.00	1.00
	444279	U62432	cholinergic receptor, nicotinic, alpha p	0.80	7.80
65	444371	BE540274	forkhead box M1	2.91	1.14
	444378	R41339	ESTs	1.00	1.00
	444381	BE387335	ESTs, Weakly similar to S64054 hypotheti	469.00	556.00
	444461	R53734	ESTs, Weakly similar to 2109260A B cell	12.88	105.00
	444471	AB020684	KIAA0877 protein	24.91	90.00
70	444489	AI151010	ESTs	1.00	111.00
	444619	BE538082	ESTs, Moderately similar to A46010 X-in	1.00	70.00
	444665	BE613126	B aggressive lymphoma gene	30.56	139.00
	444707	AI188613	desmocollin 3	1.00	1.00
	444735	BE019923	hypothetical protein FLJ13057 similar to	77.02	90.00
75	444781	NM_014400	GPI-anchored metastasis-associated prote	1.57	1.31
	444783	AK001468	anillin (Drosophila Scraps homolog), act	77.55	2.00
	445236	AK001676	hypothetical protein FLJ10814	1.00	27.00
	445258	AI635931	ESTs	1.00	73.00
	445413	AA151342	CGI-147 protein	28.14	50.00
80	445417	AK001058	Homo sapiens cDNA FLJ10196 fis, clone HE	1.81	2.62
	445443	AV653838	ESTs	1.00	1.00
	445462	AA378776	hypothetical protein MGC3077	2.09	1.70
	445517	AF208855	hypothetical protein	1.87	70.00
	445537	AJ245671	EGF-like domain, multiple 6	1.71	2.72
85	445580	AF167572	skb1 (S. pombe) homolog	1.52	1.34
	445654	X91247	thioredoxin reductase 1	1.51	1.52

	445669	AI570830	Hs.174870	ESTs	10.95	11.45
	445818	BE045321	Hs.136017	ESTs	1.00	1.00
	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-I	49.42	54.00
5	445885	AI734009	Hs.127699	KIAA1603 protein	1.00	132.00
	445898	AF070823	Hs.13423	Homo sapiens clone 24468 mRNA sequence	1.00	1.00
	445903	AI347487	Hs.132781	class I cytokine receptor	1.00	36.00
	445932	BE046441	Hs.333555	Homo sapiens clone 24859 mRNA sequence	2.41	2.88
	445982	BE410233	Hs.13501	pescadillo (zebrafish) homolog 1, contai	1.60	1.35
10	446078	AI339982	Hs.158061	ESTs	1.00	42.00
	446102	AW168067	Hs.317694	ESTs	1.00	1.00
	446157	BE270828	Hs.131740	Homo sapiens cDNA: FLJ22562 fis, clone H	1.70	1.53
	446269	AW263155	Hs.14559	hypothetical protein FLJ10540	73.01	48.00
	446292	AF081497	Hs.279682	Rh type C glycoprotein	1.55	1.26
	446293	AI420213	Hs.149722	ESTs	1.00	2.00
15	446423	AW139655	Hs.150120	ESTs	1.10	4.19
	446428	AW082270	Hs.12496	ESTs, Weakly similar to ALU4_HUMAN ALU S	0.53	3.26
	446432	AI377320	Hs.150058	ESTs	1.00	5.00
	446528	AU076640	Hs.15243	nucleolar protein 1 (120kD)	1.36	1.31
	446574	AI310135	Hs.335933	ESTs	3.89	72.00
20	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	32.03	20.23
	446636	AC002553	Hs.15767	citron (rho-interacting, serine/threonin	4.19	5.07
	446783	AW138343	Hs.141867	ESTs	2.82	9.47
	446839	BE091926	Hs.16244	mitotic spindle coiled-coil related prot	110.28	28.00
25	446849	AU076617	Hs.16251	cleavage and polyadenylation specific fa	3.26	2.94
	446856	AI814373	Hs.164175	ESTs	6.38	11.30
	446872	X97058	Hs.16362	pyrimidinergic receptor P2Y, G-protein c	1.98	2.03
	446880	AI811807	Hs.108646	Homo sapiens cDNA FLJ14934 fis, clone PL	94.90	113.00
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	1.67	3.90
30	446989	AK001898	Hs.16740	hypothetical protein FLJ11036	2.82	3.12
	447022	AW291223	Hs.157573	ESTs	1.00	170.00
	447033	AI357412	Hs.157601	ESTs	7.15	107.00
	447078	AW885727	Hs.9914	ESTs	47.24	24.00
	447081	Y13896	Hs.17287	potassium inwardly-rectifying channel, s	0.12	17.88
35	447131	NM_004585	Hs.17468	retinoic acid receptor responder (tazaro	0.97	1.48
	447149	BE299857	Hs.326	TAR (HIV) RNA-binding protein 2	1.24	1.28
	447153	AA805202	Hs.315582	ESTs	1.00	54.00
	447164	AF026941	Hs.17518	Homo sapiens cig5 mRNA, partial sequence	1.00	67.00
	447178	AW594641	Hs.192417	ESTs	3.42	50.00
40	447250	AI878909	Hs.17883	protein phosphatase 1G (formerly 2C), ma	1.60	1.52
	447289	AW247017	Hs.36978	melanoma antigen, family A, 3	1.00	1.00
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	28.63	1.00
	447343	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m	146.62	51.00
	447350	AI375572	Hs.172634	ESTs	1.00	12.00
45	447377	N27687	Hs.334334	transcription factor AP-2 alpha (activat	2.55	63.00
	447415	AW937335	Hs.28149	ESTs, Weakly similar to KF3B_HUMAN KINES	0.91	1.13
	447425	AI963747	Hs.18573	acylphosphatase 1, erythrocyte (common)	1.00	35.00
	447519	U46258	Hs.339665	ESTs	59.89	49.00
	447532	AK000614	Hs.18791	hypothetical protein FLJ20607	1.23	1.63
50	447534	AA401369	Hs.190721	ESTs	1.00	17.00
	447636	Y10043		high-mobility group (nonhistone chromoso	1.41	1.11
	447688	N87079	Hs.19236	Target CAT	1.00	39.00
	447733	AF157482	Hs.19400	MAD2 (mitotic arrest deficient, yeast, h	1.17	1.12
	447769	AW873704	Hs.320831	Homo sapiens cDNA FLJ14597 fis, clone NT	6.47	5.95
55	447802	AW593432	Hs.161455	ESTs	0.73	2.34
	447850	AB018298	Hs.19822	SEC24 (S. cerevisiae) related gene famil	86.45	116.00
	447924	AI817226	Hs.313413	ESTs, Weakly similar to T23110 hypotheti	1.00	1.00
	447973	AB011169	Hs.20141	similar to S. cerevisiae SSM4	3.50	4.27
	448030	N30714	Hs.326960	membrane-spanning 4-domains, subfamily A	4.13	142.00
60	448105	AI538613	Hs.298241	Transmembrane protease, serine 3	1.15	2.24
	448243	AW369771	Hs.52620	integrin, beta 8	15.84	1.00
	448278	W07369	Hs.11782	ESTs	0.97	1.90
	448290	AK002107	Hs.20843	Homo sapiens cDNA FLJ11245 fis, clone PL	1.00	1.00
	448296	BE622756	Hs.10949	Homo sapiens cDNA FLJ14162 fis, clone NT	2.42	2.17
65	448357	BE274396	Hs.108923	RAB38, member RAS oncogene family	1.44	1.08
	448390	AL035414	Hs.21068	hypothetical protein	1.00	43.00
	448469	AW504732	Hs.21275	hypothetical protein FLJ11011	2.63	2.49
	448569	BE382657	Hs.21486	signal transducer and activator of trans	1.84	2.53
	448663	BE614589	Hs.106823	hypothetical protein MGC14797	3.29	46.00
70	448672	AI955511	Hs.225106	ESTs	1.00	21.00
	448733	NM_005629	Hs.187958	solute carrier family 6 (neurotransmitte	1.82	1.08
	448741	BE614567	Hs.19574	hypothetical protein MGC5469	2.48	1.92
	448757	AI386784	Hs.48820	TATA box binding protein (TBP)-associate	23.53	20.00
	448775	AB025237	Hs.388	nudix (nucleoside diphosphate linked moi	2.34	1.97
75	448826	AI580252	Hs.293246	ESTs, Weakly similar to putative p150 [H]	74.07	62.67
	448830	AL031658	Hs.22181	hypothetical protein dJ310013.3	1.37	1.31
	448844	AI581519	Hs.177164	ESTs	1.00	31.00
	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	1.84	1.95
	448993	AI471630		KIAA0144 gene product	1.63	1.49
80	449003	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu o	1.00	1.00
	449029	N28989	Hs.22891	solute carrier family 7 (cationic amino	1.97	2.26
	449040	AF040704	Hs.149443	putative tumor suppressor	0.97	1.56
	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	27.13	90.00
	449053	AI625777	Hs.344766	ESTs	8.33	44.00
85	449054	AF148848	Hs.22934	myoneurin	73.85	104.00
	449101	AA205847	Hs.23016	G protein-coupled receptor	2.58	27.00

	449167	T05095	Hs.19597	KIAA1694 protein	1.61	2.36
	449207	AL044222	Hs.23255	nucleoporin 155kD	2.36	1.56
	449228	AJ403107	Hs.148590	protein related with psoriasis	1.15	1.15
5	449230	BE613348	Hs.211579	melanoma cell adhesion molecule	206.65	151.00
	449305	AI638293		gb:tt09b07.x1 NCL_CGAP_GC6 Homo sapiens	17.28	45.00
	449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	26.39	35.00
	449448	D60730	Hs.57471	ESTs	1.00	1.00
	449467	AW205006	Hs.197042	ESTs	1.00	1.00
10	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	56.80	216.86
	449722	BE280074	Hs.23860	cyclin B1	150.03	1.00
	449976	H06350	Hs.135056	Human DNA sequence from clone RP5-850E9	2.16	2.85
	450001	NM_001044	Hs.406	solute carrier family 6 (neurotransmitter)	1.17	1.45
	450098	W27249	Hs.8109	hypothetical protein FLJ21080	1.79	2.38
	450101	AV649989	Hs.24385	Human hbc647 mRNA sequence	1.00	69.00
15	450149	AW969781	Hs.132863	Zic family member 2 (odd-paired Drosophila)	1.00	1.00
	450193	AI916071	Hs.15607	Homo sapiens Fanconi anemia complementation	29.85	34.00
	450221	AA328102	Hs.24641	cytoskeleton associated protein 2	1.00	1.00
	450372	BE218107	Hs.202436	ESTs	1.00	1.00
20	450375	AA008647	Hs.8850	a disintegrin and metalloproteinase domain	51.26	93.00
	450447	AF212223	Hs.25010	hypothetical protein P15-2	123.20	181.00
	450568	AL050078	Hs.25159	Homo sapiens cDNA FLJ10784 f1s, clone NT	1.00	19.00
	450589	AI701505	Hs.202526	ESTs	1.00	23.00
	450684	AA872605	Hs.25333	Interleukin 1 receptor, type II	1.00	100.00
25	450701	H39960	Hs.288467	Homo sapiens cDNA FLJ12280 f1s, clone MA	1.89	1.55
	450705	U90304	Hs.25351	Iroquois homeobox protein 2A (IRX-2A) (1.00	45.00
	450832	AA401369	Hs.190721	ESTs	25.17	17.00
	450937	R49131	Hs.26267	ATP-dependant interferon response protein	90.92	90.00
	450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	3.33	1.70
30	451105	AI761324		gb:wi60b11.x1 NCL_CGAP_Co16 Homo sapiens	15.02	124.00
	451110	AI955040	Hs.265398	ESTs, Weakly similar to transformation-r	1.00	143.00
	451253	H48289	Hs.26126	claudin 10	3.02	2.29
	451291	R39288	Hs.6702	ESTs	1.00	1.00
	451320	AW498874		diacylglycerol kinase, zeta (104kD)	2.92	18.00
35	451380	H09280	Hs.13234	ESTs	6.90	6.67
	451386	AB029006	Hs.26334	spastic paraplegia 4 (autosomal dominant)	35.75	72.00
	451437	H24143	Hs.31945	hypothetical protein FLJ11071	1.00	69.00
	451462	AK000367	Hs.26434	hypothetical protein FLJ20360	1.83	2.10
	451524	AK001466	Hs.26516	hypothetical protein FLJ10604	1.13	1.07
40	451541	BE279383	Hs.26557	plakophilin 3	1.88	1.33
	451592	AI805416	Hs.213897	ESTs	1.00	1.00
	451635	AA018899	Hs.127179	cryptic gene	1.52	1.92
	451743	AA401369	Hs.190721	ESTs	4.95	17.00
	451806	NM_003729	Hs.27076	RNA 3'-terminal phosphate cyclase	13.55	31.00
45	451807	W52854		hypothetical protein FLJ23293 similar to	1.55	35.00
	451871	AI821005	Hs.118599	ESTs	1.81	2.53
	451952	AL120173	Hs.301663	ESTs	1.00	22.00
	452012	AA307703	Hs.279766	kinesin family member 4A	3.43	2.26
	452046	AB018345	Hs.27657	KIAA0802 protein	56.59	19.00
50	452194	AI694413	Hs.332549	olfactory receptor, family 2, subfamily	1.67	4.09
	452206	AW340281	Hs.33074	Homo sapiens, clone IMAGE:3606519, mRNA,	9.31	53.00
	452240	AA401369	Hs.190721	ESTs	13.42	17.00
	452256	AK000933	Hs.28861	Homo sapiens cDNA FLJ10071 f1s, clone HE	39.03	94.00
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 f1s, clone PL	153.01	340.00
55	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisiae)	1.95	23.00
	452295	BE379936	Hs.28866	programmed cell death 10	42.33	61.00
	452304	AA025386	Hs.61311	ESTs, Weakly similar to S10590 cysteine	1.17	2.14
	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodomain	1.00	13.00
	452349	AB028944	Hs.29189	ATPase, Class VI, type 11A	1.09	1.42
60	452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	54.49	53.00
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced protein	1.00	32.00
	452410	AL133619		Homo sapiens mRNA; cDNA DKFZp434E2321 (f	1.26	1.99
	452461	N78223	Hs.108106	transcription factor	24.47	35.00
	452571	W31518	Hs.34685	ESTs	54.61	102.00
65	452613	AA461599	Hs.23459	ESTs	1.39	1.32
	452699	AW295390	Hs.213062	ESTs	1.00	26.00
	452705	H49805	Hs.246005	ESTs	1.00	1.00
	452747	AF160477	Hs.61460	lg superfamily receptor LNIR	112.87	1.29
	452787	AW294022	Hs.222707	KIAA1718 protein	1.00	1.00
70	452795	AW392555	Hs.18878	hypothetical protein FLJ21620	1.00	1.00
	452823	AB012124	Hs.30696	transcription factor-like 5 (basic helix	7.91	75.00
	452833	BE559681	Hs.30736	KIAA0124 protein	3.16	1.92
	452838	U65011	Hs.30743	preferentially expressed antigen in melanoma	174.35	1.00
	452862	AA401369	Hs.190721	ESTs	98.26	17.00
75	452865	AW173720	Hs.345805	ESTs, Weakly similar to A47582 B-cell granule	1.55	1.00
	452934	AA581322	Hs.4213	hypothetical protein MGC16207	1.73	1.19
	452946	X95425	Hs.31092	EphA5	1.00	1.00
	452976	R44214	Hs.101189	ESTs	1.58	1.98
	453028	AB006532	Hs.31442	RecQ protein-like 4	1.60	1.60
80	453095	AW295660	Hs.252756	ESTs	0.77	1.50
	453102	NM_007197	Hs.31664	frizzled (Drosophila) homolog 10	1.00	1.00
	453103	AI301052	Hs.153444	ESTs	1.00	1.00
	453120	AA292891	Hs.31773	pregnancy-induced growth inhibitor	1.23	1.20
	453153	N53893	Hs.24360	ESTs	1.00	83.00
	453160	AI263307	Hs.239884	H2B histone family, member L	1.00	30.00
85	453197	AI916269	Hs.109057	ESTs, Weakly similar to ALU5_HUMAN ALU 5	1.00	134.00

5	453210	AL133161	Hs.32360	hypothetical protein FLJ10867	1.69	1.93		
	453240	AI969564	Hs.166254	hypothetical protein DKFZp5661133	1.00	1.00		
	453317	NM_002277	Hs.41696	keratin, hair, acidic, 1	1.19	1.27		
	453323	AF034102	Hs.32951	solute carrier family 29 (nucleoside tra	4.90	4.11		
	453331	AI240665	Hs.8850	ESTs	199.42	340.00		
	453392	U23752	Hs.32954	SRY (sex determining region Y)-box 11	1.00	18.00		
	453431	AF094754	Hs.32973	glycine receptor, beta	1.00	1.00		
	453439	AI572438	Hs.32976	guanine nucleotide binding protein 4	3.44	5.17		
10	453459	BE047032	Hs.257789	ESTs	2.84	5.58		
	453563	AW608906.comp	Hs.181163	hypothetical protein MGC5629	4.58	90.00		
	453633	AA357001	Hs.34045	hypothetical protein FLJ20764	1.74	1.60		
	453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	19.49	1.00		
	453830	AA534296	Hs.20953	ESTs	24.92	25.00		
15	453857	AL080235	Hs.35861	DKFZP586E1621 protein	167.59	66.00		
	453867	AI929383	Hs.33032	hypothetical protein DKFZp434N185	1.00	39.00		
	453883	AI638516	Hs.347524	cofactor required for Sp1 transcription	1.97	1.58		
	453884	AA355925	Hs.36232	KIAA0186 gene product	63.89	20.00		
	453900	AW003582	Hs.226414	ESTs, Weakly similar to ALU8_HUMAN ALU S	20.41	16.00		
20	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	7.09	22.00		
	453941	U39817	Hs.36820	Bloom syndrome	29.75	19.00		
	453964	AI981486	Hs.12744	ESTs	1.00	1.00		
	453988	AA847843	Hs.62711	Homo sapiens, clone IMAGE:3351295, mRNA	2.06	1.81		
	453976	BE463830	Hs.163714	ESTs	3.02	131.00		
25	454024	AA993527	Hs.293907	hypothetical protein FLJ23403	1.00	131.00		
	454034	NM_000691	Hs.575	aldehyde dehydrogenase 3 family, member	1.23	1.02		
	454042	T19228	Hs.172572	hypothetical protein FLJ20093	30.63	171.00		
	454059	NM_003154	Hs.37048	stathmin	1.00	1.00		
	454066	X00356	Hs.37058	calcitonin/calcitonin-related polypeptid	1.01	1.45		
30	454098	W27953	Hs.292911	ESTs, Highly similar to S60712 band-6-pr	1.26	1.11		
	454241	BE144666		gb:CM2-HT0176-041099-017-c02 HT0176 Homo	6.33	5.04		
	454417	AI244459	Hs.110826	trinucleotide repeat containing 9	4.30	7.82		
	454439	AW819152	Hs.164320	DKFZP566O1646 protein	1.00	1.00		
	455175	AW993247		gb:RC2-BN0033-180200-014-h09 BN0033 Homo	13.75	103.00		
35	455601	AI368680	Hs.816	SRY (sex determining region Y)-box 2	206.11	1.00		
	456237	AA203682		gb:zx52e07.r1 Soares_fetal_liver_spleen_	1.00	1.00		
	456321	NM_001327	Hs.87225	cancer/testis antigen	1.14	1.10		
	456475	NM_000144	Hs.95998	Friedreich ataxia	1.00	48.00		
	456508	AA502764	Hs.123469	ESTs, Weakly similar to AF208855 1 BM-01	162.25	189.00		
40	456534	X91195	Hs.100623	phospholipase C, beta 3, neighbor pseudo	2.12	1.80		
	456736	AW248217	Hs.1619	achaete-scute complex (Drosophila) homol	1.15	1.94		
	456759	BE259150	Hs.127792	delta (Drosophila)-like 3	1.00	1.00		
	456990	NM_004504	Hs.171545	HIV-1 Rev binding protein	16.42	84.00		
	457200	U33749	Hs.197764	thyroid transcription factor 1	0.57	1.76		
45	457234	AW968360	Hs.14355	Homo sapiens cDNA FLJ13207 fis, clone NT	2.71	4.15		
	457465	AW301344	Hs.122908	DNA replication factor	46.37	47.00		
	457489	AI693815	Hs.127179	cryptic gene	1.12	1.35		
	457646	AA725650	Hs.112948	ESTs	1.55	2.51		
	457733	AW974812	Hs.291971	ESTs	1.00	55.00		
50	457819	AA057484	Hs.35406	ESTs, Highly similar to unnamed protein	4.36	3.18		
	458092	BE545684	Hs.343566	KIAA0251 protein	1.00	1.32		
	458098	BE550224		metallothionein 1E (functional)	1.00	22.00		
	458207	T28472	Hs.7655	U2 small nuclear ribonucleoprotein auxil	2.06	1.88		
	458242	BE299588	Hs.29465	Homo sapiens cDNA: FLJ21669 fis, clone H	1.00	1.00		
55	458247	R14439	Hs.209194	ESTs	7.00	9.85		
	458679	AW975460	Hs.142913	ESTs	1.00	3.00		
	458778	AW451034	Hs.326525	arylsulfatase D	1.31	2.01		
	458933	AI638429	Hs.24763	RAN binding protein 1	1.98	1.71		
	459352	AW810383	Hs.206828	ESTs	12.60	63.00		
	459670	F01020	Hs.172004	Utin	1.00	1.00		
60	459702	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	1.00	237.00		

TABLE 9B

65	Pkey:	Unique Eos probeset identifier number	
	CAT number:	Gene cluster number	
	Accession:	Genbank accession numbers	
70	Pkey	CAT Number	Accession
	407746	10125_1	AK001962 R69415 BE464605 AA418699 AA053293 AA149075 AA058396 AW338226 AW272659 AA454607 AI139535 AW469852 AI275461
			AW271982 AA730033 AA576507 AA991217 AA782067 AI985851 AA805864 AA505598 AW469857 R69546 AA988279 AW001647 N63320
			D82661 T27343 AA306950 AA360989 R58778
	408070	1036688_1	AW148852 BE350895
	408660	107294_1	AA525775 AA056342 AI538978 AW975281 AA664986
75	409522	113735_1	AA075382 AA075431
	409866	1156522_1	AW502152 H41202 H29772
	410032	1170435_1	BE065985 BE065944 BE066008 BE066083 BE066093
	411089	123172_1	AA456454 AA713730 AA091294 AA584921 N86077 AW836781 AA601031 AA579676 AA551106 AA633188 AW905577 AI955808 AI679386
80	411152	1234028_1	AI679895 AA514764 AA454562 AI082382 AA595822 AA551351 AA586369 AA666384 AA188934 AA666398 AA551297 AA565188
			BE069199 AW936012 AW877466 AW819782 AW935798 AW835546 AW936042 BE069121 AW835625 AW877536 AW935685 BE069202
			AW820019 AW935937 BE160180 AW935946 BE069101 BE069125 AW877527 BE160316 BE160398 AW935794 AW835701 AW935784
			AL031778 X59711 NM_002505 M59079 AI870439 AI494259 AW664010 AA405063 AA436132 BE174516 AA412691 AI400314 AA436024
			T29403 BE079412 BE079428 N90322 AI631202 AI141758 AI016793 AI167566 AI862075 AI375230 AI208445 AW235763 AI044113 AA382556
			AW953918 AA927051 AA889823 BE003094 AW390155 AW360805 AW360823 AW360810 AA425472 AI694282 AL044114 AI684577 AI809865

WO 02/086443

PCT/US02/12476

			AI478773 AI160445 AI674630 N69088 AW665529 N49278 AI129239 AI457890 AI621264 AW297152 AI268215 AA907787 AI286170 AI017982 AI963541 AI469807 AI969353 BE552356 N66509 AA736741 AA382555 AW075811 AW292026 H06382 AW957730 AA352014 R13591 AA121201 D60420 BE263253 BE047862 Z41952 AI424991 AI693507 AI863108 AA599060 AI091148 AA598689 R39887 AA813482 AW016452 H06383 R41807 AI364268 AA620528 AI241940 AW089149 AW090733 AW088875 Z38240 AA121202 R17734 BE157489 BE157560 AA926960 AA926959 W76521 W24270 W21526 AA037172 BE267636 H83186 AA469909 N86396 AA001348 BE535736 AA081745 BE566245 AA082436 H72525 H77575 N49786 W80565 H78746 BE569085 W04339 R98127 T59598 BE279271 AW960304 T29812 AA476873 BE297387 AA292753 AA177048 NM_001826 X54941 BE314366 AA908783 AI719075 BE270172 BE269819 AA889955 AI204630 W25243 AI935150 AA872039 W72395 T99630 AI422691 H98460 N31428 BE255916 H03265 AI857576 AA776920 AA910644 AA459522 AA293140 AW514667 R75953 AW662396 AA662522 AI865147 AI423153 AW262230 AA584410 AA583187 AW024595 AW069734 AI828996 AA282997 AA876046 AW613002 AA527373 AW972459 AI831360 AA621337 AA100926 AA772418 AA594628 AI033892 W95096 AI034317 AA398727 AI065031 N95210 AI459432 AI041437 AA932124 AA627684 AA935829 AI004827 AI423513 AI094597 H42079 R54703 AI630359 AA617681 AA978045 AA643280 W44561 AI991988 AI537692 AI090262 AA740817 AI312104 AI911822 AA416871 AI185409 AA129784 AA701623 AI075239 AI139549 AA633648 AI339996 AI336880 AA399239 AI078708 AI085351 AI362835 AI346618 AI146955 AI989380 AI348243 N92892 AA765850 AI494230 AI278887 AA962596 AI492600 W80435 AA001979 R97424 AI129015 N24127 AA157451 AA235549 AA459292 AA037114 AA129785 AI494211 AW059601 AW886710 R92790 N59755 AI361128 AW589407 H47725 H97534 H48076 H48450 T99531 AW300758 H03431 R76789 AA954344 H77576 R96823 AI457100 N92845 N49682 H42038 BE220698 BE220715 H99552 AA701624 N74173 R54704 H79520 H72923 H03266 BE261919 AA769633 AA480310 AA507454 AA910586 AI203723 AW104725 W25611 W25071 T88980 H03513 T77589 R99156 W95095 R97470 AA702275 T77551 AA911952 H82956 N83673 AA283672 AI267700 AI720344 AA191424 AI023543 AI469633 AA172056 AW958465 AA172236 AW953397 AA355086 AW265494 AA455904 AA195677 AW265432 AW991605 AA456370 N28754 N28747 AI568146 AI979339 AA322671 AA322672 AW955043 AI990326 AA776406 AI016250 AA843678 AW451882 N23137 N23129 W70051 AI038748 AA831327 AI2925845 AW945895 Z42183 T31621 T97478 D62703 AA242966 D79798 AU076704 T74854 T74860 T72098 T73265 T73873 T69180 T74658 T58786 T60385 T73410 T68781 T76845 T67593 T73952 T67864 T60630 T68367 T68401 T53959 T72360 T72099 T60377 T58961 T71712 T72821 T64738 T74645 T72037 T68688 T72063 T73258 T72826 T64242 T68220 T74673 T71800 T68355 T61227 T62738 T69317 T53850 T64692 T73768 T73962 T73382 T69914 T70975 T73400 T60631 T73277 T73203 T70498 T61409 T58925 NM_000508 M64982 T68301 T73729 T69445 T60424 T76922 T67736 T68716 T67755 T74765 T73819 T58719 T74756 T60477 T74863 T61109 T68329 T58850 T71857 T73425 T53736 T68607 T58898 T64309 T72031 T72079 T64306 T71908 T68107 T71916 T73787 T56035 T64425 T71870 T60476 T61376 T67820 T71895 T41006 T69441 T68170 T74617 T71958 T69440 T61875 R06789 H48353 T71914 T53939 T64121 AA693996 T72525 T67779 T68078 AA011465 AA345378 AV654847 AV654272 AV656001 AI064470 T82897 N33594 AA344542 AW805054 AI207457 T61743 AA026737 H94389 AA382695 AA918409 T68044 S82092 T39959 AI017721 AA312395 AA312919 T40158 H66239 AV652989 H38728 R98521 AV655200 R95790 W03250 W00913 AA344136 AV660126 R97923 AA343595 AW470774 AV651266 N54417 AA812862 AW182929 AI111192 H61463 H72060 AA344503 H38639 AI277511 AV661108 AI207625 T47810 AA235252 T7853 T47778 R95746 H70620 AA701463 AW827166 R98475 C02925 AV657287 T71959 T71313 T73920 T73333 T61618 T69293 T69283 T73931 T72178 T72456 AV645639 AV653476 T72957 T72300 T68906 T71457 T70494 T72956 T70495 T68257 T74407 T55778 AA344726 T7854 T74485 T74101 T73868 T71518 T72304 AA343853 T73909 T68070 T72065 H72149 T73493 T73495 AV645993 R02293 T70475 T64751 AA344441 AA343657 AA345732 AA344328 AI110639 AA344603 AF063513 T64696 T68516 T72223 T60507 T67633 R29500 T72517 R02292 T60599 T69206 T70452 T74677 R29366 T61277 T74914 T60352 R29675 T74843 AV645792 AA344408 T69197 T72057 T69368 T69358 T68258 AV650429 T73341 T61702 T74598 T40095 K02272 T40106 AA343045 AA341908 AA341907 AA342807 AA341964 T53747 T72042 T62764 AI064899 AA343060 T67832 T72440 T71770 T68091 T69108 T72449 T69167 T71289 T68261 AV654844 T64375 AA345234 T67598 AA011414 T68036 H48262 AI207557 T68219 W86031 T69081 T64232 R93196 T62136 AV650539 H67459 T72978 AA344583 T60362 H58121 T95711 T72803 T68055 T71715 R29038 T72793 T69122 T64595 T62888 T69139 T68291 T64652 T67971 T46862 AA693592 AI248502 R29454 T64764 T57001 T73052 T71429 T51176 T58866 AV655414 H90426 AA342489 T73666 T67848 T72512 T53835 T67837 T73317 T74273 T69420 T68245 T74380 T67862 T74474 T56068 AI792788 BE142230 AA252019 AI910275 X00474 X52003 X05030 NM_003225 AA314326 AA308400 AA506787 AA314825 AI571948 AA507595 AA614579 AA587613 R83818 AA568312 AA614409 AA307578 AI925552 AW950155 AI910083 M12075 BE074052 AW004668 AA578674 AA582084 BE074053 BE074126 BE074140 AA514776 AA588034 BE074051 BE074058 AW009769 AW050690 AA858276 R55389 AI001051 AW050700 AW750216 AA614539 BE074045 AI307407 AW602303 BE073575 AI202532 AA524242 AI970839 AI909751 BE076078 AI909749 R55292 AW881145 AA490718 M85637 AA304575 T06067 AA331991 AL119930 AA320696 AW752565 AL031985 AL137241 AI792366 AI733664 AI857654 AI049911 AA337221 AA335756 AW966196 AW953120 R56325 AA349562 AI483134 AI498691 AW771508 AI498457 AI768408 AI783624 AI383985 AI580267 D79813 AA393768 AK001536 AA191092 AW510354 AI554256 AL353968 AA134266 AA663848 AA400100 AA401424 AL038843 AA161338 BE268213 AA425597 N87306 AA092969 BE566038 AA247451 N47392 AI928802 AW182584 AW027872 AI819831 AI936994 W56258 AI653448 AI278611 AI283557 AI824306 AW338658 AW150899 AA687514 N47393 N29885 AA973469 AI038904 AI292064 AI034339 AW674593 N72156 AI079733 AI038683 AI291616 AA491599 AA93675 AA837380 BE006554 BE006473 AI087090 T33044 AA652043 AI203503 AA583959 W35283 AI129926 Z41844 AW020925 AW575848 AI684603 AA493297 AI140689 AI277175 AA425444 AI932767 W02632 BE396786 R37261 AW207206 AW341473 AA448195 AI951341 AA249027 AL038984 AK001993 AL080066 AV652725 BE566226 AA345557 AA315222 AA090585 AA375688 AA301092 AA298454 W05762 AW607939 H51658 C83880 N84323 BE296821 AW947007 D61461 AW079261 AA329482 AW901780 AI354442 AA772275 R31663 AI354441 AI767525 H92431 AI916735 H93575 AI394255 AW014741 AI573090 C06195 AW612857 AW265195 AI339558 AI377532 AI038821 AI919424 AI589705 AW055215 AI36532 AI338051 AA806547 C75509 C0618 AW071172 AW769904 AA630381 AI678018 AI863985 D79662 BE221049 AW265018 AI589700 AW196655 N76573 AI370908 BE042393 N75017 AI698870 AW960115 AL133561 AL041090 AL117481 AL122069 AW439292 AI968826 AW072916 AI184913 AA489195 AW466994 AW469044 N59350 AI819642 AI280239 AI220572 AA789302 AI473611 AW841126 D60937 BE041395 AA491826 AA621946 AA715980 AA666102 AW970622 AA503009 AA502989 AA502805 T92188 AA221036 R87170 BE537068 BE544757 C18935 AW812058 T92565 AA227415 AA233942 AA223237 AA668403 AA601627 AW869639 BE061833 BE000620 AW961170 AW847519 AA308542 AW821833 AW945688 C46899 AA205504 AA377241 AW821687 AA055720 AW817981 AW856468 AA155719 AA179928 T03007 AW754298 AA227407 AA113928 AA307904 C16859 AI798378 S46400 AW811617 AW811616 W00557 BE142245 AW858232 AW861851 AW858362 AA232351 AA218567 AA055556 AW858231 AW857541 AW814172 H66214 AW814398 AF134164 AA243093 AA173345 AA199942 AA223384 AA227092 AA227080 T12379 AA092174 T61139 AA149776 AA698929 AW879188 AW813567 AW813538 AI267168 AA157718 AA157719 AA100472 AA100774 AA130756 AA157705 AA157730 AA157715 AA053524 AW849581 AW854566 C05254 AW882836 T92637 AW812621 AA206583 AA209204 BE156909 AA226824 AI829309 AW991957 N66951 AA527374 H66215 AA045564 AI694265 H60808 AA149726 AW195620 BE081333 BE073424 AW817662 AW817705 AW817703 AW817659 BE081531 H59570 AA628980 AI126603 BE504035
5	412811	132943_1	
	413690	1383256_1	
	414883	15024_1	
10			
15			
20	415989	156454_1	
	417324	166714_1	
	418574	17690_1	
25	418712	1784125_1	
	419443	184788_1	
	419502	18355_1	
30			
35			
40			
45	419936	189181_1	
	421582	2041_1	
50	422128	211994_1	
	423034	224122_1	
	423816	23234_1	
	424200	236595_1	
	424999	245835_1	
	426966	273896_1	
	426991	27415_1	
60	427260	276598_1	
	428023	28589_2	
65	429220	301384_1	
	429978	31150_1	
70	430439	31808_1	
	430935	325772_1	
	431089	327825_1	
	431322	331543_1	
	432407	34624_1	
75	434414	38585_1	
80			
85	436608	42361_3	

WO 02/086443

PCT/US02/12476

438091 44964_1 AW373062 T55662 AI299190 BE174210 AW575001 H01811 W40186 R67100 AI923886 AW952164 AA628440 AW898607 AW898616
AA709126 AW898628 AW898644 AA947932 AW898625 AW898622 AI276125 AI185720 AW510698 AA987230 T52522 BE487708 AW243400
AW043642 AI288245 AI186932 D52654 D55017 D52715 D52477 D53933 D54679 AI298739 AI146984 AI922204 N98343 BE174213 AA845571
AI813854 AI214518 AI635262 AI139455 AI707807 AI698085 AW884528 AI024768 AI004723 AW087420 AI565133 N94964 AI268939
AW513280 AI061126 AI435818 AI859106 AI360506 AI024767 AA513019 AA757598 X56196 AA902959 AI334784 AI860794 AA010207
AW890091 AW513771 AI951391 AI337671 T52499 AA890205 AI640908 H75966 AA463487 AA358688 AI961767 AI866295 AA780994
AI985913 BE174196 AA029094 AW592159 T55581 N79072 AI611201 AA910812 AI220713 AW149306 AI758412 AA045713 R79750 N76096
AW979121 AA847986 AA829098
AL133916 N79113 AF086101 N76721 AW950828 AA364013 AW955684 AI346341 AI867454 N54784 AI655270 AI421279 AW014882
AA775552 N62351 N59253 AA626243 AI341407 BE175639 AA456968 AI358918 AA457077
AL109688 R23665 R26578
AA570256 AW014761 AA573721 AI473237 AI022165 AA554071 AA127551 N90525 AW973623 AA447991 AA243852 BE328850 AI148171
AI359627 AI005068 AI356567 AA232991 AW016855 AA906902 AA233101 AA127550 BE512923
AI188710 AI032142 AW078833 N30308 AW675632 AI219028 AI341201 N22181 H95390
W24187 W24194 R17789
Y10043 NM_005342 L05085 AL034450 BE614226 AW749053 AA379173 AA248230 BE514634 AA334622 R70656 AA367593 AA214649
AA369318 AW957081 R05760 AA039903 AI886597 AW630122 AA906264 AA041527 R01145 AI088688 BE463637 AA398795 AI354883
AI768938 AI569996 AI452952 AI168582 AI189869 AI086670 AW262560 AW613854 AA862839 AA435840 AA670197 AI024032 AI990659
AI990089 N81095 AA847919 AW960150 AA211075 AA044704 AA367594 AW582587 AW858854 AW818630 AW818281 AW818433 AW582595
AA096002 N83992
AI471630 BE540637 BE265481 AW07710 BE513882 BE546739 AA053597 BE140503 BE218514 AW956702 AI656234 AI636283 AI567265
AW340858 BE207794 AA053085 R69173 AA292343 AA454908 AA293504 AI659741 AI927478 AA399460 AI760441 AA345416 BE047245
AA730380 AA394063 AA454833 AI982791 AI567270 AI813332 AI767858 AA427705 D02084 AI221458 BE048537 AI263048 AA346417
AA911497 BE537702
AI638293 AW813561
AI761324 AW880941 AW880937
AW118072 AI631982 T15734 AA224195 AI701458 W20198 F26326 AA890570 N90552 AW071907 AI671352 AI375892 T03517 R88265
AI124088 AA224388 AI084316 AI354686 T33652 AI140719 AI720211 T03490 AI372637 T15415 AW205836 AA630384 T03515 T33230
AA017131 AA443303 T33623 AI222556 T33511 T33785 AI419606 D55612
W52854 AL117600 BE208118 BE208432 BE208239 BE082291 AW963423 AA351619 BE180648 BE140560 W60080 AA865478 N90291
AW450652 AW449519 AA993634 AI806539 AA351618 AW449522 AI827626 AA904788 AA380381 AA886045 AA774409 BE003229 Z41756
AL133819 AA488118 AA383064 AI76447 T09430 AI673758 AA524895 AI581345 AI300820 AW498812 AA256162 AI559724 AI685732
AA602400 AA905453 AI204595 AW166541 AA157456 AA156269 AA383652 AA431072 AW592707 AI435410 AW272464 AI215594 AA622747
R74039 N35031 AI804128 AW513621 AA868351 AI026826 AI493388 AA614641 W81604 AI567080 AI214351 AA730140 AI125754 AI200813
AI269603 AI665082 AI807095 AI476629 AA505909 AI368449 AI686077 AI582930 AW085038 AA757863 AA730154 AI767072 AA468316
AI734130 AI734138 AA426284 AA433997 AI741241 AW043563 AI732741 AI732734 AA437369 AA425820 AA664048 R74130
BE144656 BE184942 AW238414 BE184946
AW993247 AW861464
AA203682 R11958
BE550224 AA832519 N45402 AW885857 N29245 BE465409 W07677 AW970089 AI299731 AA482971 BE503548 H18151 W79223 AF086393
AA461301 W74510 R34182 AI090689 N46003 BE071550 R28075 AW134982 AI240204 AI138906 AW026179 AI572316 BE466182 AI206395
AI276164 AI273269 AI422817 AI371014 AI421274 AI188525 AA939164 BE549810 AW137865 AI694996 BE503841 AA459718 BE327407
BE467534 BE218421 BE467767 AA989054 BE467063 AI797130 BE327761

TABLE 9C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

	Pkey	Ref	Strand	Nt_position
55	400512	9796593	Minus	1439-1616
	400517	9796686	Minus	49996-50346
	400560	9843598	Plus	94182-94323,97056-97243,101095-101236,102824-103005
	400664	8118496	Plus	13558-13721,13942-14090,14554-14679
60	400665	8118496	Plus	16879-17023
	400666	8118496	Plus	17982-18115,20297-20456
	400749	7331445	Minus	9162-9293
	400763	8131616	Minus	35537-35784
	401027	7230983	Minus	70407-70554,71060-71160
65	401093	8516137	Minus	22335-23166
	401203	9743387	Minus	172961-173056,173868-173928
	401212	9858408	Plus	87839-88028
	401411	7799787	Minus	144144-144329
	401435	8217934	Minus	54508-55233
70	401464	6682291	Minus	170688-170834
	401714	6715702	Plus	96484-96681
	401747	9789672	Minus	118596-118816,119119-119244,119609-119761,120422-120990,130161-130381,130468-130593,131097-131258,131866-131932,132451-132575,133580-134011
	401760	9929699	Plus	83126-83250,85320-85540,94719-95287
75	401780	7249190	Minus	28397-28617,28920-29045,29135-29296,29411-29567,29705-29787,30224-30573
	401781	7249190	Minus	83215-83435,83531-83656,83740-83901,84237-84393,84955-85037,86290-86814
	401785	7249190	Minus	165776-165996,166189-166314,166408-166569,167112-167268,167387-167469,168634-168942
	401797	6730720	Plus	6973-7118
	401961	4581193	Minus	124054-124209
80	401985	2580474	Plus	61542-61750
	401994	4153858	Minus	42904-43124,43211-43336,44607-44763,45199-45281,46337-46732
	402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125872-126076
	402260	3399665	Minus	113765-113910,116653-116765,116808-116940
	402285	3287673	Plus	21059-21168
85	402297	6598824	Plus	35279-35405,35573-35659
	402408	9796239	Minus	110326-110491

	402420	9798339	Plus	129750-129919
	402674	8077108	Minus	39290-39502
	402802	3287156	Minus	53242-53432
5	402994	2996643	Minus	4727-4869
	403137	9211494	Minus	92349-92572,92958-93084,93579-93712,93949-94072,94591-94748,95214-95337
	403308	8099945	Plus	127100-127251
	403329	8516120	Plus	96450-96598
	403381	9438267	Minus	26009-26178
10	403478	9958258	Plus	116458-116564
	403485	9966528	Plus	2888-3001,3198-3532,3855-4117
	403627	8569879	Minus	23868-24342
	403715	7239669	Plus	85128-85292
	404044	9558573	Minus	225757-225939
15	404076	9931752	Minus	3848-3967
	404101	8076925	Minus	125742-125997
	404140	9843520	Plus	37761-38147
	404165	9926489	Minus	69025-69128
	404185	4572584	Minus	129171-129327
20	404210	5006246	Plus	169926-170121
	404253	9367202	Minus	55675-56055
	404287	2326514	Plus	53134-53281
	404298	9944263	Minus	73591-73723
	404347	9838195	Plus	74493-74829
25	404440	7528051	Plus	80430-81581
	404721	9856648	Minus	173763-174294
	404794	4826439	Plus	101618-101898
	404854	7143420	Plus	14260-14537
	404877	1519284	Plus	1095-2107
30	404927	7342002	Plus	68690-69563
	404996	6007890	Plus	37999-38145,38652-38998,39727-39872,40557-40674,42351-42450
	405449	7622497	Plus	42238-42570
	405568	6008906	Plus	35912-36065
	405572	3800891	Plus	85230-85938
35	405646	4914350	Plus	741-969
	405676	4557087	Plus	73195-73917
	405770	2735037	Plus	61057-62075
	405932	7767812	Minus	123525-123713
40	406137	9166422	Minus	30487-31058
	406360	9256107	Minus	7513-7673
	406399	9256288	Minus	63448-63554
	406467	9795551	Plus	182212-182958

TABLE 10A: Potential Therapeutic, Diagnostic and Prognostic targets for Therapy of Lung Cancer and Non-malignant Lung Disease

Table 2A shows about 307 genes up-regulated in non-malignant lung disease relative to lung tumors and normal body tissues and/or down-regulated in lung tumors relative to normal lung and non-malignant lung disease. These genes were selected from about 59680 probesets on the Eos/Affymetrix Hu03 Genechip array.

Table 10B show the accession numbers for those Pkey's lacking UnigenelD's for table 10A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Table 10C show the genomic positioning for those Pkey's lacking UnigenelD's and accession numbers in table 10A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigenel number
 Unigenel Title: Unigenel gene title
 R1: Average of lung tumors (including squamous cell carcinomas, adenocarcinomas, small cell carcinomas, granulomatous and carcinoid tumors) divided by the average of normal lung samples
 R2: Average of non-malignant lung disease samples (including bronchitis, emphysema, fibrosis, atelectasis, asthma) divided by the average of normal lung samples

	Pkey	ExAccn	UnigenelD	Unigenel Title	R1	R2
	404394			ENSP00000241075:TRRAP PROTEIN.	0.79	3.10
	404916			Target Exon	1.00	159.00
	405257			Target Exon	1.00	422.00
70	407228	M25079	Hs.155376	hemoglobin, beta	0.47	2.33
	407568	AA740964	Hs.62699	ESTs	1.00	123.00
	408562	AI436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,	1.00	230.00
	409031	AA376836	Hs.76728	ESTs	1.00	128.00
	410434	AF051152	Hs.63668	tol-like receptor 2	39.65	149.00
75	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	1.00	109.00
	410808	T40326	Hs.167793	ESTs	1.14	13.14
	412351	AL135960	Hs.73828	T-cell acute lymphocytic leukemia 1	0.37	2.27
	412372	R65998	Hs.285243	hypothetical protein FLJ22029	1.00	173.00
	413795	AL040178	Hs.142003	ESTs	0.10	11.90
80	414154	AW205314	Hs.323060	ESTs	0.62	2.09
	414214	O49958	Hs.75819	glycoprotein MGA	0.03	4.55
	414998	NM_002543	Hs.77729	oxidised low density lipoprotein (lectin	0.64	2.97
	415122	D60708	Hs.22245	ESTs	0.07	8.97
	415765	NM_005424	Hs.78824	tyrosine kinase with immunoglobulin and	0.67	1.65
85	415775	H00747	Hs.29792	ESTs, Weakly similar to I38022 hypotheti	0.29	2.64
	415910	U20350	Hs.78913	chemokine (C-X3-C) receptor 1	1.00	145.00

WO 02/086443

PCT/US02/12476

	416319	AI815601	Hs.79197	CD83 antigen (activated B lymphocytes, i	15.32	237.00
	416402	NM_000715	Hs.1012	complement component 4-binding protein,	0.64	4.00
	417355	D13168	Hs.82002	endothelin receptor type B	0.01	3.90
5	417421	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, m	36.30	357.00
	417511	AL049176	Hs.82223	chordin-like	1.00	179.00
	418489	U76421	Hs.85302	adenosine deaminase, RNA-specific, B1 (h	0.02	6.00
	418726	BE241812	Hs.87860	protein tyrosine phosphatase, non-recept	1.00	113.00
	418741	H83265	Hs.8881	ESTs, Weakly similar to S41044 chromosom	0.44	1.90
10	418883	BE387036	Hs.1211	acid phosphatase 5, tartrate resistant	0.96	2.04
	419086	NM_000216	Hs.89591	Kallmann syndrome 1 sequence	0.62	2.74
	419150	T29618	Hs.89640	TEK tyrosine kinase, endothelial (venous	0.03	6.90
	419235	AW470411	Hs.288433	neurotrophin	1.48	5.13
	419407	AW410377	Hs.41502	hypothetical protein FLJ21276	37.55	336.00
15	420556	AA278300	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	0.80	3.65
	420656	AA279098	Hs.187636	ESTs	1.66	8.07
	420729	AW984897	Hs.290825	ESTs	2.99	25.82
	421177	AW070211	Hs.102415	Homo sapiens mRNA; cDNA DKFZp586N0121 (f	0.46	1.95
	422080	R20893	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	1.00	156.00
20	422426	W79117	Hs.58559	ESTs	0.03	7.44
	422652	AW967969	Hs.118958	syntaxin 11	0.14	3.62
	423099	NM_002837	Hs.123641	protein tyrosine phosphatase, receptor t	0.01	3.16
	424433	H04607	Hs.9218	ESTs	0.75	141.75
	424585	AA484840	Hs.131987	ESTs	1.00	167.00
25	424711	NM_005795	Hs.152175	calcitonin receptor-like	0.43	3.01
	424973	X92521	Hs.154057	matrix metalloproteinase 19	0.37	19.45
	425023	AW556889	Hs.154210	endothelial differentiation, sphingolipid	0.14	3.35
	425664	AJ006276	Hs.159003	transient receptor potential channel 6	1.00	94.00
	425998	AU076629	Hs.165950	fibroblast growth factor receptor 4	0.68	1.42
30	426657	NM_015865	Hs.171731	solute carrier family 14 (urea transport	0.03	3.74
	426753	T89832	Hs.170278	ESTs	1.00	141.00
	427558	D49493	Hs.2171	growth differentiation factor 10	1.00	117.00
	427983	M17708	Hs.2233	colony stimulating factor 3 (granulocyte	0.75	2.20
	428467	AK002121	Hs.184465	hypothetical protein FLJ11259	0.76	2.25
35	428927	AA441837	Hs.90250	ESTs	0.01	3.62
	429498	AA453800	Hs.192793	ESTs	1.00	138.00
	430468	NM_004673	Hs.241519	angiotensin-like 1	1.00	132.00
40	431385	BE178536	Hs.11090	membrane-spanning 4-domains, subfamily A	1.00	167.00
	431728	NM_007351	Hs.268107	multimerin	1.00	157.00
	431848	AI378857	Hs.126758	ESTs, Highly similar to AF175283 1 zinc	0.34	2.24
	432128	AA127221	Hs.117037	ESTs	0.00	1.15
	432519	AI221311	Hs.130704	ESTs, Weakly similar to BCHUIA S-100 pro	0.01	2.06
	433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	1.00	267.00
	433803	AI823593	Hs.27688	ESTs	1.00	105.00
45	434730	AA644669	Hs.193042	ESTs	1.05	3.15
	435472	AW972330	Hs.283022	triggering receptor expressed on myeloid	0.83	1.94
	436532	AA721522		gbmv54h12.r1 NCI_CGAP_Ew1 Homo sapiens	1.00	218.00
	437119	AI379921	Hs.177043	ESTs	1.00	133.00
	437140	AA312799	Hs.283689	activator of CREM in testis	0.67	122.67
50	437211	AA382207	Hs.5509	ecotropic viral integration site 2B	1.00	142.00
	437960	AI669586	Hs.222194	ESTs	1.00	147.00
	438202	AW169287	Hs.22588	ESTs	1.00	141.00
	438873	AI302471	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	0.71	3.66
	438875	AA827640	Hs.189059	ESTs	23.32	370.00
55	441048	AA913488	Hs.192102	ESTs	0.77	8.50
	441188	AW292830	Hs.255609	ESTs	3.43	16.36
	441499	AW298235	Hs.101689	ESTs	1.00	167.00
	444513	AL120214	Hs.7117	glutamate receptor, ionotropic, AMPA 1	1.00	151.00
	444527	NM_005408	Hs.11383	small inducible cytokine subfamily A (Cy	46.47	153.00
60	444561	NM_004469	Hs.11392	c-fos induced growth factor (vascular en	0.01	3.08
	445279	R41900	Hs.22245	ESTs	0.60	141.00
	446017	N98238	Hs.55185	ESTs	0.18	2.39
	446984	AB020722	Hs.16714	Rho guanine exchange factor (GEF) 15	0.10	2.16
	446998	N99013	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	0.01	2.53
65	447357	AI375922	Hs.159367	ESTs	0.46	2.64
	448106	AI800470	Hs.171941	ESTs	18.05	296.00
	448253	H25899	Hs.201591	ESTs	1.00	141.00
	449276	AW450848	Hs.205457	perlecan	0.56	1.38
70	450400	AI694722	Hs.279744	ESTs	0.88	4.33
	450698	AI654223	Hs.16026	hypothetical protein FLJ23191	0.52	2.08
	450726	AW204600	Hs.250505	retinoic acid receptor, alpha	0.79	2.01
	451497	H83294	Hs.284122	Wnt inhibitory factor-1	0.35	2.03
	451533	NM_004657	Hs.26530	serum deprivation response (phosphatidyl	0.13	2.25
	453636	R67837	Hs.169872	ESTs	1.00	116.00
75	458332	AI000341	Hs.220491	ESTs	1.00	192.00
	459580	AA022888	Hs.176065	ESTs	0.20	2.98
	400269			Eos Control	0.40	2.40
	403421			NM_016369*:Homo sapiens claudin 18 (CLDN	0.53	1.77
80	407570	Z19002	Hs.37096	zinc finger protein 145 (Krueppel-like, e	0.01	3.18
	412295	AW088826	Hs.117176	poly(A)-binding protein, nuclear 1	0.56	1.74
	414517	M24461	Hs.78305	surfactant, pulmonary-associated protein	0.64	1.50
	417204	N81037	Hs.1074	surfactant, pulmonary-associated protein	0.33	1.16
	418307	U70867	Hs.83974	solute carrier family 21 (prostaglandin	0.53	1.55
	418935	T28499	Hs.89485	carbonic anhydrase IV	0.20	1.28
85	421502	AF111856	Hs.105039	solute carrier family 34 (sodium phospho	0.78	1.90
	421798	N74880	Hs.29877	N-acylsphingosine amidohydrolase (acid c	0.59	1.54

	423354	AB011130	Hs.127438	calcium channel, voltage-dependent, alph	0.59	1.55
	423738	AB002134	Hs.132195	airway trypsin-like protease	10.14	51.00
	425211	M18667	Hs.1867	progastricsin (pepsinogen C)	0.35	1.62
5	425438	T62216	Hs.270840	ESTs	0.23	9.45
	426828	NM_000020	Hs.172670	activin A receptor type II-like 1	0.03	1.71
	427019	AA001732	Hs.173233	hypothetical protein FLJ10970	0.01	1.49
	428043	T92248	Hs.2240	uteroglobin	0.42	1.26
	430280	AA381258	Hs.237868	interleukin 7 receptor	0.46	2.43
10	431433	X65018	Hs.253495	surfactant, pulmonary-associated protein	0.57	1.59
	431723	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	0.29	1.80
	432985	T92363	Hs.178703	ESTs	0.32	2.27
	441835	AB036432	Hs.184	advanced glycosylation end product-speci	0.31	1.51
	442275	AW449467	Hs.54795	ESTs	0.55	1.78
	443709	AI082692	Hs.134662	ESTs	0.00	3.02
15	444325	AW152618	Hs.16757	ESTs	0.32	2.49
	450954	AI904740	Hs.25691	receptor (calcitonin) activity modifying	0.46	1.74
	451558	NM_001089	Hs.26630	ATP-binding cassette, sub-family A (ABC1	0.52	1.87
	453310	X70697	Hs.553	solute carrier family 8 (neurotransmitte	0.00	3.30
	456855	AF035528	Hs.153863	MAD (mothers against decapentaplegic, Dr	0.01	2.31
20	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	0.66	2.20
	400754			Target Exon	1.00	297.00
	401045			C11001883:g j6753278 ref NP_033938.1 c	1.00	109.00
	401083			NM_016582*:Homo sapiens peptide transp	0.89	1.39
	402474			NM_004079:Homo sapiens cathepsin S (CTSS	1.45	4.47
25	402808			ENSP00000235229:SEMB.	1.00	1.87
	403021			C21000030:g j9955960 ref NP_063957.1 AT	1.00	149.00
	403438			NM_031419*:Homo sapiens molecule possess	1.06	2.96
	403687			NM_007037*:Homo sapiens a disintegrin-li	0.04	4.89
30	403764			NM_005463:Homo sapiens heterogeneous nuc	1.00	225.00
	404277			NM_019111*:Homo sapiens major histocompa	0.97	1.93
	404288			NM_002944*:Homo sapiens v-ros avlan UR2	1.00	68.00
	404518	AI815601		CD83 antigen (activated B lymphocytes, I	0.02	1.83
	405106			C11001637*:g j5032241 ref NP_005732.1 z	1.00	235.00
35	405381			Target Exon	1.00	93.00
	406387			Target Exon	1.37	6.02
	406646	M33600		major histocompatibility complex, class	0.86	2.46
	408714	AI219304	Hs.266959	hemoglobin, gamma G	0.01	3.19
	406753	AA505665	Hs.217493	annexin A2	1.00	147.00
40	406973	M34996	Hs.198253	major histocompatibility complex, class	1.03	2.04
	407248	U82275	Hs.94498	leukocyte immunoglobulin-like receptor,	1.00	64.00
	407510	U96191		gb:Human trophoblast hypoxia-regulated f	1.00	90.00
	407731	NM_000068	Hs.38069	complement component 8, beta polypeptide	1.00	67.00
	407830	NM_001086	Hs.587	arylacetamide deacetylase (esterase)	1.00	102.00
45	408045	AW138959	Hs.245123	ESTs	1.00	70.00
	408074	R20723		ESTs	1.00	112.00
	408374	AW025430	Hs.155591	forkhead box F1	0.07	10.17
	409064	AA062954	Hs.141883	ESTs	0.39	2.31
	409083	AF050083	Hs.673	interleukin 12A (natural killer cell sti	1.00	95.00
50	409153	W03754	Hs.50813	hypothetical protein FLJ20022	0.01	4.55
	409203	AA780473	Hs.687	cytochrome P450, subfamily IVB, polypept	0.01	3.72
	409238	AL049990	Hs.51515	Homo sapiens mRNA; cDNA DKFZp564G112 (fr	1.00	79.00
	409389	AB007979	Hs.301281	Homo sapiens mRNA, chromosome 1 specific	0.14	27.35
	409718	D86640	Hs.56045	src homology three (SH3) and cysteine ri	1.00	113.00
55	410798	BE178622	Hs.16291	gb:PM3-HT0605-270200-001-a02 HT0605 Homo	0.64	2.47
	411020	NM_006770	Hs.67726	macrophage receptor with collagenous str	0.55	2.40
	411667	BE160198		gb:QV1-HT0413-010200-059-h03 HT0413 Homo	1.00	111.00
	412000	AW576555	Hs.15780	ATP-binding cassette, sub-family A (ABC1	1.00	95.00
	412358	BE047490	Hs.24172	ESTs	1.00	87.00
60	412420	AL035668	Hs.73853	bone morphogenetic protein 2	1.43	8.07
	412564	X83703	Hs.31432	cardiac ankyrin repeat protein	0.02	3.07
	412869	AA290712	Hs.82407	CXC chemokine ligand 16	0.93	1.72
	412870	N22788	Hs.82407	CXC chemokine ligand 16	0.97	1.51
	413529	U11874	Hs.846	interleukin 8 receptor, beta	0.02	2.42
65	413533	BE146973		gb:QV4-HT0222-011199-019-e05 HT0222 Homo	0.65	1.50
	413689	BE157286	Hs.20631	zinc finger protein, subfamily 1A, 5 (Pe	20.87	232.00
	413724	AA131466	Hs.23767	hypothetical protein FLJ12666	1.00	80.00
	413800	AI129238	Hs.192235	ESTs	1.00	85.00
	413802	AW964490	Hs.32241	ESTs, Weakly similar to S65567 alpha-1C-	1.00	213.00
70	413829	NM_001872	Hs.75572	carboxypeptidase B2 (plasma)	0.02	3.93
	414376	BE393856	Hs.66915	ESTs, Weakly similar to 16.7Kd protein [1.00	115.00
	414577	AI056548	Hs.72116	hypothetical protein FLJ20992 similar to	0.49	1.94
	414700	H63202	Hs.38163	ESTs	0.03	3.75
	415078	AA311223	Hs.283091	found in inflammatory zone 3	0.86	1.95
75	415120	N84464	Hs.34950	ESTs	1.00	120.00
	415323	BE269352	Hs.949	neutrophil cytosolic factor 2 (65kD, chr	0.60	2.48
	415335	AA847758	Hs.111030	ESTs	1.00	95.00
	415582	W92445	Hs.165195	Homo sapiens cDNA FLJ14237 fis, clone NT	1.00	136.00
	416030	H15261	Hs.21948	ESTs	0.02	8.07
80	416427	BE244050	Hs.79307	Rac/Cdc42 guanine exchange factor (GEF)	1.00	73.00
	416464	NM_000132	Hs.79345	coagulation factor VIII, procoagulant co	0.70	3.36
	416585	X54162	Hs.79386	leiocodin 1 (smooth muscle)	0.06	6.56
	416847	L43821	Hs.80261	enhancer of filamentation 1 (cas-like do	0.70	3.66
	417148	AA359896	Hs.293885	hypothetical protein FLJ14902	1.00	114.00
85	417370	T28651	Hs.82030	tryptophanyl-tRNA synthetase	0.85	1.30
	417673	T87281	Hs.16355	ESTs	0.16	15.54

	418067	AI127958	Hs.83393	cystatin E/M	0.81	1.74
	418296	C01566	Hs.86671	ESTs	1.00	99.00
	418643	J03798	Hs.86948	small nuclear ribonucleoprotein D1 polyp	1.00	60.00
5	418832	X04011	Hs.88974	cytochrome b-245, beta polypeptide (chro	2.40	14.74
	418945	BE246762	Hs.89499	arachidonate 5-lipoxygenase	0.67	3.16
	419261	X07876	Hs.89791	wingless-type MMTV integration site faml	1.00	73.00
	419564	U08989	Hs.91139	solute carrier family 1 (neuronal/epithe	1.00	192.00
	419574	AK001989	Hs.91165	hypothetical protein	1.00	94.00
10	419968	X04430	Hs.93913	interleukin 6 (interferon, beta 2)	61.16	500.00
	420256	U84722	Hs.76206	cadherin 5, type 2, VE-cadherin (vascula	0.52	1.70
	420285	AA258124	Hs.293878	ESTs, Moderately similar to ZN91_HUMAN Z	1.00	172.00
	420577	AA278436	Hs.186649	ESTs	1.00	97.00
	421262	AA286746	Hs.9343	Homo sapiens cDNA FLJ14265 fis, clone PL	1.00	64.00
15	421445	AA913059	Hs.104433	Homo sapiens, clone IMAGE:4054868, mRNA	0.88	1.51
	421470	R27496	Hs.1378	annaxin A3	0.05	11.26
	421478	AI683243	Hs.97258	ESTs, Moderately similar to S29539 ribos	1.00	73.00
	421563	NM_006433	Hs.105806	granulysin	0.82	2.42
	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	5.50	31.57
20	421855	F06504	Hs.27384	ESTs, Moderately similar to ALLJ4_HUMAN A	1.00	129.00
	421913	AI934365	Hs.109439	osteoglycin (osteoinductive factor, mime	1.00	101.00
	421952	AA300900	Hs.98849	ESTs, Moderately similar to AF161511 H	0.60	63.60
	422232	D43945	Hs.113274	transcription factor EC	1.00	148.00
	422386	AF105374	Hs.115830	heparan sulfate (glucosamine) 3-O-sulfot	1.40	3.98
25	423168	R34385	Hs.124940	GTP-binding protein	0.34	3.59
	423196	AK001866	Hs.125139	hypothetical protein FLJ11004	0.55	2.00
	423387	AJ012074		vasoactive intestinal peptide receptor 1	0.09	2.13
	423424	AF150241	Hs.128433	prostaglandin D2 synthase, hematopoietic	1.00	141.00
	423456	AL110151	Hs.128797	DKFZP586D0824 protein	1.00	66.00
30	423698	Z92546		Sushi domain (SCR repeat) containing	0.73	1.27
	424027	AW337575	Hs.201591	ESTs	0.54	2.58
	424212	NM_005814	Hs.143131	glycoprotein A33 (transmembrane)	0.77	2.47
	425087	R62424	Hs.126059	ESTs	1.00	74.00
	425175	AF020202	Hs.155001	UNC13 (C. elegans)-like	0.85	1.98
35	425771	BE561776	Hs.159494	Bruton agammaglobulinemia tyrosine kinas	1.18	2.56
	426486	BE178285	Hs.170056	Homo sapiens mRNA; cDNA DKFZp586B0220 (f	1.00	76.00
	427507	AF240467	Hs.179152	toll-like receptor 7	1.00	63.00
	427618	NM_000760	Hs.2175	colony stimulating factor 3 receptor (gr	0.60	2.19
	427732	NM_002980	Hs.2199	secretin receptor	0.97	1.42
40	427952	AA765368	Hs.293941	ESTs, Moderately similar to A53959 throm	1.00	105.00
	428709	BE268717	Hs.104916	hypothetical protein FLJ21940	1.00	80.00
	428769	AW207175	Hs.106771	ESTs	0.09	2.65
	428780	AI478578	Hs.50636	ESTs	1.00	98.00
	428833	AI928355	Hs.185805	ESTs	1.00	113.00
45	428657	D13626	Hs.2465	KIAA0001 gene product; putative G-protei	1.00	52.00
	430212	AA469153		gb:nc67f04.s1 NCI_CGAP_Pr1 Homo sapiens	1.00	132.00
	430226	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	0.11	15.60
	430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	1.00	103.00
	430414	AW365665	Hs.120388	ESTs	0.50	6.96
50	430656	AA482900	Hs.162080	ESTs	1.00	70.00
	430843	AI734149	Hs.119514	ESTs	1.00	90.00
	430998	AF128847	Hs.204038	indolethylamine N-methyltransferase	0.29	1.84
	431217	NM_013427	Hs.260830	Rho GTPase activating protein 6	1.00	79.00
	431921	N46466	Hs.58879	ESTs	0.91	1.67
55	432176	AW090386	Hs.112278	arrestin, beta 1	0.66	2.63
	432203	AA305745	Hs.49	macrophage scavenger receptor 1	1.00	76.00
	432231	AA339977	Hs.274127	CLST 11240 protein	0.46	1.46
	432485	N90866	Hs.276770	CDW52 antigen (CAMPATH-1 antigen)	0.79	2.25
	432522	D11466	Hs.51	phosphatidylinositol glycan, class A (pa	1.93	4.83
60	432596	AJ224741	Hs.278461	matrilin 3	0.04	5.79
	432850	X87723	Hs.3110	angiotensin receptor 2	1.00	167.00
	433138	AB029496	Hs.59729	semaphorin sem2	0.04	9.16
	433563	AI732637	Hs.277901	ESTs	1.00	91.00
	433588	AI056872	Hs.133386	ESTs	120.16	315.00
65	434445	AI349306	Hs.11782	ESTs	0.60	1.84
	435496	AW840171	Hs.265398	ESTs, Weakly similar to transformation-r	1.00	128.00
	435974	U29690	Hs.37744	Homo sapiens beta-1 adrenergic receptor	1.00	108.00
	436061	AI248584	Hs.190745	Homo sapiens cDNA: FLJ21326 fis, clone C	1.00	91.00
	437157	BE048860	Hs.120655	ESTs	1.00	87.00
70	437207	T27503	Hs.15929	hypothetical protein FLJ12910	1.00	105.00
	437311	AA370041	Hs.9456	SWI/SNF related, matrix associated, acti	1.00	71.00
	437439	H29796	Hs.269622	ESTs	1.00	115.00
	438199	AW016531	Hs.122147	ESTs	1.00	80.00
	439551	W72062	Hs.11112	ESTs	0.30	3.10
75	440615	AJ131245	Hs.7239	SEC24 (S. cerevisiae) related gene famil	1.00	77.00
	440887	AI799488	Hs.135905	ESTs	1.00	85.00
	441025	AA913880	Hs.176379	ESTs	1.00	82.00
	441384	AA447849	Hs.288660	Homo sapiens cDNA: FLJ22182 fis, clone H	0.79	1.89
	441735	AI738675	Hs.127346	ESTs	1.00	75.00
80	442200	AW590572	Hs.235768	ESTs	0.78	6.83
	442832	AW206560	Hs.253569	ESTs	0.03	10.88
	442957	AI949952	Hs.49397	ESTs	1.00	70.00
	443282	T47764	Hs.132917	ESTs	1.00	197.00
	443547	AW271273	Hs.23767	hypothetical protein FLJ12666	1.00	253.00
85	443951	F13272	Hs.111334	fertilin, light polypeptide	0.55	2.09
	444330	AI597655	Hs.49265	ESTs	1.00	90.00

	444515	AW204908	Hs.169979	ESTs	1.00	84.00
	445769	AI741471	Hs.23666	ESTs	0.02	4.38
	445908	R13580	Hs.13436	Homo sapiens clone 24425 mRNA sequence	1.00	97.00
5	446291	BE397753	Hs.14623	Interferon, gamma-inducible protein 30	0.93	1.69
	446917	AI347863	Hs.166672	ESTs	1.00	106.00
	447261	NM_006691	Hs.17917	extracellular link domain-containing 1	0.40	47.20
	447432	AW958473	Hs.301957	nudix (nucleoside diphosphate linked moi	1.00	100.00
	447482	AB033059	Hs.18705	KIAA1233 protein	0.05	8.21
10	447997	H00656	Hs.29792	ESTs, Weakly similar to I38022 hypotheli	0.02	5.42
	448299	AA497044	Hs.20887	hypothetical protein FLJ10392	1.00	79.00
	448782	AL050295	Hs.22039	KIAA0758 protein	0.42	1.56
	450575	NM_005859	Hs.29117	purine-rich element binding protein A	0.17	11.33
	450584	AA040403	Hs.60371	ESTs	1.00	94.00
15	450693	AW450461	Hs.203965	ESTs	1.00	91.00
	450715	AI266484	Hs.31570	ESTs, Weakly similar to KIAA1324 protein	1.00	152.00
	451103	R52804	Hs.25956	DKFZP564D206 protein	1.00	86.00
	451220	AF124251	Hs.26054	novel SH2-containing protein 3	0.60	1.30
	451668	Z43948	Hs.326444	cartilage acidic protein 1	0.54	1.91
20	452197	AW023595	Hs.232048	ESTs	1.00	67.00
	452331	AA598509	Hs.29117	purine-rich element binding protein A	4.53	11.07
	452353	C18825	Hs.29191	epithelial membrane protein 2	0.72	2.24
	453049	BE537217	Hs.30343	ESTs	1.00	68.00
	453107	NM_016113	Hs.279746	vanilloid receptor-like protein 1	0.83	1.70
25	453355	AW295374	Hs.31412	Homo sapiens cDNA FLJ11422 fis, clone HE	1.00	132.00
	453390	AA862496	Hs.28482	ESTs	1.00	72.00
	453531	AA417940		ESTs, Weakly similar to JC5795 CDEP prot	1.00	68.00
	454741	BE154396		gb:CM2-HT0342-091299-050-b05 HT0342 Homo	0.57	2.89
	456579	AA287827	Hs.284205	up-regulated by BCG-CWS	1.00	82.00
30	456672	AK002016	Hs.114727	Homo sapiens, clone MGC:16327, mRNA, com	0.79	1.96
	457400	AF032906	Hs.252549	cathepsin Z	1.03	3.25
	457718	F18572	Hs.22978	ESTs, Weakly similar to ALU4_HUMAN ALU S	1.00	113.00
	459696	F03027		gb:HSC1KA072 normalized infant brain cDN	1.00	544.00

TABLE 10B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

40	Pkey	CAT Number	Accession
	408074	103684_1	R20723 AA263003 AA333976 AA334725 AA334151 AW965490 AA310513 AI810530 D31302 AW134897 AA830127 AA046953 AI668930 C06094 AW104534
	411667	1253334_1	BE160198 AW935898 T11520 AW935930 AW856073 AW861034
45	413533	1375344_1	BE146973 BE146972 BE147042 BE147018 BE146783 BE147020 BE146781 BE147019 BE146766 BE147021 BE146952 BE146767 BE147044 BE146797 BE146776 BE146985 BE146793 BE146768 BE146771 BE146954 BE146760 BE147048 BE147025 BE147030
	423387	22779_1	AJ012074 U11087 L13288 X75299 L20295 AW630780 H14880 T28037 AI872991 R72136 AW449839 T81622 T79697 T29519 R94105 T83923 R73300 AI797007 R73390 AA981010 H74168 AI689932 BE045543 AI808418 AI608912 AI806573 AW884084 AW872978 AW872985 AA565655 AI022915 R50647 R73210 H45098 R46451 AW166269 T71132 AI264547 R52146 AI304920 R73391 AW884059 AW884085 H73241 T60038 T79612 R73145 R50549 AI094557 AI668793 R72302 AI564366 W01956 AA418962 W32571 R72840 H45409 R72085 R46356 R46758
50	423698	23112_1	AA508805 AA418798 T83751 R94072 T16182 AA928785 AA903896 Z92546 AA330586 AI570568 AW341487 AI827050 AW298668 AI792189 AI015693 AI733599 AI572251 AI672488 AW193262 AI244716 AI864375 AI206100 AA912444 AI269365 AI640254 AW772466 AI867336 AA627604 H16914 AA358477 AA338009
	430212	314437_1	AA469153 AI718503 AA469225
55	436532	421802_1	AA721522 AW975443 T93070
	453531	97026_1	AA417940 AA036735 T07025
	454741	1232559_1	BE154396 AW817959 BE154393

TABLE 10C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NT_position: Indicates nucleotide positions of predicted exons.

	Pkey	Ref	Strand	NT_position
	400754	7331445	Plus	144559-144684
70	401045	8117619	Plus	90044-90184,91111-91345
	401083	3242744	Plus	33192-33360
	402474	7547175	Minus	53526-53628,55755-55920,57530-57757
	402808	6456148	Minus	114964-115136,115461-115585,115931-116047,117666-117771,118004-118102
	403021	7547270	Plus	120799-120965
	403421	9665041	Minus	126609-126773,139988-140205
75	403438	9719679	Plus	90792-90938
	403687	7387384	Plus	9009-9534
	403764	7717105	Minus	118692-118853
	404277	1834458	Minus	91665-91946
80	404288	2769644	Plus	3512-3691
	404394	3135305	Minus	37121-37205,37491-37762,41053-41140,41322-41593,41773-41919
	404518	8151988	Plus	84494-84603
	404916	7341826	Plus	91057-91188
	405106	8079395	Minus	80877-81418
	405257	7329310	Plus	73121-73273
85	405381	6006920	Minus	7636-8054

WO 02/086443
406387 9256180 Plus

116229-116371,117512-117651

PCT/US02/12476

TABLE 11A: Genes Distinguishing Adenocarcinoma from Other Lung Diseases and Normal Lung

Table 11A shows about 84 genes upregulated in lung adenocarcinomas relative to other lung tumors, non-malignant lung disease, and normal lung. These genes were selected from about 59680 probesets on the Eos/Affymetrix Hu03 Genechip array.

Table 11B show the accession numbers for those Pkey's lacking UnigenelD's for table 11A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Table 11C show the genomic positioning for those Pkey's lacking UnigenelD's and accession numbers in table 11A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique Eos probeset Identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Average of lung tumors (including squamous cell carcinomas, adenocarcinomas, small cell carcinomas, granulomatous and carcinoid tumors) divided by the average of normal lung samples
 R2: Average of non-malignant lung disease samples (including bronchitis, emphysema, fibrosis, atelectasis, asthma) divided by the average of normal lung samples

Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2
403329			Target Exon	1.00	61.00
406399			NM_003122*:Homo sapiens serine protease	1.00	39.00
406690	M29540	Hs.220529	cardioembryonic antigen-related cell ad	226.37	350.00
407869	A1827976	Hs.24391	hypothetical protein FLJ13612	0.77	1.18
407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfot	1.00	10.00
408908	BE296227	Hs.250822	serine/threonine kinase 15	7.76	1.00
409103	AF251237	Hs.112208	XAGE-1 protein	80.44	40.00
409187	AF154830	Hs.50966	carbamoyl-phosphate synthetase 1, mitoch	1.00	1.00
409269	AA576953	Hs.22972	hypothetical protein FLJ13352	1.00	1.00
410076	T05387	Hs.7991	ESTs	1.12	1.50
410102	AW248508	Hs.278727	Homo sapiens cDNA FLJ14035 fls, clone HE	9.89	1.00
410399	BE068889		synuclein, gamma (breast cancer-specific	0.92	1.06
411908	L27943	Hs.72924	cytidine deaminase	1.00	1.00
412612	NM_000047	Hs.74131	arylsulfatase E (chondrodysplasia puncta	1.02	1.03
414075	U11862	Hs.75741	amiloride binding protein 1 (amine oxida	0.84	1.07
416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	3.67	1.00
417542	J04129	Hs.82269	progesterone-associated endometrial prote	1.28	1.35
419183	U60669	Hs.89663	cytochrome P450, subfamily XXIV (vitamin	1.00	1.00
419502	AU076704		fibrinogen, A alpha polypeptide	13.05	115.00
419631	AW188117	Hs.303154	popeye protein 3	1.00	13.00
420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	1.00	8.00
421155	H87879	Hs.102267	lysyl oxidase	1.00	15.00
421190	U95031	Hs.102482	mucin 5, subtype B, tracheobronchial	1.17	1.55
421474	U76362	Hs.104637	solute carrier family 1 (glutamate trans	1.46	1.78
421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase 1, l	1.00	3.00
421582	A1910275		trefoil factor 1 (breast cancer, estroge	1.23	1.00
422026	U80736	Hs.110826	trinucleotide repeat containing 9	1.00	52.00
422085	A1868872	Hs.282804	hypothetical protein FLJ22704	4.37	2.34
422311	AF073515	Hs.114948	cytokine receptor-like factor 1	1.16	1.78
422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	1.69	3.17
423472	AF041260	Hs.129057	breast carcinoma amplified sequence 1	48.13	72.00
423554	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	1.00	50.00
424502	AF242388	Hs.149585	lengsin	1.00	1.00
424544	M88700	Hs.150403	dopa decarboxylase (aromatic L-amino aci	1.00	59.00
424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	21.35	1.00
424960	BE245380	Hs.153952	5' nucleotidase (CD73)	1.00	1.00
425523	AB007948	Hs.158244	KIAA0479 protein	1.00	35.00
426230	AA367019	Hs.241395	protease, serine, 1 (trypsin 1)	1.00	83.00
427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	7.41	34.00
428585	AB007863	Hs.185140	KIAA0403 protein	1.00	6.00
428758	AA433988	Hs.98502	hypothetical protein FLJ14303	1.06	1.13
429170	NM_001394	Hs.2359	dual specificity phosphatase 4	16.18	105.00
429263	AA019004	Hs.198396	ATP-binding cassette, sub-family A (ABC1	1.07	1.00
429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas	1.59	1.69
430508	A1015435	Hs.104637	ESTs	4.75	7.27
430985	AA490232	Hs.27323	ESTs, Weakly similar to I7885 serine/th	0.94	1.28
431548	A1834273	Hs.9711	novel protein	5.66	15.00
431566	AF176012	Hs.260720	J domain containing protein 1	49.76	37.00
431986	AA536130	Hs.149018	Novel human gene mapping to chromosome 20	1.19	1.47
432375	BE536069	Hs.2962	S100 calcium-binding protein P	1.65	1.06
432677	NM_004482	Hs.278611	UDP-N-acetyl-alpha-D-galactosamine:polyp	1.00	48.00
433558	W56321	Hs.111460	calcium/calmodulin-dependent protein kin	1.00	19.00
433819	AW511097	Hs.112765	ESTs	3.71	8.00
434001	AW950905	Hs.3697	serine (or cysteine) proteinase inhibito	29.31	72.00
434424	A1811202	Hs.325335	Homo sapiens cDNA: FLJ23523 fls, clone L	1.00	64.00
434792	AA649253	Hs.132458	ESTs	8.52	44.00
436217	T53925	Hs.107	fibrinogen-like 1	57.97	31.00
436749	AA584890	Hs.5302	lectin, galactoside-binding, soluble, 4	1.10	1.41
436972	AA284679	Hs.25640	claudin 3	1.59	1.46
437866	AA156781		metallothionein 1E (functional)	3.62	101.00
437935	AW939591	Hs.5940	mucin 13, epithelial transmembrane	1.60	1.39
438915	AA260174	Hs.285681	Williams-Beuren syndrome chromosome regi	1.00	1.00
439451	AF096270	Hs.278554	heterochromatin-like protein 1	23.28	52.00

439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN	1.00	21.00
441031	AI110684	Hs.7645	fibrinogen, B beta polypeptide	1.41	99.00
441377	BE218239	Hs.202656	ESTs	22.03	1.00
443614	AV655386	Hs.7645	fibrinogen, B beta polypeptide	1.00	18.00
443813	AA876372	Hs.93961	Homo sapiens mRNA; cDNA DKFZp667D095 (fr	1.20	1.99
443991	NM_002250	Hs.10082	potassium intermediate/small conductance	5.71	6.87
444670	H58373	Hs.332938	hypothetical protein MGC5370	1.98	38.00
444931	AV652066	Hs.75113	general transcription factor IIIA	1.00	54.00
446102	AW168067	Hs.317694	ESTs	1.00	1.00
446163	AA026880	Hs.25252	Homo sapiens cDNA FLJ13603 fis, clone PL	1.00	36.00
446469	BE094848	Hs.15113	homogenisate 1,2-dioxygenase (homogenit	1.00	11.00
447388	AW630534	Hs.76277	Homo sapiens, clone MGC:9381, mRNA, comp	1.24	1.16
447532	AK000614	Hs.18791	hypothetical protein FLJ20607	1.23	1.63
448243	AW369771	Hs.52620	integrin, beta 8	15.84	1.00
448844	AI591519	Hs.177164	ESTs	1.00	31.00
449444	AW818436	Hs.23590	solute carrier family 16 (monocarboxylic	1.00	83.00
451807	W52854		hypothetical protein FLJ23293 similar to	1.55	35.00
452689	F33868	Hs.284176	transferrin	1.54	1.44
453392	U23762	Hs.32964	SRY (sex determining region Y)-box 11	1.00	16.00
453464	AI884911	Hs.32989	receptor (calcitonin) activity modifying	1.55	2.45
453735	AI066629	Hs.125073	ESTs	1.01	1.30

TABLE 11B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

410399	11995_1	BE068889 BE068882 AF044311 AF017256 NM_003087 AF037207 AF010126 AA633976 AA872836 BE298825 BE299889 AI016464 AI684600 AI936527 AA804675 AA394097 AI139933 AA946606 BE171313 AA722407 AA293803 AI468480 AA056035 AA055968 AW796957 AI637713 AA410737 H49348 AA486472 AA411094 AA235594 AA402624 AA443638 AW452137 AA421708 AW265211 AI493266 AA365132 AW966044 AU076704 T74854 T74860 T72098 T73265 T73873 T69180 T74658 T68786 T60385 T73410 T68781 T67845 T67593 T73952 T67884 T60830 T68367 T68401 T53959 T72360 T72099 T60377 T58961 T71712 T72821 T64738 T74645 T72037 T68688 T72063 T73258 T72826 T64242 T68220 T74673 T71800 T68355 T61227 T62738 T69317 T53850 T64692 T73768 T73962 T73382 T68914 T70975 T73400 T60631 T73277 T73203 T70498 T61409 T58925 NM_000508 M54982 T68301 T73729 T69445 T60424 T67922 T67736 T68716 T76755 T74765 T73819 T58719 T74756 T60477 T74863 T61109 T68329 T58850 T71857 T73425 T53736 T68607 T58898 T64309 T72031 T72079 T64305 T71908 T68107 T71916 T73787 T56035 T64425 T71870 T60476 T61376 T67820 T71895 T41006 T69441 T68170 T74617 T71958 T69440 T61875 R06796 H48353 T71914 T53939 T64121 AA693996 T72525 T67779 T68078 AA011465 AA345378 AV654847 AV654272 AV656001 AI064740 T82897 N33594 AA344542 AW805054 AI207457 T61743 AA026737 H94389 AA382695 AA918409 T68044 S82092 T39959 AI017721 AA312395 AA312919 T40156 H66239 AV652989 H38728 R85521 AV655200 R95790 W03250 W00913 AA344136 AV660126 R97923 AA343596 AW470774 AV651256 N54417 AA812862 AW182929 AI111192 H61463 H72060 AA344503 H38639 AI277511 AV661108 AI207625 T47810 AA235252 T27853 T47778 R95746 H70620 AA701463 AW827166 R98475 C20925 AV657287 T71959 T71313 T73920 T73333 T61618 T69293 T69283 T73931 T72178 T72456 AV645639 AV653476 T72957 T72300 T58906 T71457 T70494 T72956 T70495 T68267 T74407 T85778 AA344726 T27854 T74485 T74101 T73868 T71518 T72304 AA343853 T73909 T68070 T72055 H72149 T73493 T73495 AV645993 R02293 T70475 T64751 AA344441 AA343657 AA345732 AA344328 AI110639 AA344603 AF063513 T64696 T68516 T72223 T60507 T67633 R29500 T72517 R02292 T60599 T69206 T70452 T74677 R29366 T61277 T74914 T60352 R29675 T74843 AV645792 AA344408 T69197 T72057 T69368 T69358 T68258 AV650429 T73341 T61702 T74598 T40095 K02272 T40106 AA343045 AA341908 AA341907 AA342807 AA341964 T53747 T72042 T62764 AI064899 AA343080 T67832 T72440 T71770 T68091 T69108 T72449 T69167 T71289 T68251 AV654844 T64375 AA345234 T67598 AA011414 T68036 H48262 AI207557 T68219 W86031 T69081 T64232 R93196 T62136 AV650539 H67459 T72978 AA344583 T60362 H58121 T95711 T72803 T68055 T71715 R29036 T72793 T69122 T64595 T62888 T69139 T68291 T64652 T67971 T46862 AA693592 AI248502 R29454 T64764 T57001 T73052 T71429 T51176 T58866 AV655414 H90426 AA342489 T73666 T67848 T72512 T53835 T67837 T73317 T74273 T69420 T68245 T74380 T67862 T74474 T56068 AI910275 X00474 X52003 X05030 NM_003225 AA314326 AA308400 AA506787 AA314825 AI571948 AA507595 AA614579 AA587613 R83818 AA568312 AA614409 AA307678 AI925552 AW950155 AI910083 M12075 BE074052 AW004668 AA578674 AA582084 BE074053 BE074126 BE074140 AA514776 AA588034 BE074051 BE074068 AW009769 AW050690 AA588276 R55389 AI001051 AW050700 AW750216 AA614539 BE074045 AI307407 AW602303 BE073575 AI202532 AA524242 AI970839 AI909751 BE078078 AI909749 R55292 AA156781 AW293839 U52054 AA024963 AA778446 BE073977 AW444904 AW602574 BE164040 BE164012 BE163972 BE163974 BE163992 AA837481 AW468444 BE185091 AW468002 AA687333 AA811830 AA581806 AI866686 AI572124 AA043777 AA040926 D20160 AI536733 AA812489 AW874142 AI471883 W84421 AA156850 W52854 AL117600 BE208116 BE208432 BE206239 BE082291 AW953423 AA351619 BE180648 BE140560 W60080 AA865478 N90291 AW450652 AW449519 AA993634 AI806539 AA351618 AW449522 AI827628 AA904788 AA380381 AA886045 AA774409 BE003229 Z41758
--------	---------	---

TABLE 11C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
403329	8516120	Plus	96450-96598
406399	9256288	Minus	63448-63554

TABLE 12A: Genes Distinguishing Squamous Cell Carcinoma from Other Lung Diseases and Normal Lung

Table 12A shows about 72 genes upregulated in squamous cell carcinomas of the lung relative to other lung tumors, non-malignant lung disease, and normal lung. These genes were selected from about 59680 probesets on the Eos/Affymetrix Hu03 Genechip array.

Table 12B show the accession numbers for those Pkey's lacking UnigenelD's for table 12A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Table 12C show the genomic positioning for those Pkey's lacking UnigenelD's and accession numbers in table 12A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigenes number
 Unigenes Title: Unigenes gene title
 R1: Average of lung tumors (including squamous cell carcinomas, adenocarcinomas, small cell carcinomas, granulomatous and carcinoid tumors) divided by the average of normal lung samples
 R2: Average of non-malignant lung disease samples (including bronchitis, emphysema, fibrosis, atelectasis, asthma) divided by the average of normal lung samples

Pkey	ExAccn	UnigenelD	Unigenes Title	R1	R2
400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	132.45	4.00
400666			NM_002425:Homo sapiens matrix metallopro	3.26	3.22
401780			NM_005557:Homo sapiens keratin 16 (foca	26.47	10.50
401781			Target Exon	10.33	4.61
401785			NM_002275:Homo sapiens keratin 15 (KRT1	4.13	2.70
401994			Target Exon	61.84	47.00
402075			ENSP00000251056*:Plasma membrane calcium	1.00	1.00
404996			Target Exon	1.00	1.00
407839	AA045144	Hs.161566	ESTs	173.91	108.00
408000	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	151.17	8.00
408522	AI541214	Hs.46320	Small proline-rich protein SPRK [human,	1.98	1.24
410561	BE540255	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	10.04	1.00
415091	AL044872	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A sy	1.00	30.00
415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-l	24.30	1.00
416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	53.29	51.00
417034	NM_006183	Hs.80962	neurotensin	1.00	1.00
417366	BE185289	Hs.1076	small proline-rich protein 1B (cornifin)	8.97	3.27
418663	AK001100	Hs.41690	desmocollin 3	112.17	19.00
418678	NM_001327	Hs.87225	cancer/testis antigen	1.18	1.10
419121	AA374372	Hs.89626	parathyroid hormone-like hormone	1.00	1.00
420783	AI659838	Hs.99923	lectin, galactoside-binding, soluble, 7	3.04	1.25
421773	W69233	Hs.112457	ESTs	1.12	1.14
421948	L42583	Hs.334309	keratin 6A	51.83	20.25
421978	AJ243662	Hs.110196	NICE-1 protein	1.01	0.91
422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	2.37	1.10
422440	NM_004812	Hs.116724	aldo-keto reductase family 1, member B10	47.53	32.00
423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	76.02	1.00
423725	AJ403108	Hs.132127	hypothetical protein LOC57822	4.20	1.00
423738	AB002134	Hs.132195	airway trypsin-like protease	10.14	51.00
424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	233.42	68.00
424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibito	1.00	1.00
424098	AF077374	Hs.139322	small proline-rich protein 3	137.82	54.00
424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	56.19	12.00
425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	33.45	1.00
427099	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	4.24	17.00
427335	AA448542	Hs.251677	G antigen 7B	51.83	4.00
428182	BE386042	Hs.293317	ESTs, Weakly similar to GGC1_HUMAN G ANT	1.00	1.00
428645	AA431400	Hs.98729	ESTs, Weakly similar to 2017205A dihydro	1.00	16.00
428748	AW593206	Hs.98785	Ksp37 protein	1.00	87.00
429259	AA420450	Hs.292911	ESTs, Highly similar to S60712 band-6-pr	2.01	1.18
429538	BE182592	Hs.11261	small proline-rich protein 2A	4.43	2.90
429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	11.80	1.00
430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	12.28	41.00
430890	X54232	Hs.2699	glypican 1	1.58	1.40
431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3	60.25	28.00
431846	BE019924	Hs.271580	uroplakin 1B	4.49	2.51
433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	1.20	1.09
434360	AW015415	Hs.127780	ESTs	40.98	27.00
434880	U02388	Hs.101	cytochrome P450, subfamily IVF, polypept	1.00	1.00
435505	AF200492	Hs.211238	Interleukin-1 homolog 1	1.00	38.00
435793	AB037734	Hs.4993	KIAA1313 protein	23.68	42.00
436511	AA721252	Hs.291502	ESTs	16.76	14.00
438403	AA806607	Hs.292206	ESTs	1.00	1.00
439285	AL133916		hypothetical protein FLJ20093	46.23	139.00
439606	W79123	Hs.58561	G protein-coupled receptor 87	33.61	1.00
439670	AF088076	Hs.59507	ESTs, Weakly similar to AC004858 3 U1 sm	1.00	1.00
439706	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	86.55	11.00
440325	NM_003812	Hs.7164	a disintegrin and metalloproteinase doma	62.88	147.00
441525	AW241867	Hs.127728	ESTs	1.53	1.42
443162	T49951	Hs.8029	DKFZP434G032 protein	31.11	38.00
444378	R41339	Hs.12569	ESTs	1.00	1.00

WO 02/086443

PCT/US02/12476

446292	AF081497	Hs.279682	Rh type C glycoprotein	1.55	1.26
447078	AW885727	Hs.9914	ESTs	47.24	24.00
447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	28.63	1.00
449003	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu o	1.00	1.00
449101	AA205847	Hs.23016	G protein-coupled receptor	2.58	27.00
450832	AW970602	Hs.105421	ESTs	25.17	36.00
452240	AI591147	Hs.61232	ESTs	13.42	1.00
453317	NM_002277	Hs.41698	keratin, hair, acidic, 1	1.19	1.27
453830	AA534296	Hs.20953	ESTs	24.92	25.00
454098	W27953	Hs.292911	ESTs, Highly similar to S60712 band-6-pr	1.26	1.11
455601	AI368680	Hs.816	SRY (sex determining region Y)-box 2	208.11	1.00

TABLE 12B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
439285	47065_1	AL133916 N79113 AF086101 N76721 AW950828 AA364013 AW955684 AI346341 AI867464 N54784 AI655270 AI421279 AW014882 AA775552 N62351 N59253 AA626243 AI341407 BE175639 AA456968 AI358918 AA457077

TABLE 12C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400666	8118496	Plus	17982-18115,20297-20456
401780	7249190	Minus	28397-28617,28920-29045,29135-29296,29411-29567,29705-29787,30224-30573
401781	7249190	Minus	83215-83435,83531-83656,83740-83901,84237-84393,84955-85037,86290-86814
401785	7249190	Minus	165776-165996,166189-166314,166408-166569,167112-167268,167387-167469,168634-168942
401994	4153858	Minus	42904-43124,43211-43336,44607-44763,45199-45281,46337-46732
402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076
404996	6007890	Plus	37999-38145,38652-38998,39727-39872,40557-40674,42351-42450

TABLE 13A: Genes Distinguishing Non-Malignant Lung Disease from Lung Tumors and Normal lung

Table 13A shows about 23 genes upregulated in non-malignant lung disease relative to lung tumors and normal lung. These genes were selected from about 59680 probesets on the Eos/Affymetrix Hu03 Genechip array.

Table 13B show the accession numbers for those Pkey's lacking UnigeneID's for table 13A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Table 13C show the genomic positioning for those Pkey's lacking Unigene ID's and accession numbers in table 13A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 R1: Average of lung tumors (including squamous cell carcinomas, adenocarcinomas, small cell carcinomas, granulomatous and carcinoid tumors) divided by the average of normal lung samples
 R2: Average of non-malignant lung disease samples (including bronchitis, emphysema, fibrosis, atelectasis, asthma) divided by the average of normal lung samples

Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2
408562	AI436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,	1.00	230.00
409031	AA376836	Hs.76728	ESTs	1.00	128.00
412372	R65998	Hs.285243	hypothetical protein FLJ22029	1.00	173.00
415910	U20350	Hs.78913	chemokine (C-X3-C) receptor 1	1.00	145.00
417511	AL049176	Hs.82223	chordin-like	1.00	179.00
418819	AA228776	Hs.191721	ESTs	1.00	140.00
422060	R20893	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	1.00	156.00
424585	AA464840	Hs.131987	ESTs	1.00	167.00
426753	T89832	Hs.170278	ESTs	1.00	141.00
429496	AA453800	Hs.192793	ESTs	1.00	138.00
430719	AA488988	Hs.293796	ESTs	1.00	133.00
431089	BE041395		ESTs, Weakly similar to unknown protein	23.32	941.00
431385	BE178536	Hs.11090	membrane-spanning 4-domains, subfamily A	1.00	157.00
431728	NM_007351	Hs.268107	multimerin	1.00	157.00
436532	AA721522		gb:mv54h12.r1 NCL_CGAP_Ew1 Homo sapiens	1.00	218.00
437960	AI669586	Hs.222194	ESTs	1.00	147.00
438202	AW169287	Hs.22588	ESTs	1.00	141.00
441499	AW298235	Hs.101689	ESTs	1.00	167.00
444513	AL120214	Hs.7117	glutamate receptor, ionotropic, AMPA 1	1.00	151.00
448253	H25899	Hs.201591	ESTs	1.00	141.00
453636	R67837	Hs.169872	ESTs	1.00	116.00
458332	AI000341	Hs.220491	ESTs	1.00	192.00
459587	AA031956		gb:zk15e04.s1 Soares_pregnantUterus_NbH	1.00	154.00

TABLE 13B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
431089	327825_1	BE041395 AA491826 AA621946 AA715980 AA666102
436532	421802_1	AA721522 AW975443 T93070

TABLE 13C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076

TABLE 14A: Preferred Utility and Subcellular Localization for Potential Lung Disease Targets

Table 14A shows the subcellular localization and preferred utility for the genes appearing in Tables 9A and 10A. mAb symbolizes monoclonal antibody, diag symbolizes diagnostic, s.m. symbolizes small molecule, and CTL symbolizes cytotoxic lymphocytic ligand. These genes were selected from 59680 probesets on the Eos/Affymatrix Hu03 Genechip array.

Table 14B show the accession numbers for those Pkey's lacking UnigeneID's for table 14A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Table 14C show the genomic positioning for those Pkey's lacking Unigene ID's and accession numbers in table 14A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique Eos probeset identifier number

ExAccn: Exemplar Accession number, Genbank accession number

UnigeneID: Unigene number

Unigene Title: Unigene gene title

Pref.Utility: Preferred Utility

Pred.Loc: Predicted subcellular localization

Pkey	ExAccn	UnigeneID	Unigene Title	Pref Utility	Pred. Loc
400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	mAb & diag & s.m.	extracellular
400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	mAb	plasma membrane
402075			ENSP00000251056*:Plasma membrane calcium	mAb & diag	secreted
407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	diag	secreted
408243	Y00787	Hs.624	interleukin 8	diag	secreted
408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	mAb & s.m.	plasma membrane
408908	BE296227	Hs.250822	serine/threonine kinase 15	s.m.	cytoplasm
409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	CTL & diag	secreted
409103	AF251237	Hs.112208	XAGE-1 protein	CTL	nuclear
409420	Z16008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalni	diag	secreted
409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	diag	secreted
409757	NM_001898	Hs.123114	cystatin SN	diag	extracellular
409893	AW247090	Hs.57101	minichromosome maintenance deficient (S.	CTL	nuclear
409956	AW103364	Hs.727	inhibin, beta A (activin A, activin AB a	diag	extracellular
410001	AB041036	Hs.57771	kallikrein 11	diag	extracellular
410407	X66839	Hs.63287	carbonic anhydrase IX	mAb & s.m.	plasma membrane
410418	D31382	Hs.63325	transmembrane protease, serine 4	mAb & diag & s.m.	plasma membrane
412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	s.m.	
412719	AW018610	Hs.816	ESTs	s.m.	nuclear
414774	X02419	Hs.77274	plasminogen activator, urokinase	diag	extracellular
414883	AA926960		CDC28 protein kinase 1	s.m.	
415138	C18356	Hs.295944	tissue factor pathway inhibitor 2	CTL & diag	extracellular
415669	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibito	mAb & diag & s.m.	secreted
415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	mAb & s.m.	plasma membrane
416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	diag	extracellular
417034	NM_008183	Hs.80962	neurotensin	diag	extracellular
417079	U65590	Hs.81134	Interleukin 1 receptor antagonist	diag	extracellular
417308	H60720	Hs.81892	KIAA0101 gene product	s.m.	mitochondrial
417389	BE260984	Hs.82045	midkine (neurite growth-promoting factor	mAb & diag	secreted
417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	mAb	plasma membrane
417933	X02308	Hs.82962	thymidylate synthetase	s.m.	endoplasmic reticulum
418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	s.m.	cytoplasm
418506	AA084248	Hs.85339	G protein-coupled receptor 39	mAb & s.m.	plasma membrane
418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)	CTL	cytoplasmic
419121	AA374372	Hs.89626	parathyroid hormone-like hormone	diag	secreted
419171	NM_002846	Hs.89655	protein tyrosine phosphatase, receptor t	mAb & s.m.	plasma membrane
419183	U60669	Hs.89663	cytochrome P450, subfamily XXIV (vitamin	CTL & s.m.	mitochondrial
419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	diag	secreted
419235	AW470411	Hs.288433	neurotrophin	mAb & diag	plasma membrane
419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	mAb & s.m.	plasma membrane
419556	U29615	Hs.91093	chitinase 1 (chitotriosidase)	mAb & diag	extracellular*
420610	AI683183	Hs.99348	distal-less homeo box 5	CTL	nuclear
421110	AJ250717	Hs.1355	cathepsin E	sm & diag	extracellular
421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	diag	secreted
421474	U76362	Hs.104637	solute carrier family 1 (glutamate trans	mAb & s.m.	plasma membrane
421552	AF026692	Hs.105700	secreted frizzled-related protein 4	diag	secreted
421753	BE314828	Hs.107911	ATP-binding cassette, sub-family B (MDR/	mAb & s.m.	plasma membrane
421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	mAb & s.m.	plasma membrane
422109	S73265	Hs.1473	gastrin-releasing peptide	diag	secreted
422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	diag	secreted
422282	AF019225	Hs.114309	apolipoprotein L	diag	secreted
422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	s.m.	nuclear
422424	AI186431	Hs.296638	prostate differentiation factor	diag	extracellular
422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	s.m.	cytoplasm
422809	AK001379	Hs.121028	hypothetical protein FLJ10549	s.m.	nuclear
422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	diag	extracellular
422956	BE545072	Hs.122579	ECT2 protein (Epithelial cell transformi	CTL & s.m.	
423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	diag	
423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	mAb & diag & s.m.	secreted
423961	D13666	Hs.136348	perforin (OSF-2os)	mAb & diag	extracellular
424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibito	diag	secreted
424381	AA285249	Hs.146329	protein kinase Chk2	s.m.	nuclear

	424502	AF242388	Hs.149585	lengsin	s.m.	cytoplasmic
	424503	NM_002205	Hs.149609	Integrin, alpha 5 (fibronectin receptor,	mAb & s.m.	plasma membrane
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	diag	extracellular
5	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin	mAb & diag & s.m.	secreted
	425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	s.m.	cytoplasmic
	425550	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	mAb	plasma membrane
	425734	AF056209	Hs.159396	peptidylglycine alpha-amidating monooxyg	s.m.	
	425776	U25128	Hs.159499	parathyroid hormone receptor 2	mAb & diag	plasma membrane
10	425852	AK001504	Hs.159651	death receptor 6, TNF superfamily member	mAb & s.m.	plasma membrane
	426215	AW963419	Hs.155223	stanniocalcin 2	mAb & diag	secreted
	426427	M86699	Hs.169840	TTK protein kinase	CTL & s.m.	nuclear
	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	mAb & diag	secreted
	427335	AA448542	Hs.251877	G antigen 7B	CTL	cytoplasmic
	427747	AW411425	Hs.180655	serine/threonine kinase 12	s.m.	cytoplasmic
15	428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	diag	
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	mAb & diag & s.m.	extracellular
	428450	NM_014791	Hs.184339	KIAA0175 gene product	s.m.	nuclear
	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to	s.m.	nuclear
20	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	mAb & s.m.	plasma membrane
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	CTL & s.m.	nuclear
	428698	AA852773	Hs.334838	KIAA1866 protein	mAb	
	428748	AW593206	Hs.98785	Ksp37 protein	diag	extracellular
	428758	AA433988	Hs.98502	CA125 antigen; mucin 16	diag	mitochondria*
	428969	AF120274	Hs.194689	artemin	diag	extracellular
25	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	mAb & s.m.	plasma membrane
	429263	AA019004	Hs.198396	ATP-binding cassette, sub-family A (ABC1	mAb & s.m.	plasma membrane
	429547	AW009166	Hs.99376	ESTs	diag	secreted
	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas	mAb & diag	secreted
30	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	s.m.	
	430488	BE062109	Hs.241551	chloride channel, calcium activated, fam	mAb & s.m.	plasma membrane
	431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precu	diag	extracellular
	431515	NM_012152	Hs.258583	endothelial differentiation, lysophospha	mAb & s.m.	plasma membrane
	431846	BE019924	Hs.271580	uroplakin 1B	mAb & diag	plasma membrane
35	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	mAb & diag	plasma membrane
	432201	AI538613	Hs.298241	Transmembrane protease, serine 3	mAb & diag & s.m.	plasma membrane
	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	s.m.	nuclear
	435505	AF200492	Hs.211238	interleukin-1 homolog 1	diag	secreted
	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	s.m.	
40	437016	AU076916	Hs.5398	guanine monophosphate synthetase	s.m.	cytoplasm
	437044	AL035864	Hs.69517	differentially expressed in Fanconi's an	CTL	ER
	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti	CTL	nuclear
	437852	BE001836	Hs.256897	ESTs, Weakly similar to dJ365012.1 [H.sa	mAb & s.m.	plasma membrane
	439223	AW238299	Hs.250618	UL16 binding protein 2	mAb	plasma membrane
45	439477	W69813	Hs.58042	ESTs, Moderately similar to GFR3_HUMAN G	mAb & s.m.	
	439606	W79123	Hs.58561	G protein-coupled receptor 87	mAb & s.m.	plasma membrane
	439738	BE246502	Hs.9598	sema domain, immunoglobulin domain (Ig),	mAb & s.m.	plasma membrane
	440006	AK000517	Hs.6844	NALP2 protein; PYRIN-Containing APAF1-II	s.m.	nuclear
	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	s.m.	
50	442117	AW664964	Hs.128899	ESTs; hypothetical protein for IMAGE:447	mAb & s.m.	plasma membrane
	443247	BE614387	Hs.333893	c-Myc target JPO1	CTL	extracellular*
	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	CTL	
	443859	NM_013409	Hs.9914	folliculin	diag	extracellular
	444006	BE395085	Hs.10086	type I transmembrane protein Fn14	mAb	plasma membrane
55	444371	BE540274	Hs.239	forkhead box M1	s.m.	nuclear
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	diag	secreted
	444781	NM_014400	Hs.11850	GPI-anchored metastasis-associated prote	mAb & diag	plasma membrane
	445537	AJ245671	Hs.12844	EGF-like domain, multiple 6	mAb & diag	secreted
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	diag	secreted
60	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	diag	extracellular
	447033	AI357412	Hs.157601	ESTs	CTL & diag	secreted
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	CTL	
	448243	AW369771	Hs.52620	Integrin, beta 8	mAb & s.m.	plasma membrane
	448844	AI581519	Hs.177164	ESTs	mAb & s.m.	
65	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	mAb	plasma membrane
	449722	BE280074	Hs.23960	cyclin B1	s.m.	cytoplasm
	450001	NM_001044	Hs.406	solute carrier family 6 (neurotransmitte	mAb & s.m.	plasma membrane
	450376	AA009647		a disintegrin and metalloproteinase doma	mAb & diag & s.m.	plasma membrane
	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-	mAb & diag	plasma membrane
70	450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	diag	secreted
	451668	Z43948	Hs.326444	cartilage acidic protein 1	mAb & diag	plasma membrane
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	diag	
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	diag	extracellular
	452747	BE153855	Hs.61460	Ig superfamily receptor LNIR	mAb	plasma membrane
75	452838	U65011	Hs.30743	preferentially expressed antigen in mela	CTL	nuclear
	453968	AA847843	Hs.62711	High mobility group (nonhistone chromoso	CTL & s.m.	nuclear
	457489	AI693815	Hs.127179	cryptic gene	diag	secreted

TABLE 14B

80 Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey CAT Number Accession

WO 02/086443

PCT/US02/12476

414883 15024_1 AA926960 AA926959 W76521 W24270 W21526 AA037172 BE267636 H83186 AA469909 N86396 AA001348 BE535736 AA081745 BE566245
AA082436 H72525 H77575 N49786 W80565 H78746 BE569085 W04339 R98127 T55938 BE279271 AW960304 T29812 AA476873 BE297387
AA292753 AA177048 NM_001826 X54941 BE314366 AA908783 AI719075 BE270172 BE269819 AA869955 AI204630 W25243 AI935150
AA872039 W72395 T99630 AI422691 H98460 N31428 BE265916 H03265 AI857576 AA776920 AA910844 AA459522 AA293140 AW514667
R75953 AW662396 AA662522 AI865147 AI423153 AW262230 AA584410 AA583187 AW024595 AW069734 AI828996 AA282997 AA876046
AW613002 AA527373 AW972459 AI831360 AA621337 AA100926 AA772418 AA594628 AI033892 W95096 AI034317 AA398727 AI085031
N95210 AI459432 AI041437 AA932124 AA627684 AA935829 AI004827 AI423513 AI094597 H42079 R54703 AI630359 AA617681 AA978045
AA643280 W44561 AI991988 AI537692 AI090262 AA740817 AI312104 AI911822 AA416871 AI185409 AA129784 AA701623 AI075239
AI139549 AA633648 AI339996 AI336880 AA399239 AI078708 AI085351 AI362835 AI346618 AI146955 AI989380 AI348243 N92892 AA765850
AI494230 AI278887 AA962596 AI492600 W80435 AA001979 R97424 AI129015 N24127 AA157451 AA235549 AA459292 AA037114 AA129785
AI494211 AW059601 AW886710 R92790 N59755 AI361128 AW589407 H47725 H97534 H48076 H48450 T99631 AW300758 H03431 R76789
AA954344 H77576 R96823 AI457100 N92845 N49682 H42038 BE220698 BE220715 H99552 AA701624 N74173 R54704 H79520 H72923
H03266 BE261919 AA769633 AA480310 AA507454 AA910586 AI203723 AW104725 W25611 W25071 T88980 H03513 T77589 R99156
W95095 R97470 AA702275 T77551 AA911952 H82956 N83673 AA283672
15 450375 83327_1 AA009647 AA131254 AA374293 AW954405 H04410 AW606284 AA151166 BE157467 BE157601 H04384 W46291 AW663674 H04021 H01532
AA190993 H03231 H59605 H01642 AA852676 AA113758 AA626915 AA746952 AI181014 AA099554 R69067

TABLE 14C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA
sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:469-495.
Strand: Indicates DNA strand from which exons were predicted.
25 NT_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NT_position
402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076

TABLE 15A: Information for all sequences in Table 16

Table 15A shows the Seq ID No, Pkey, ExAccn, UnigenelD, and Unigene Title for all of the sequences in Table 16.

5 Table 15B show the accession numbers for those Pkey's lacking UnigenelD's for table 15A. For each probaset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

10 Table 15C show the genomic positioning for those Pkey's lacking Unigene ID's and accession numbers in table 15A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

15 Seq ID No: Sequence ID number
Pkey: Unique Eos probaset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigenelD: Unigene number
Unigene Title: Unigene gene title

20	Seq ID No:	Pkey	ExAccn	UnigenelD	Unigene Title
	Seq ID No: 1 & 2	410407	X66839	Hs.63287	carbonic anhydrase IX
	Seq ID No: 3 & 4	412719	AW016610	Hs.816	ESTs
	Seq ID No: 5 & 6	417034	NM_006183	Hs.80862	neurotensin
25	Seq ID No: 7 & 8	430486	BE082109	Hs.241551	chloride channel, calcium activated, fam
	Seq ID No: 9 & 10	407788	BE514982	Hs.38991	S100 calcium-binding protein A2
	Seq ID No: 11 & 12	407788	BE514982	Hs.38991	S100 calcium-binding protein A2
	Seq ID No: 13 & 14	407788	BE514982	Hs.38991	S100 calcium-binding protein A2
	Seq ID No: 15 & 16	407788	BE514982	Hs.38991	S100 calcium-binding protein A2
30	Seq ID No: 17 & 18	439285	AL133916		hypothetical protein FLJ20093
	Seq ID No: 19 & 20	413753	U17760	Hs.75517	laminin, beta 3 (nlcin (125kD), kalinin
	Seq ID No: 21 & 22	120486	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog
	Seq ID No: 23 & 24	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen
	Seq ID No: 25 & 26	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines
35	Seq ID No: 27 & 28	423573	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage
	Seq ID No: 29 & 30	452838	U65011	Hs.30743	preferentially expressed antigen in mela
	Seq ID No: 31 & 32	418663	AK001100	Hs.41690	desmocollin 3
	Seq ID No: 33 & 34	418663	AK001100	Hs.41690	desmocollin 3
	Seq ID No: 35 & 36	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibitor
40	Seq ID No: 37 & 38	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas
	Seq ID No: 39 & 40	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad
	Seq ID No: 41 & 42	431846	BE019924	Hs.271580	uropod 1B
	Seq ID No: 43 & 44	418830	BE513731	Hs.88959	hypothetical protein MGC4816
	Seq ID No: 45 & 46	424098	AF077374	Hs.139322	small proline-rich protein 3
45	Seq ID No: 47 & 48	443648	AI085377	Hs.143610	ESTs
	Seq ID No: 49	311034	BE567130	Hs.311389	ESTs, Highly similar to NKGD_HUMAN NKG2-
	Seq ID No: 50 & 51	408522	AI541214	Hs.46320	Small proline-rich protein SPRK (human,
	Seq ID No: 52 & 53	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL
	Seq ID No: 54 & 55	435505	AF200492	Hs.211238	interleukin-1 homolog 1
50	Seq ID No: 56 & 57	417366	BE185289	Hs.1076	small proline-rich protein 1B (cornifin)
	Seq ID No: 58 & 59	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta
	Seq ID No: 60 & 61	441020	W79283	Hs.35962	ESTs
	Seq ID No: 62 & 63	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys
	Seq ID No: 64 & 65	429538	BE182592	Hs.11261	small proline-rich protein 2A
55	Seq ID No: 66 & 67	448733	NM_005629	Hs.187958	solute carrier family 6 (neurotransmitte
	Seq ID No: 68 & 69	444371	BE540274	Hs.239	forkhead box M1
	Seq ID No: 70 & 71	444371	BE540274	Hs.239	forkhead box M1
	Seq ID No: 72 & 73	444371	BE540274	Hs.239	forkhead box M1
	Seq ID No: 74 & 75	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias
60	Seq ID No: 76 & 77	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias
	Seq ID No: 78 & 79	429259	AA420450	Hs.292911	Plakophilin
	Seq ID No: 80 & 81	426440	BE382756	Hs.169902	solute carrier family 2 (facilitated glu
	Seq ID No: 82 & 83	437044	AL035864	Hs.69517	differentially expressed in Fanconi's an
	Seq ID No: 84 & 85	423662	AK001035	Hs.130881	B-cell CLL/lymphoma 11A (zinc finger pro
65	Seq ID No: 86 & 87	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino
	Seq ID No: 88 & 89	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3
	Seq ID No: 90 & 91	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor
	Seq ID No: 92 & 93	423634	AW559908	Hs.1690	heparin-binding growth factor binding pr
	Seq ID No: 94 & 95	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated
70	Seq ID No: 96 & 97	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E. coli Re
	Seq ID No: 98 & 99	425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic
	Seq ID No: 100 & 101	449003	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu o
	Seq ID No: 102 & 103	431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3
	Seq ID No: 104 & 105	409103	AF251237	Hs.112208	XAGE-1 protein
75	Seq ID No: 106 & 107	417542	J04129	Hs.82269	progesterone-associated endometrial prote
	Seq ID No: 108 & 109	428471	X57348	Hs.184510	stratiferin
	Seq ID No: 110 & 111	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member
	Seq ID No: 112 & 113	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2
	Seq ID No: 114 & 115	418203	X54942	Hs.83758	CDC28 protein kinase 2
80	Seq ID No: 116	447343	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m
	Seq ID No: 117 & 118	437018	AU076916	Hs.5398	guanine monophosphate synthetase
	Seq ID No: 119 & 120	449230	BE613348	Hs.211579	melanoma cell adhesion molecule
	Seq ID No: 121 & 122	446989	AK001898	Hs.16740	hypothetical protein FLJ11036
	Seq ID No: 123 & 124	457819	AA057484	Hs.35406	ESTs, Highly similar to unnamed protein
85	Seq ID No: 125 & 126	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B

5	Seq ID No: 127 & 128	414430	AI346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1
	Seq ID No: 129 & 130	418462	BE001596	Hs.85266	integrin, beta 4
	Seq ID No: 131 & 132	100688	L05424	Hs.169610	CD44 antigen (homing function and Indian
	Seq ID No: 133 & 134	458933	AI638429	Hs.24763	RAN binding protein 1
	Seq ID No: 135 & 136	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me
10	Seq ID No: 137 & 138	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me
	Seq ID No: 139 & 140	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me
	Seq ID No: 141 & 142	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me
	Seq ID No: 143 & 144	446269	AW263155	Hs.14559	hypothetical protein FLJ10540
	Seq ID No: 145 & 146	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur
15	Seq ID No: 147 & 148	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con
	Seq ID No: 149 & 150	440325	NM_003812	Hs.7164	a disintegrin and metalloproteinase doma
	Seq ID No: 151 & 152	439606	W79123	Hs.58561	G protein-coupled receptor 87
	Seq ID No: 153 & 154	453884	AA355925	Hs.36232	KIAA0186 gene product
	Seq ID No: 155 & 156	453884	AA355925	Hs.36232	KIAA0186 gene product
20	Seq ID No: 157 & 158	453884	AA355925	Hs.36232	KIAA0186 gene product
	Seq ID No: 159 & 160	453884	AA355925	Hs.36232	KIAA0186 gene product
	Seq ID No: 161 & 162	404877			NM_005365:Homo sapiens melanoma antigen,
	Seq ID No: 163 & 164	413129	AF292100	Hs.104613	RP42 homolog
	Seq ID No: 165 & 166	413281	AA861271	Hs.222024	transcription factor BMAL2
25	Seq ID No: 167 & 168	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote
	Seq ID No: 169 & 170	416819	U77735	Hs.80205	pim-2 oncogene
	Seq ID No: 171 & 172	451320	AW118072		diacylglycerol kinase, zeta (104kD)
	Seq ID No: 173 & 174	418543	NM_005329	Hs.85962	hyaluronan synthase 3
	Seq ID No: 175 & 176	454034	NM_000691	Hs.575	aldehyde dehydrogenase 3 family, member
30	Seq ID No: 177 & 178	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)
	Seq ID No: 179 & 180	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 181 & 182	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 183 & 184	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 185 & 186	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
35	Seq ID No: 187 & 188	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 189 & 190	419121	AA374372	Hs.89626	parathyroid hormone-like hormone
	Seq ID No: 191 & 192	448993	AI471630	Hs.8127	KIAA0144 gene product
	Seq ID No: 193 & 194	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR
	Seq ID No: 195 & 196	430393	BE185030	Hs.241305	estrogen-responsive B box protein
40	Seq ID No: 197 & 198	425057	AA826434	Hs.1619	achaete-scute complex (Drosophila) homol
	Seq ID No: 199 & 200	420462	AF050147	Hs.97932	chondromodulin 1 precursor
	Seq ID No: 201 & 202	102963	X02404	Hs.274534	calcitonin-related polypeptide, beta
	Seq ID No: 203 & 204	100576	X00356	Hs.37058	calcitonin/calcitonin-related polypeptid
	Seq ID No: 205 & 206	101175	U82671	Hs.36980	melanoma antigen, family A, 2
45	Seq ID No: 207 & 208	429038	AL023513	Hs.194766	seizure related gene 6 (mouse)-like
	Seq ID No: 209 & 210	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)
	Seq ID No: 211 & 212	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)
	Seq ID No: 213 & 214	131927	AJ003112	Hs.34780	doublecortin; lissencephaly, X-linked (d
	Seq ID No: 215 & 216	428182	BE386042	Hs.293317	ESTs, Weakly similar to GGC1_HUMAN G ANT
50	Seq ID No: 217 & 218	427335	AA448542	Hs.251677	G antigen 78
	Seq ID No: 219 & 220	409420	Z15008	Hs.54451	laminin, gamma 2 (niclin (100kD), kalini
	Seq ID No: 221 & 222	114346	AL137256	Hs.130489	ATPase, aminophospholipid transporter-II
	Seq ID No: 223 & 224	438956	W00847	Hs.135056	Human DNA sequence from clone RP5-850E9
	Seq ID No: 225 & 226	404440			NM_021048:Homo sapiens melanoma antigen,
55	Seq ID No: 227 & 228	415669	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibitor
	Seq ID No: 229 & 230	103312	Y12642	Hs.3185	lysosomal
	Seq ID No: 231 & 232	320843	BE069288	Hs.34744	Homo sapiens mRNA; cDNA DKFZp547C136 (fr
	Seq ID No: 233	429065	AI753247	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT
	Seq ID No: 234 & 235	446102	AW166067	Hs.317694	ESTs
60	Seq ID No: 236 & 237	330495	U47924	Hs.71642	guanine nucleotide binding protein (G pr
	Seq ID No: 238	413573	AI733859	Hs.149089	ESTs
	Seq ID No: 239 & 240	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to
	Seq ID No: 241 & 242	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to
	Seq ID No: 243 & 244	332180	AF134160	Hs.7327	claudin 1
65	Seq ID No: 245	437915	AI637993	Hs.202312	Homo sapiens clone N11 Ntera2D1 teratoca
	Seq ID No: 246 & 247	441553	AA281219	Hs.121296	ESTs
	Seq ID No: 248 & 249	331692	AI683487	Hs.152213	wingless-type MMTV integration site fami
	Seq ID No: 250 & 251	429413	NM_014058	Hs.201877	DESC1 protein
	Seq ID No: 252 & 253	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis
70	Seq ID No: 254 & 255	448357	N20169	Hs.108923	RAB38, member RAS oncogene family
	Seq ID No: 256 & 257	446292	AF081497	Hs.279682	Rh type C glycoprotein
	Seq ID No: 258 & 259	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h
	Seq ID No: 260 & 261	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1
	Seq ID No: 262 & 263	424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibitor
75	Seq ID No: 264 & 265	439223	AW238299	Hs.250618	UL16 binding protein 2
	Seq ID No: 266 & 267	429228	AI553633	Hs.326447	ESTs
	Seq ID No: 268 & 269	409757	NM_001898	Hs.123114	cystatin SN
	Seq ID No: 270 & 271	411089	AA456454	Hs.214291	cell division cycle 2-like 1 (PITSLRE pr
	Seq ID No: 272 & 273	436511	AA721252	Hs.291502	ESTs
80	Seq ID No: 274 & 275	428969	AF120274	Hs.194689	artemin
	Seq ID No: 276 & 277	428969	AF120274	Hs.194689	artemin
	Seq ID No: 278 & 279	428969	AF120274	Hs.194689	artemin
	Seq ID No: 280 & 281	428969	AF120274	Hs.194689	artemin
	Seq ID No: 282	407137	T97307		gbye53h05.s1 Soares fetal liver spleen
85	Seq ID No: 283 & 284	412723	AA648459	Hs.335951	hypothetical protein AF301222
	Seq ID No: 285 & 286	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-
	Seq ID No: 287 & 288	405770			NM_002362:Homo sapiens melanoma antigen,
	Seq ID No: 289 & 290	439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13
	Seq ID No: 291 & 292	414774	X02419	Hs.77274	plasminogen activator, urokinase

5	Seq ID No: 293 & 294	424629	M90656	Hs.151393	glutamate-cysteine ligase, catalytic sub
	Seq ID No: 295 & 296	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypothe
	Seq ID No: 297 & 298	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypothe
	Seq ID No: 299 & 300	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypothe
	Seq ID No: 301 & 302	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypothe
	Seq ID No: 303 & 304	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypothe
	Seq ID No: 305 & 306	453968	AA847843	Hs.62711	High mobility group (nonhistone chromoso
	Seq ID No: 307 & 308	403478			NM_022342:Homo sapiens kinesin protein 9
10	Seq ID No: 309	441526	AW241867	Hs.127728	ESTs
	Seq ID No: 310 & 311	434105	AW952124	Hs.13094	presenilins associated rhomboid-like pro
	Seq ID No: 312 & 313	428810	AF068236	Hs.193788	nitric oxide synthase 2A (inducible, hep
	Seq ID No: 314 & 315	413691	AB023173	Hs.75478	ATPase, Class VI, type 11B
	Seq ID No: 316 & 317	423934	U89995	Hs.159234	forkhead box E1 (thyroid transcription f
15	Seq ID No: 318 & 319	409228	R16811	Hs.22010	ESTs, Weakly similar to 2109260A B cell
	Seq ID No: 320 & 321	425734	AF056209	Hs.159396	peptidylglycine alpha-amidating monoox
	Seq ID No: 322 & 323	413582	AW295647	Hs.71331	hypothetical protein MGC5350
	Seq ID No: 324 & 325	438403	AA806607	Hs.292206	ESTs
	Seq ID No: 326 & 327	403329			unnamed protein product [Homo sapiens]
20	Seq ID No: 328 & 329	409893	AW247090	Hs.57101	minichromosome maintenance deficient (S
	Seq ID No: 330 & 331	119073	BE245360	Hs.279477	v-ets erythroblastosis virus E26 oncogen
	Seq ID No: 332 & 333	113195	H83265	Hs.8881	ESTs, Weakly similar to S41044 chromosom
	Seq ID No: 334 & 335	102283	AW161552	Hs.83381	guanine nucleotide binding protein 11
	Seq ID No: 336 & 337	101345	NM_005795	Hs.152175	calcitonin receptor-like
25	Seq ID No: 338 & 339	103280	U84722	Hs.76206	cadherin 5, type 2, VE-cadherin (vascula
	Seq ID No: 340 & 341	102012	BE259035	Hs.118400	singed (Drosophila)-like (sea urchin fas
	Seq ID No: 342 & 343	105729	H46612	Hs.293815	Homo sapiens HSPC285 mRNA, partial cds
	Seq ID No: 344 & 345	134299	AW580939	Hs.97199	complement component C1q receptor
	Seq ID No: 346 & 347	412719	AW016610	Hs.816	ESTs
30	Seq ID No: 348 & 349	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL
	Seq ID No: 350 & 351	128924	BE279383	Hs.26557	plakophilin 3
	Seq ID No: 352 & 353	100486	T19006	Hs.10842	RAN, member RAS oncogene family
	Seq ID No: 354 & 355	419121	AA374372	Hs.89626	parathyroid hormone-like hormone
	Seq ID No: 356 & 357	409469	D86407	Hs.54481	low density lipoprotein receptor-related
35	Seq ID No: 358 & 359	330493	M27826		endogenous retroviral protease
	Seq ID No: 360 & 361	417866	AW067903	Hs.82772	collagen, type XI, alpha 1
	Seq ID No: 362 & 363	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4
	Seq ID No: 364 & 365	437016	AU076916	Hs.5398	guanine monophosphate synthetase
	Seq ID No: 366 & 367	429612	AF062649	Hs.252587	pituitary tumor-transforming 1
40	Seq ID No: 368 & 369	440704	M69241	Hs.162	insulin-like growth factor binding prote
	Seq ID No: 370 & 371	431221	AA449015	Hs.286145	SRB7 (suppressor of RNA polymerase B, ye
	Seq ID No: 372 & 373	431565	AF161470	Hs.260622	butyrate-induced transcript 1
	Seq ID No: 374 & 375	431565	AF161470	Hs.260622	butyrate-induced transcript 1
	Seq ID No: 376 & 377	132354	BE185289	Hs.1076	small proline-rich protein 1B (cornifin)
45	Seq ID No: 378 & 379	424441	X14850	Hs.147097	H2A histone family, member X
	Seq ID No: 380 & 381	103768	AF086009	Hs.296398	gb:Homo sapiens full length insert cDNA
	Seq ID No: 382 & 383	417512	X76534	Hs.82226	glycoprotein (transmembrane) numb
	Seq ID No: 384 & 385	425266	J00077	Hs.155421	alpha-fetoprotein
	Seq ID No: 386 & 387	424503	NM_002205	Hs.149609	Integrin, alpha 5 (fibronectin receptor,
50	Seq ID No: 388 & 389	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin
	Seq ID No: 390 & 391	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial
	Seq ID No: 392 & 393	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial
	Seq ID No: 394 & 395	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino
	Seq ID No: 396 & 397	415138	C18356	Hs.295944	tissue factor pathway inhibitor 2
55	Seq ID No: 398 & 399	418506	AA084248	Hs.85339	G protein-coupled receptor 39
	Seq ID No: 400 & 401	423961	D13666	Hs.136348	perostin (OSF-2os)
	Seq ID No: 402 & 403	414812	X72755	Hs.77367	monokine induced by gamma interferon
	Seq ID No: 404 & 405	417433	BE270268	Hs.82128	ST4 oncofetal trophoblast glycoprotein
	Seq ID No: 406 & 407	417433	BE270266	Hs.82128	ST4 oncofetal trophoblast glycoprotein
60	Seq ID No: 408 & 409	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse
	Seq ID No: 410 & 411	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy
	Seq ID No: 412 & 413	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypothe
	Seq ID No: 414 & 415	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated
	Seq ID No: 416 & 417	411789	AF245505	Hs.72167	Adfcan
65	Seq ID No: 418 & 419	428698	AA852773	Hs.334838	KIAA1866 protein
	Seq ID No: 420 & 421	450098	W27249	Hs.8109	hypothetical protein FLJ21080
	Seq ID No: 422 & 423	421552	AF026692	Hs.105700	secreted frizzled-related protein 4
	Seq ID No: 424 & 425	452747	BE153855	Hs.61460	Ig superfamily receptor LNIR
	Seq ID No: 426 & 427	450375	AA009647		a disintegrin and metalloproteinase doma
70	Seq ID No: 428 & 429	426215	AW963419	Hs.155223	stanniocalcin 2
	Seq ID No: 430 & 431	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin
	Seq ID No: 432 & 433	432201	AI538613	Hs.298241	Transmembrane protease, serine 3
	Seq ID No: 434 & 435	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph
	Seq ID No: 436 & 437	442117	AW664964	Hs.128899	ESTs; hypothetical protein for IMAGE:447
75	Seq ID No: 438 & 439	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn
	Seq ID No: 440 & 441	447033	AI357412	Hs.157601	ESTs
	Seq ID No: 442 & 443	447033	AI357412	Hs.157601	ESTs
	Seq ID No: 444 & 445	447033	AI357412	Hs.157601	ESTs
	Seq ID No: 446 & 447	115522	BE614387	Hs.333893	c-Myc target JPO1
80	Seq ID No: 448 & 449	410418	D31382	Hs.63325	transmembrane protease, serine 4
	Seq ID No: 450 & 451	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119
	Seq ID No: 452 & 453	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119
	Seq ID No: 454 & 455	452461	N78223	Hs.108106	transcription factor
	Seq ID No: 456 & 457	412420	AL035668	Hs.73853	bone morphogenetic protein 2
85	Seq ID No: 458 & 459	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara
	Seq ID No: 460 & 461	407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon

	Seq ID No: 462 & 463	437852	BE001836	Hs.256897	ESTs, Weakly similar to dJ365O12.1 [H.s.a
	Seq ID No: 464 & 465	402075			ENSP00000251056*:Plasma membrane calcium
	Seq ID No: 466 & 467	421110	AJ260717	Hs.1355	cathepsin E
5	Seq ID No: 468 & 469	451668	Z43948	Hs.326444	cartilage acidic protein 1
	Seq ID No: 470 & 471	451668	Z43948	Hs.326444	cartilage acidic protein 1
	Seq ID No: 472 & 473	451668	Z43948	Hs.326444	cartilage acidic protein 1
	Seq ID No: 474 & 475	422282	AF019225	Hs.114309	apolipoprotein L
	Seq ID No: 476 & 477	425852	AK001504	Hs.159651	death receptor 6, TNF superfamily member
10	Seq ID No: 478 & 479	439738	BE246502	Hs.9598	sema domain, immunoglobulin domain (Ig),
	Seq ID No: 480 & 481	427747	AW411425	Hs.180655	serine/threonine kinase 12
	Seq ID No: 482 & 483	420281	AI623693	Hs.323494	Predicted cation efflux pump
	Seq ID No: 484 & 485	405932			C15000305:gi 3806122 gb AAC69198.1 (AF0
	Seq ID No: 486 & 487	405932			C15000305:gi 3806122 gb AAC69198.1 (AF0
15	Seq ID No: 488 & 489	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane
	Seq ID No: 490 & 491	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy
	Seq ID No: 492 & 493	417079	U65590	Hs.81134	Interleukin 1 receptor antagonist
	Seq ID No: 494 & 495	430890	X54232	Hs.2699	glypican 1
	Seq ID No: 496 & 497	419721	NM_001650	Hs.288650	aquaporin 4
20	Seq ID No: 498 & 499	444471	AB020684	Hs.11217	KIAA0877 protein
	Seq ID No: 500 & 501	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote
	Seq ID No: 502 & 503	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly
	Seq ID No: 504 & 505	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro
	Seq ID No: 506 & 507	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro
25	Seq ID No: 508 & 509	450001	NM_001044	Hs.406	solute carrier family 6 (neurotransmitte
	Seq ID No: 510 & 511	410407	X66839	Hs.63287	carbonic anhydrase IX
	Seq ID No: 512 & 513	309931	AW341683		gb:hd13d01.x1 Soares_NFL_T_GBC_S1 Homo s
	Seq ID No: 514 & 515	412719	AW016610	Hs.816	ESTs
	Seq ID No: 516 & 517	417034	NM_006183	Hs.80962	neurotensin
30	Seq ID No: 518 & 519	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam
	Seq ID No: 520 & 521	413753	U17760	Hs.75517	laminin, beta 3 (nicein (125kD), kalini
	Seq ID No: 522 & 523	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen
	Seq ID No: 524 & 525	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage
	Seq ID No: 526 & 527	418663	AK001100	Hs.41690	desmocollin 3
35	Seq ID No: 528 & 529	418663	AK001100	Hs.41690	desmocollin 3
	Seq ID No: 530 & 531	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas
	Seq ID No: 532 & 533	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad
	Seq ID No: 534 & 535	431846	BE019924	Hs.271580	uroplakin 1B
	Seq ID No: 536 & 537	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL
40	Seq ID No: 538 & 539	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta
	Seq ID No: 540 & 541	437044	AL035864	Hs.69517	differentially expressed in Fanconi's an
	Seq ID No: 542 & 543	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino
	Seq ID No: 544 & 545	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3
	Seq ID No: 546 & 547	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor
45	Seq ID No: 548 & 549	431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3
	Seq ID No: 550 & 551	417542	J04129	Hs.82269	progesterone-associated endometrial prote
	Seq ID No: 552 & 553	449230	BE613348	Hs.211579	melanoma cell adhesion molecule
	Seq ID No: 554 & 555	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma
	Seq ID No: 556 & 557	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma
50	Seq ID No: 558 & 559	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B
	Seq ID No: 560 & 561	418462	BE001596	Hs.85266	Integrin, beta 4
	Seq ID No: 562 & 563	410274	AA381807	Hs.61762	hypoxia-inducible protein 2
	Seq ID No: 564 & 565	439606	W79123	Hs.58561	G protein-coupled receptor 87
	Seq ID No: 566 & 567	404877			NM_005365:Homo sapiens melanoma antigen,
55	Seq ID No: 568 & 569	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote
	Seq ID No: 570 & 571	418543	NM_005329	Hs.85962	hyaluronan synthase 3
	Seq ID No: 572 & 573	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 574 & 575	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 576 & 577	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
60	Seq ID No: 578 & 579	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 580 & 581	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 582 & 583	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 584 & 585	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR
	Seq ID No: 586 & 587	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)
65	Seq ID No: 588 & 589	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)
	Seq ID No: 590 & 591	409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini
	Seq ID No: 592 & 593	332180	AF134160	Hs.7327	claudin 1
	Seq ID No: 594 & 595	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,
	Seq ID No: 596 & 597	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,
70	Seq ID No: 598 & 599	439223	AW238299	Hs.250618	UL16 binding protein 2
	Seq ID No: 600 & 601	409757	NM_001898	Hs.123114	cystatin SN
	Seq ID No: 602 & 603	428969	AF120274	Hs.194689	artemin
	Seq ID No: 604 & 605	428969	AF120274	Hs.194689	artemin
	Seq ID No: 606 & 607	428969	AF120274	Hs.194689	artemin
75	Seq ID No: 608 & 609	428969	AF120274	Hs.194689	artemin
	Seq ID No: 610 & 611	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-
	Seq ID No: 612 & 613	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-
	Seq ID No: 614 & 615	414774	X02419	Hs.77274	plasminogen activator, urokinase
	Seq ID No: 616 & 617	407944	R34008	Hs.239727	desmocollin 2
	Seq ID No: 618 & 619	407944	R34008	Hs.239727	desmocollin 2
80	Seq ID No: 620 & 621	457489	AI693815	Hs.127179	cryptic gene
	Seq ID No: 622 & 623	429547	AW009166	Hs.99376	ESTs
	Seq ID No: 624 & 625	407242	M18728		gb:Human nonspecific crossreacting anti
	Seq ID No: 626 & 627	407242	M18728		gb:Human nonspecific crossreacting anti
	Seq ID No: 628 & 629	407242	M18728		gb:Human nonspecific crossreacting anti
85	Seq ID No: 630 & 631	444006	BE395085	Hs.10086	type 1 transmembrane protein Fn14

Seq ID No: 632 & 633	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase domain
Seq ID No: 634 & 635	422109	S73265	Hs.1473	gastrin-releasing peptide
Seq ID No: 636 & 637	419235	AW470411	Hs.288433	neurotrophin
Seq ID No: 638 & 639	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induced
Seq ID No: 640 & 641	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cyt)
Seq ID No: 642 & 643	431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precursor
Seq ID No: 644 & 645	448243	AW369771	Hs.52620	integrin, beta 8
Seq ID No: 646 & 647	426427	M86699	Hs.169840	TTK protein kinase
Seq ID No: 648 & 649	445537	AJ245871	Hs.12844	EGF-like domain, multiple 6
Seq ID No: 650 & 651	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6
Seq ID No: 652 & 653	428450	NM_014791	Hs.184339	KIAA0175 gene product
Seq ID No: 654 & 655	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,
Seq ID No: 656 & 657	453392	U23752	Hs.32964	SRX (sex determining region Y)-box 11
Seq ID No: 658 & 659	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic)
Seq ID No: 660 & 661	425776	U25128	Hs.159499	parathyroid hormone receptor 2
Seq ID No: 662 & 663	425776	U25128	Hs.159499	parathyroid hormone receptor 2
Seq ID No: 664 & 665	431515	NM_012152	Hs.258583	endothelial differentiation, lysophosphatidyl
Seq ID No: 666 & 667	419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7
Seq ID No: 668 & 669	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino acid
Seq ID No: 670 & 671	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino acid
Seq ID No: 672 & 673	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino acid
Seq ID No: 674 & 675	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino acid
Seq ID No: 676 & 677	410001	AB041036	Hs.57771	kalikrein 11
Seq ID No: 678 & 679	426501	AW043782	Hs.293616	ESTs
Seq ID No: 680 & 681	408369	R38438	Hs.182575	solute carrier family 15 (H ⁺ ???) transport
Seq ID No: 682 & 683	445413	AA151342	Hs.12677	CGI-147 protein
Seq ID No: 684 & 685	422424	AI186431	Hs.296638	prostate differentiation factor
Seq ID No: 686 & 687	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,
Seq ID No: 688 & 689	420610	AI683183	Hs.99348	distal-less homeo box 5

TABLE 15B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
309931	AW341683	
330493	33264_5	M27826 R78416 AA307645 AW957879 AW957800 AA633529 H03662
439285	47065_1	AL133916 N79113 AF086101 N76721 AW950828 AA364013 AW955684 AI346341 AI887454 N54784 AI655270 AI421279 AW014882
		AA775552 N62351 N59253 AA626243 AI341407 BE175639 AA456968 AI358918 AA457077
450375	83327_1	AA009647 AA131254 AA374293 AW954405 H04410 AW606284 AA151186 BE157467 BE157601 H04384 W46291 AW663674 H04021 H01532
		AA190993 H03231 H59605 H01642 AA852876 AA113758 AA626915 AA746952 AI161014 AA099554 R69067
451320	86576_1	AW118072 AI631982 T15734 AA224195 AI701458 W20198 F26326 AA890570 N90552 AW071907 AI671352 AI375892 T03517 R88265
		AI124088 AA224388 AI084316 AI354686 T33652 AI140719 AI720211 T03490 AI372637 T15415 AW205836 AA630384 T03515 T33230
		AA017131 AA443303 T33623 AI222556 T33511 T33785 AI419606 D55612

TABLE 15C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
402075	8117407	Plus	121907-122035, 122804-122921, 124019-124161, 124455-124610, 126672-126076
403329	8518120	Plus	96450-96598
403478	9958258	Plus	116458-116564
404440	7528051	Plus	80430-81581
404877	1519284	Plus	1095-2107
405770	2735037	Plus	61057-62075
405932	7767812	Minus	123525-123713

Table 16

Seq ID NO: 1 DNA sequence
Nucleic Acid Accession #: NM_001216
Coding sequence: 43..1422

5	1	11	21	31	41	51	
10	GCCCGTACAC	ACCGTGTGCT	GGGACACCCC	ACAGTCAGCC	GCATGGCTCC	CCTGTGCCCC	60
	AGCCCTGGC	TCCCTCTGTT	GATCCCGGCC	CCTGCTCCAG	GCCTCACTGT	GCAACTGCTG	120
	CTGTCACTGC	TGCTTCTGAT	GCCTGTCCAT	CCCCAGAGGT	TGCCCCGGAT	GCAGGAGGAT	180
	TCCCCCTTGG	GAGGAGGCTC	TTCTGGGGAA	GATGACCCAC	TGGGCGAGGA	GGATCTGCCC	240
	AGTGAAGAGG	ATTCAACCCAG	AGAGGAGGAT	CCACCGGAG	AGGAGGATCT	ACCTGGAGAG	300
15	GAGGATCTAC	CTGGAGAGGA	GGATCTACCT	GAAGTTAAGC	CTAAATCAGA	AGAAGAGGGC	360
	TCCCTGAAGT	TAGAGGATCT	ACCTACTGTT	GAGGCTCCTG	GAGATCTCTA	AGAACCCAG	420
	AATAATGCCC	ACAGGGACAA	AGAAGGGGAT	GACCAGAGTC	ATTGGCGCTA	TGGAGCGCAC	480
	CGCCCTGGC	TCGCGGTGTC	CCCAGCCTGC	CGCGGCCGCT	TCCAGTCCCC	GGTGGATATC	540
	CGCCCCAGC	TCGCGCGCTT	CTGCCCCGCC	CTGCGCCCCC	TGGAATCTCT	GGGCTTCCAG	600
20	CTCCGCGCGC	TCCCTGCTGCT	GGCCTGCGC	AACAATGGCC	ACAGTGTGCA	ACTGACCTG	660
	CCTCCTGGGC	TAGAGATGGC	TCTGGGTCCC	GGGCGGGAGT	ACCGGCTCT	GCAGCTGCAT	720
	CTGCACTGGG	GGGCTCGAGG	TCGTCGCGGC	TCGGAGCACA	CTGTGGAAGG	CCACCGTTTC	780
	CCTGCGGAGA	TCACAGTGGT	TCACCTCAGC	ACCGCCTTTG	CCAGAGTTGA	CGAGGCCCTT	840
	GGGCGCCCGG	GAGGCGTGGC	CGTGTGTGGC	GCCTTTCTGG	AGGAGGGCCC	GGAGAAAAC	900
25	AGTGCTATG	AGCAGTGTCT	GTCTCGCTTG	GAAGAAATCG	CTGAGGAAGG	CTCAGAGACT	960
	CAGGTCCAG	GACTGGACAT	ATCTGCACTC	CTGCCCTCTG	ACTTCAGCCG	CTACTTCCAA	1020
	TATGAGGGGT	CTCTGACTAC	ACCGCCCTGT	GCCCAGGGTG	TCATCTGGAC	TGTGTTTAA	1080
	CAGACAGTGA	TGCTAGTGGC	TAAGCAGCTC	CACACCTCT	CTGACACCT	GTGGGACCT	1140
	GGTGAATCTC	GGCTACAGCT	GAATCTCCGA	CGCAGCGAGC	CTTTGAATGG	GCGAGTGATT	1200
30	GAGGCTCTCT	TCCCTGCTGCT	AGTGGACAGC	AGTCTCTGGG	CTGCTGAGCC	AGTCCAGCTG	1260
	AATTCCTGCC	TGGCTGCTGG	TGACATCTTA	GCCCTGTTT	TTGGCTCTCT	TTTGTCTGTC	1320
	ACCAGCGTCG	CGTTCCTTGT	CGAGATGAGA	AGGCAGCACA	GAAGGGGAAC	CAAAGGGGGT	1380
	GTGAGCTACC	GCCCAGCAGA	GGTAGCCGAG	ACTGGAGCCT	AGAGGCTGGA	TCTTGAGAAA	1440
	TGTGAGAAGC	CAGCCAGAGG	CATCTGAGGG	GGAGCCGGTA	ACTGTCTCTG	CCTGCTCATT	1500
35	ATGCCACTTC	CTTTAACTG	CCAAGAAATT	TTTTAAATA	AATATTATTA	AT	

Seq ID NO: 2 Protein sequence:
Protein Accession #: NP_001207

40	1	11	21	31	41	51	
	MAPLCPSPWL	PLLIPAPAPG	LTVQLLSLL	LMPVHPQRL	PRMOEDSPLG	GGSSGEDDPL	60
	GEEDLPSEED	SPREEDPPGE	EDLPGEEDLP	GEEDLPVKP	KSEEGSLKL	EDLPVTRAPG	120
	DPQEPQNNAH	RDKEGDDQSH	WRYGGDFPWF	RVSPACAGRF	QSPVDIRPQL	AAFCPALRPL	180
45	ELLGFLPEPL	PELRLRNNGH	SVQLTLPPGL	EMALGPGREY	RALQLHLHWG	AAGRPGSEHT	240
	VEGHRFPABE	HVHLSTAFAT	RVDEALGRPG	GLAVLAAPLE	EGPEENSAYE	QLLSRLIEIA	300
	EEGSETQVPG	LDISALLPSD	PSRYFQYEGS	LTPPCAQGV	IWTVFNQTVM	LSAKQLHTLS	360
	DTLWPGDSR	LQLNFRATQP	LNGRVIEASF	PAGVDSPPRA	AEFVQLNSCL	AAGDILALVF	420
	GLLPAVTSVA	FLVQMRQRH	RGTGKGVSYR	PAEVAETGA			

Seq ID NO: 3 DNA sequence
Nucleic Acid Accession #: BC013923
Coding sequence: 438-1391

55	1	11	21	31	41	51	
	AGCGGGGTG	TCTATTAAC	TGTTCAAAA	GTATCAGGAG	TTGTCAAGGC	AGAGAAGAGA	60
	GTGTTTGCA	AAGGGGAAA	GTAGTTTGCT	GCCTCTTTAA	GACTAGGACT	GAGAGAAAGA	120
	AGAGGAGAGA	GAAAGAAAGG	GAGAGAAGTT	TGAGCCCCAG	GCTTAAGCCT	TCCAAAAA	180
60	TAATAATAAC	AATCATCGGC	GGCGGCAGGA	TCGGCCAGAG	GAGGAGGGAA	CGGCTTTTT	240
	TGATCCTGAT	TCCAGTTTGC	CTCTCTCTTT	TTTTCCCCCA	AATTATTTCT	CGCCTGATTT	300
	TCCTCGGGGA	GCCCTGCGCT	CCCGACACCC	CGGCCCGCCT	CCCCTCCTCC	TCTCCCCCG	360
	CCCGCGGGCC	CCCCAAAGTC	CCGCGCGGGC	CGAGGGTCGG	CGGCCGCGG	CGGGCCGGGC	420
	CCGCGCACAG	CGCCCGCATG	TACAACATGA	TGGAGACGGA	GCTGAAGCCG	CGGGCCCGGC	480
65	AGCAAACTTC	GGGGGGCGGC	GGCGGCAACT	CCACCGCGGC	GGCGGCGGC	GGCAACCAGA	540
	AAAACAGCCC	GGACCGCGTC	AAGCGGCCCA	TGAATGCCTT	CATGTGTGG	TCCGCGGGC	600
	AGCGGCGCAA	GATGGCCAG	GAGAAACCCA	AGATGCACAA	CTCGGAGATC	AGCAAGCGCC	660
	TGGGCGCGGA	GTGAAACTT	TGTGCGGAGA	CGGAGAAAGC	GCCGTTTCAT	GACGAGGCTA	720
	AGCGGCTGCG	AGCGCTGCAC	ATGAAGGAGC	ACCGGATTA	TAAATACCGG	CCCGGGGGA	780
70	AAACCAAGAC	GCTCATGAAG	AAGGATAAGT	ACACGCTGCC	CGCGGGCTG	CTGGCCCCCG	840
	GCGGCAATAG	CATGGCGAGC	GGGGTCGGGG	TGGGCGCGGG	CCTGGGCGCG	GGCGTGAACC	900
	AGCGCATGGA	CAGTTACGCG	CACATGAACG	GCTGGAGCAA	CGGCAGCTAC	AGCATGATGC	960
	AGGACAGGCT	GGGCTACCGG	CAGCACCCGG	GCCTCAATGC	GCACGCGCAG	GCGCAGATGC	1020
	AGCCCATGCA	CCGCTACGAC	GTGAGCGCCC	TGCAGTACAA	CTCCATGACC	AGCTCGCAGA	1080
75	CCTACATGAA	CGGCTCGCCC	ACCTACAGCA	TGTCCTACTC	GCAGCAGGGC	ACCCCTGGCA	1140
	TGGCTCTTGG	CTCCATGGGT	TCGGTGGTCA	AGTCCGAGGC	CAGCTCCAGC	CCCCCTGTGG	1200
	TTACTCTTTC	CTCCCATCTC	AGGGCGCCCT	GCCAGGCGGG	GGACCTCCGG	GACATGATCA	1260
	GCATGTATCT	CCCGGGCGCC	GAGGTGCCGG	AACCGCGCGC	CCCCAGCAGA	CTTCACATGT	1320
	CCAGCACTA	CGAGAGCGGC	CCGGTGCCCG	GCACGGCCAT	TAACGGGCACA	CTGCCCTCT	1380
80	CACACATGTG	AGGGCCGGAC	AGCGAACTGG	AGGGGGGAGA	AATTTTCAAA	GAAAAACGAG	1440
	GGAAATGGGA	GGGGTGCAAA	AGAGGAGAGT	AAGAAACAGC	ATGGAGAAAA	CCCCGTACGC	1500
	TCAAAAAAAA	AAAAAATCCAT	CACCCACAGC	AAATGACAGC	AAATGACAGC	TGCAAAAGAG	1560
	AACACCAATC	CCATCCACAC	TCACGCAAAA	ACCGCGATGC	CGACAAGAAA	ACTTTTATGA	1620
	GAGAGATCCT	GAGACTTCTT	TTGGGGGACT	ATTTTGTAC	AGAGAAAAAC	TGGGGAGGGT	1680
85	GGGGAGGGCG	GGGGAATGGA	CCTTGTATAG	ATCTGGAGGA	AAGAAAGCTA	CGAAAACTT	1740
	TTTAAAGATT	CTAGTGGTAC	GGTAGGAGCT	TTGCGAGGAG	TTTGCAGGAG	TCTTTACCAA	1800
	TAATATTAG	AGCTGTGCTC	CAAGCGACGA	AAAAAATGTT	TTAATATTG	CAAGCAACTT	1860
	TGTACAGTA	TTTATCGAGA	TAAACATGGC	AATCAAAATG	TCCATTGTTT	ATAAGCTGAG	1920

AATTGGCCAA TATTTTTCAA GGAGAGGCTT CTTGCTGAAT TTTGATTCTG CAGCTGAAAT 1980
 TTAGGACAGT TGCAACCGTG AAAAGAAGAA AATTATTCAT ATTTGGACAT TTTAATTGTT 2040
 TAAAAATGT ACAAAGGAA AAAATTAGAA TAAGTACTGG CGAACCATCT CTGTGGTCTT 2100
 GTTTAAAAAG GGCAAAAGTT TTAGACTGTA CTAAATTTTA TAACCTACTG TTAAGAGCAA 2160
 AAATGGCCAT GCAGGTGAC ACCGTGTGTA ATTTATAATA GCTTTTGTTC GATCCCAACT 2220
 TTCCATTTTG TTCAGATAAA AAAAACCATG AAATTACTGT GTTTGAAATA TTTTCTTATG 2280
 GTTTGTAATA TTTCTGTAAA TTTATGTGTA TATTTTAAGG TTTTCCCCC TTTATTTTCC 2340
 GTAGTTGTAT TTTAAAGAT TCGGCTCTGT ATTATTTGAA TCAGTCTGCC GAGAATCCAT 2400
 GTATATATTT GAATAATAT CATCCTTATA ACAGGTACAT TTTCAACTTA AGTTTCTTACT 2460
 CCATTATGCA CAGTTTGAGA TAAATAAAT TTTGAAATAT GGACACTGAA AAAAAAATAA 2520
 AAAAAACAA AACAAAAAA CAAAAACAA AACACAGAAA AACAAAAAA AAAACAAAC 2580
 CACAACACA AACAAAAAA AAAAAAAGA AACAAACACA CAACACAACA CAACACAACA 2640
 CCACAACACA AACACAACA CACAGAGGG

Seq ID NO: 4 Protein sequence:
Protein Accession #: CAA83435.1

1 11 21 31 41 51
 MYNMMETELK PPGPQQTSGG GGNSTAAAA GGNQKNSPDR VKRPMNAPMV WSRGQRRKMA 60
 QENPKMHNSE ISKRLGAEWK LLSETEKRPF IDEAKRLRAL HMKEHPDYKY RPRRKTKTLM 120
 KKDKYTLPGG LLAPGGNSMA SGVGVGAGLG AGVNQRMDSY AHMNGWSNGS YSMQDQLGY 180
 PQHPGLNARG AAQMPPHRY DVSALQYNSM TSSQTYMNGS PTYSMSYSQQ GTPGMALGSM 240
 GSVVKSEASS SPVVVTSSSH SRAPCQAGDL RDMISMYLPG AEPVEPAAPS RLHMSQHYQS 300
 GPVFGTAING TLPLSHM

Seq ID NO: 5 DNA sequence
Nucleic Acid Accession #: U91618
Coding sequence: 29-541

1 11 21 31 41 51
 CGGACTTGGC TTGTTAGAAG GCTGAAAGAT GATGGCAGGA ATGAAAATCC AGCTTGATATG 60
 CATGCTACTC CTGGCTTTCA GCTCCTGGAG TCTGTGCTCA GATTGAGAAG AGGAAATGAA 120
 AGCATTAGAA GCAGATTTCT TGACCAATAT GCATACATCA AAGATTAGTA AAGCACATGT 180
 TCCCTCTGGG AAGATGACTC TGCTAAATGT TTGCAGTCTT GTAAATAATT TGAACAGCCC 240
 AGCTGAGGAA ACAGGAGAAG TTCTGAAGA GGAGCTTGTT GCAAGAAGGA AACTTCCTAC 300
 TGCTTTAGAT GGCTTTAGCT TGGAAAGCAAT GTTGACAATA TACCAGCTCC ACAAAATCTG 360
 TCACAGCAGG GCTTTTCAAC ACTGGGAGTT AATCCAGGAA GATATTCTTG ATACTGGAAA 420
 TGACAAAAAT GGAAAGGAAG AAGTCATAAA GAGAAAAATT CCTTATATTC TGAAACGGCA 480
 GCTGTATGAG AATAAACCCA GAAGACCCTA CATACTCAA AGAGATTCTT ACTATTACTG 540
 AGAGAATAAA TCATTATTTT ACATGTGATT GTGATTATC ATCCCTTAAT TAAATATCAA 600
 ATTATATTTG TGTGAAATG TGACAAACAC ACTTATCTGT CTCCTTACA ATTGTGGTTT 660
 ATTGAATGTG TTTTCTGCA CTAATAGAAA TTAGACTAAG TGTTTTCAA TAAATCTAAA 720
 TCTTCAAAAA AAAAAAATAA AAATGGGGCC GCAATT

Seq ID NO: 6 Protein sequence:
Protein Accession #: AAB50564

1 11 21 31 41 51
 MMAGMKIQLV CMLLLAPSSW SLCSDSSEEM KALEADFLTN MHTSKISKAH VPSWKMTLLN 60
 VCSLVNINLS PAETGSEVHE EELVARRKLP TALDGFSLAE MLTIYQLHKI CHSRAFQHWE 120
 LIQEDILDTG NDKNGKEEVI KRKIPYILKR QLYENKPRRP YILKRDSYFY

Seq ID NO: 7 DNA sequence
Nucleic Acid Accession #: NM_006536.2
Coding sequence: 109-2940

1 11 21 31 41 51
 ACCTAAAACC TTGCAAGTTC AGGAAGAAAC CATCTGCATC CATATTGAAA ACCTGACACA 60
 ATGTATGCAG CAGGCTCAGT GTGAGTGAAC TGGAGGCTTC TCTACAACAT GACCCAAAGG 120
 AGCATTTGAG GTCCTATTTG CAACCTGAAG TTTGTGACTC TCCTGGTTGC CTTAAGTTCA 180
 GAACCTCCAT TCCTGGGAGC TGGAGTACAG CTTCAAGACA ATGGGTATAA TGGATTGCTC 240
 ATTGCAATTA ATCTCAGGT ACCTGAGAA CAGAACCTCA TCTCAAACAT TAAGGAAATG 300
 ATAAGTGAAG CTTCAATTTA CCTATTTAAT GCTACCAAGA GAAGAGTATT TTTGAGAAAT 360
 ATAAAGATTT TAATACCTGC CACATGGAAA GCTAATAATA ACAGCAAAAT AAAACAAGAA 420
 TCATATGAAA AGGCAAAATGT CATAGTGACT GACTGGTATG GGGCACATGG AGATGATCCA 480
 TACACCTTAC AATACAGAGG GTGTGGAAAA GAGGAAAAAT ACATTCAATT CACACCTAAT 540
 TTCCTACTGA ATGATAACTT AACAGCTGGC TACGGATCAC GAGGCCGAGT GTTTGTCCAT 600
 GAATGGGCCC ACCTCGGTTG GGGTGTGTTG GATGAGTATA ACAATGACAA ACCTTTCTAC 660
 ATAAATGGGC AAAATCAAAT TAAAGTGACA AGGTGTTTCA CTGACATCAC AGGCATTTT 720
 GTGTGTGAAA AAGGTCTCTG CCCCAGAGAA AACTGTATTA TTAGTAAGCT TTTTAAAGAA 780
 GGATGCACCT TTATCTACAA TAGCACCCAA AATGCAACTG CATCAATAAT GTTCATGCAA 840
 AGTTTATCTT CTGTGTGTA ATTTTGTAA GCAAGTACCC ACAACCAAGA AGCACCACAA 900
 CTACAGAAC AGATGTGCAG CCTCAGAAAT GCATGGGATG TAATCACAGA CTCTGCTGAC 960
 TTTCAACACA GCTTTCCCAT GAATGGGACT GAGCTTCCAC CTCCTCCAC ATTCTGCTT 1020
 GTACAGGCTG GTGACAAAGT GGTCTGTTTA GTGCTGGATG TGTCCAGCAA GATGGCAGAG 1080
 GCTGACAGAC TCCTTCAACT ACAACAAGCC GCAGAAATTT ATTGTATGCA GATTGTTGAA 1140
 ATTCATACCT TCGTGGGCTT TGCCAGTTTC GACAGCAAAAG GAGAGATCAG AGCCACGCTA 1200
 CACCAATTA ACAGCAATGA TGATCGAAAG TTGCTGTTT CATATCTGCC CACCACTGTA 1260
 TCAGCTAAAA CAGACATCAG CATTGTGTTA GGGCTTAAGA AAGGATTGGA GGTGGTTGAA 1320
 AAACCTGAATG GAAAAGCTTA TGGCTCTGTG ATGATATTAG TGACCAGCGG AGATGATAAG 1380
 CTTCTTGCA ATTGCTTACC CACTGTGCTC AGCAGTGGTT CAACAATTCA CTCATTGGC 1440

	CTGGGTTTCAT	CTGCAGCCCC	AAATCTGGAG	GAATTATCAC	GTCTTACAGG	AGGTTTAAAG	1500
	TTCTTTGTTC	CAGATATATC	AAACTCCAAT	AGCATGATTG	ATGCTTTTCAG	TAGAAATTTCC	1560
	TCTGGAACTG	GAGACATTTT	CCAGCAACAT	ATTCAGCTTG	AAAGTACAGG	TGAAAAATGTC	1620
5	AAACCTCACC	ATCAATTGAA	AAACACAGTG	ACTGTGGATA	ATACTGTGGG	CAACGACACT	1680
	ATGTTTCTAG	TTACGTGGCA	GGCCAGTGGT	CCTCCTGAGA	TTATATTATT	TGATCCTGAT	1740
	GGACGAAAT	ACTACACAAA	TAATTTTATC	ACCAATCTAA	CTTTTCGGAC	AGCTAGTCTT	1800
	TGGATTCCAG	GAACAGCTAA	GCCTGGGCAC	TGGACTTACA	CCCTGAACAA	TACCCATCAT	1860
	TCTCTGCAAG	CCCTGAAAGT	GACAGTGACC	TCTCGCGCCT	CCAACTCAGC	TGTGCCCCCA	1920
10	GCCACTGTGG	AAGCCTTTGT	GGAAAGAGAC	AGCCTCCATT	TTCTCATCC	TGTGATGATT	1980
	TATGCCAATG	TGAAACAGGG	ATTTTATCCC	ATTCCTAATG	CCACTGTCAC	TGCCACAGTT	2040
	GAGCCAGAGA	CTGGAGATCC	TGTTACGCTG	AGACTCCTTG	ATGATGGAGC	AGGTGCTGAT	2100
	GTTATAAAAA	ATGATGGAAT	TTACTCGAGG	TATTTTTTCT	CCTTGTCTGC	AAATGGTAGA	2160
	TATAGCTTGA	AAGTGATGT	CAATCACTCT	CCCAGCATAA	GCACCCCAAC	CCACTCTATT	2220
	CCAGGGAGTC	TATGATGTA	TGTACCAGGT	TACACAGCAA	ACGGTAATAT	TCAGATGAAT	2280
15	GCTCCAAGGA	AATCAGTAGG	CAGAAATGAG	GAGGAGCGAA	AGTGGGGCTT	TAGCCGAGTC	2340
	AGCTCAGGAG	GCTCCTTTTC	AGTGCTGGGA	GTTCCAGCTG	GCCCCCACC	TGATGTGTTT	2400
	CCACCATGCA	AAATTATTGA	CCTGGAAGCT	GTAAGTAG	AAGAGGAATT	GACCTTATCT	2460
	TGGACAGCAC	CTGGAGAAGA	CTTTGATCAG	GGCCAGGCTA	CAAGCTATGA	AATAAGAAATG	2520
	AGTAAAGTC	TACGCAATAT	CAAGATGAC	TTTAAACATG	CTATTTTAGT	AAATACATCA	2580
20	AAGCGAAATC	CTCAGCAAGC	TGGCATCAGG	GAGATATTTA	CGTCTCACC	CCAGATTFTCC	2640
	ACGAATGGAC	CTGAACATCA	GCCAAATGGA	GAAACACATG	AAAGCCACAG	AATTTATGTT	2700
	GCAATACGAG	CAATGGATAG	GAACTCCTTA	CAGTCTGCTG	TATCTAACAT	TGCCCAGGCG	2760
	CCTCTGTTTA	TTCCCCCAA	TTCTGATCCT	GTACCTGCCA	GAGATTATCT	TATATTGAAA	2820
	GGAGTTTAA	CAGCAATGGA	TTTGATAGGA	ATCATTTCCT	TTATTATAGT	TGTGACACAT	2880
25	CATACCTTAA	GCAGGAAAAA	GAGAGCAGAC	AAGAAAGAGA	ATGGAACAAA	ATTATTATAA	2940
	ATAAATATCC	AAAGTGTCTT	CCTTCTTAGA	TATAAGACCC	ATGGCCTTCG	ACTACAAAAA	3000
	CATACTAACA	AAGTCAAAAT	AACATCAAAA	CTGTATTAAA	ATGCATTGAG	TTTTTGTACA	3060
	ATACAGATAA	GATTTTACAA	TGGTAGATCA	ACAATTCCTT	TTGGGGGTAG	ATTAGAAAAAC	3120
	CCTTACACTT	TGCTAATGAA	CAAAATAATA	AAATTATCT	TTAAAGTAAT	GTCTTTAAAG	3180
30	GCAAAGGGAA	GGGTAAAGTC	GGACCAAGTG	CAAGGAAAGT	TTGTTTTATT	GAGGTGGAAA	3240
	AATAGCCCA	AGCAGAGAAA	AGGAGGGTAG	GTCTGCATTA	TAACTGTCTG	TGTGAAGCAA	3300
	TCATTAGTT	ACTTTGATTA	ATTTTTCTTT	TCTCCTTATC	TGTGCAGTAC	AGGTGTCTTG	3360
	TTTACATGAA	GATCATGCTA	TATTTTATAT	ATGTAGCCCC	TAATGCAAGG	CTCTTACCTT	3420
	CTTGCTATTT	TGTTATATAT	ATTTACAGATG	ACATCTCCCT	GCTAATGCTC	AGAGATCTTT	3480
35	TTTCACTGTA	AGAGGTAAAC	TTTAAACAATA	TGGGTATTAC	CTTTGTCTCT	TCATACCGGT	3540
	TTTATGACAA	AGGTCTATTG	AATTTATTTG	TNTGTAAGTT	TCTACTCCCA	TCAAAGCAGC	3600
	TTTCTAAGTT	TATTGCCTTG	GGTTATTATG	GAATGATAGT	TATAGCCCN	TATAATGCCT	3660
	TACCTAGGAA	A					

Seq ID NO: 8 Protein sequence:
Protein Accession #: NP_006527.1

	1	11	21	31	41	51	
45	MTQRSIAGPI	CNLKFVTLV	ALSSSELPFLG	AGVQLQDNGY	NGLLIAINPQ	VPENQNLISS	60
	IKEMITEASF	YLFNATKRRV	FFRNKILIP	ATWKANNNSK	IKQESYEKAN	VIVTDWYGAH	120
	GDDPYTLQYR	CGCKEGKYIH	FTPNFLNDN	LTAGYGSRRG	VFVHEWAHLR	WGVFDEYNND	180
	KPFYINGNQ	IKVTRCSSDI	TGIFVCEKGP	CPQENCIISK	LFKEGCTFIY	NSTQWATASI	240
50	MEMQSLSSVV	EFCNASTHNQ	EAPNLQNMOC	SLRSANDVIT	DSADFHHSFP	MNGTELPPPP	300
	TFSLVQAGDK	VVCLVLDVSS	KMAEADRLLO	LQQAAPFYLM	QIVRIHTFVG	IASFDSKGEI	360
	RAQLHQINSN	DDRKLVLVSYL	PTTVSAKTDI	SICSLKKKGF	EVVEKLNGKA	YGSVMILVTS	420
	GDDKLLGNCL	PTVLSSGSTI	HSIALGSSAA	PNLEELSRIT	GGLKFPVPDI	SNSNSMIDAF	480
	SRISSGTGD	FQHQHILEST	GENVKPHEQL	KNTVTVDNTV	GNDTMFLVTW	QASGPPEIIL	540
55	FDPDRKYYT	NNPITNLTR	TASLWIPGTA	KPGHWYTLN	NTHSLQALK	VTVTSRASNS	600
	AVPPATVEAF	VERDLSHFPH	PVMYIANVKQ	GFYPILNATV	TATVEPETGD	PVTLRLLDDG	660
	AGADVINKND	IYGRYHFSFA	ANGRYSLKVH	VNRSPSISTP	AHSIPGSHAM	VYPGYTANGN	720
	IQMNAPRKSV	GRNEEERKWG	FSRVSSGGSF	SVLGVPAGPH	PDVFPCKII	DLEAVKVBBE	780
	LTLSTWAPGE	DFDQGGQATSY	EIRMSKSLQN	IQDDFNAIL	VNTSKRNPPQ	AGIREIFTFS	840
60	PQISTNGPEH	QPNGETHESH	RIYVAIRAMD	RNSLQSAVSN	IAQAPLFIFP	NSDPVPARDY	900
	LILKCVLTAM	GLTGICLII	VVTHHTLSRK	KRADKKENG	KLL		

Seq ID NO: 9 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 336-632

	1	11	21	31	41	51	
70	CTCCCTCAC	CCCGGTCCAG	GATGCCCACT	CCCCACGACA	CCTCCCACTT	CCCACTGTGG	60
	CCTGGGTGGG	CTCAGGGGCT	GCCCTTGACC	TGGCCTAGAG	CCCTCCCCCA	GCTGGTGGTG	120
	GAGCTGGCAC	TCTCTGGGAG	GGAGGGGGCT	GGGAGGGAAT	GAGTGGGAAT	GGCAAGAGGC	180
	CAGGGTTTGG	TGGGATCAGG	TTGAGGCAGG	TTTGGTTTCC	TTAAAATGCC	AAGTTGGGGG	240
	CCAGTGGGGC	CCACATATAA	ATCCTCACCC	TGGGAGCCTG	GCTGCCTTGC	TCTCCTTCTC	300
75	GGGTCTGTCT	CTGCCACCTG	GTCTGCCACA	GATCCATGAT	GTGCAGTTCT	CTGGAGCAGG	360
	CGCTGGCTGT	GCTGGTCACT	ACCTTCCACA	AGTACTCCTG	CCAAGAGGGC	GACAAGTTCA	420
	AGCTGAGTAA	GGGGGAAATG	AAGGAACCTC	TGCACAAGGA	GCTGCCACGC	TTTGTGGGGG	480
	AGAAAGTGGG	TGAGGAGGGG	CTGAAGAAGC	TGATGGGCAG	CCTGGATGAG	AACAGTGACC	540
	AGCAGGTGGA	CTTCCAGGAG	TATGCTGTTT	TCTTGGCACT	CATCACTGTC	ATGTGCAATG	600
80	ACTTCTTCCA	GGGCTGCCCA	GACCGACCTT	GAAGCAGAAC	TCTTGACTTC	CTGCCATGGA	660
	TCTCTTGGGC	CCAGGACTGT	TGATGCCCTT	GAGTTTGTGA	TTCAATAAAC	TTTTTTTGTG	720
	TGTTGATAAT	CTTTAAATTG	CTCAGTGATG	TTCCATAACC	CGGCTGGCTC	AGCTGGAGTG	780
	CTGGGAGATG	AGGGCTCTCT	GATCCTGCT	CCCTTCTGGG	CTCTGACTCT	CCTGGAATTC	840
	TCTCCAAGGC	CAGAGCTATG	CTTAGGTCT	CAATTTTGA	ATTTCACAAA	CCAGCAAAAA	900
85	ATTGGAATC	GAGATAGGTT	GCTGACTTTT	ATTTTGTCAA	ATAAAGATAT	TAAAAAAGGC	960
	AAATACCA						

Seq ID NO: 10 Protein sequence:

Protein Accession #: NP_005969.1

1 11 21 31 41 51
5 | | | | |
MMCSLSLEQAL AVLVTTFPHKY SCQEGDKFKL SKGEMKELLH KELPSFVGEK VDEEGLKKLM 60
GSLDENSDQQ VDFQYAVFL ALITVMCNDF FQGCPRDP

Seq ID NO: 11 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 336-626

1 11 21 31 41 51
15 | | | | |
CTCCCTCAC CCCGGTCCAG GATGCCAGT CCCCACGACA CCTCCCACT CCCACTGTGG 60
CCTGGGTGGG CTCAGGGGCT GCCCTTGACC TGGCCTAGAG CCCTCCCCCA GCTGGTGGTG 120
GAGCTGGCAC TCTCTGGGAG GGAGGGGGCT GGGAGGGAAT GAGTGGGAAT GGCAAGAGGC 180
CAGGGTTTGG TGGGATCAGG TTGAGGCAGG TTTGGTTTCC TTAAGTGGCC AAGTTGGGGG 240
CCAGTGGGGC CCACATATAA ATCCTCACCC TGGGAGCCTG GCTGCCTTGC TCTCCTTCT 300
20 GGGTCTGTCT CTGCCACCTG GTCTGCCACA GATCCATGAT GTGCAGTTCT CTGGAGCAGG 360
CGCTGGCTGT GCTGTCTACT ACCTTCCACA AGTACTCCTG CCAAGAGGGC GACAAGTTCA 420
AGCTGAGTAA GGGGGAATG AAGGAACTTC TGCACAAGGA GCTGCCCCAGC TTTGTGGGGC 480
ATTCCAGAGA ACCATGTGCT GTGAGGGCCT TCCGAGTCCA TCTGTTTAAT CCTGTCTATTG 540
25 GAGACTTGAG AAACCAAGAGC CCAGAAGGGA AAAGTGATTG TCCCAAGATC ACACAGCACT 600
GGAGAAAGTG GATGAGGAGG GGCTGAAGAA GCTGATGGGC AGCCTGGATG AGAACAGTGA 660
CCAGCAGGTG GCTTTCAGG AGTATGCTGT TTTCTGGCA CTCACTACTG TCATGTGCAA 720
TGACTTCTTC CAGGGCTGCC CAGACCGACC CTGAAGCAGA ACTCTTGACT TCCTGCCATG 780
GATCTCTTGG GCCCAGGACT GTTGATGCCT TTGAGTTTGG TATTCAATAA ACTTTTTTTG 840
30 TCTGTTGATA ATATTTTAAT TGCTCAGTGA TGTTCCATAA CCGGCTGGC TCAGCTGGAG 900
TGCTGGGAGA TGAGGGCCTC CTGGATCCTG CTCCTTCTG GGTCTGACT CTCCTGGAAA 960
TCTCTCCAAG GCCAGAGCTA TGCTTTAGGT CTCATTTTGA GAATTTCAAA CACCAGCAAA 1020
AAATTGGAAA TCGAGATAGG TTGCTGACTT TTATTTTGTG AAATAAGAT ATTAATAAAG 1080
GCAATACCA

Seq ID NO: 12 Protein sequence:
Protein Accession #: Eos sequence

1 11 21 31 41 51
40 | | | | |
MMCSLSLEQAL AVLVTTFPHKY SCQEGDKFKL SKGEMKELLH KELPSFVGHS REPCAVRAFR 60
VHLFNPVIGD LRNQSPEGKS DCPKITQHWK KWMRRG

Seq ID NO: 13 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 58-354

1 11 21 31 41 51
50 | | | | |
GTGAGCTCAC CATGTGGGGG TGAGGCTGAG AGAAAACAAG TACACAGCCA CAGATCCATG 60
ATGTGCAGTT CTCTGGAGCA GCGCGTGGCT GTGCTGGTCA CTACCTTCCA CAAGTACTCC 120
TGCCAAAGAG GCGACAAGTT CAAGCTGAGT AAGGGGGAAG TGAAGGAAGT TCTGCACAAG 180
GAGCTGGCCA GCTTTGTGGG GGAGAAAGTG GATGAGGAGG GGCTGAAGAA GCTGATGGGC 240
55 AGCCTGGATG AGAACAGTGA CCAGCAGGTG GACTTCCAGG AGTATGCTGT TTTCTGGCA 300
CTCATCACTG TCATGTGCAA TGACTTCTTC CAGGGCTGCC CAGACCGACC CTGAAGCAGA 360
ACTCTTGACT TCCTGCCATG GATCTCTTGG GCCCAGGACT GTTGATGCCT TTGAGTTTGG 420
TATTCAATAA ACTTTTTTTG TCTGTTGATA ATATTTTAAT TGCTCAGTGA TGTTCCATAA 480
CCCGCTGGC TCAGCTGGAG TGCTGGGAGA TGAGGGCCTC CTGGATCCTG CTCCTTCTG 540
60 GGCTCTGACT CTCCTGGAAA TCTCTCCAAG GCCAGAGCTA TGCTTTAGGT CTCATTTTGG 600
GAATTTCAAA CACCAGCAAA AAATTGGAAA TCGAGATAGG TTGCTGACTT TTATTTTGTG 660
AAATAAGAT ATTAATAAAG GCAATACCA

Seq ID NO: 14 Protein sequence:
Protein Accession #: NP_005969.1

1 11 21 31 41 51
65 | | | | |
MMCSLSLEQAL AVLVTTFPHKY SCQEGDKFKL SKGEMKELLH KELPSFVGEK VDEEGLKKLM 60
GSLDENSDQQ VDFQYAVFL ALITVMCNDF FQGCPRDP

Seq ID NO: 15 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 62-358

1 11 21 31 41 51
75 | | | | |
GGAGGGTGTG CCGCTGAGTC ACTGCCTGGG CATCTGGGCC TGGAACTCG GCCACAGATC 60
CATGATGTGC AGTTCTCTGG AGCAGGCGCT GGCTGTGCTG GTCACTACCT TCCACAAGTA 120
80 CTCCTGCCAA GAGGGGCGCA AGTTCAAGCT GAGTAAGGGG GAAATGAAGG AACTTCTGCA 180
CAAGGAGCTG CCCAGCTTTG TGGGGAGAA AGTGGATGAG GAGGGGCTGA AGAAGCTGAT 240
GGGAGCCTG GATGAGAACA GTGACCAGCA GGTGGACTTC CAGGAGTATG CTGTTTCTCT 300
GGCACTCATC ACTGTCATGT GCAATGACTT CTTCCAGGGC TGCCAGAGCC GACCTGAAG 360
CAGAACTCTT GACTTCTCTG CATGGATCTC TTGGGCCAG GACTGTTGAT GCCTTTGAGT 420
85 TTTGATTCA ATAAACTTTT TTTGTCTGTT GATAATATT TAATTGCTCA GTGATGTTCC 480
ATAACCCGGC TGGCTCAGT GGAATCTCTG GAGATGAGGG CCTCTGGAT CTGCTCCCT 540
TCTGGGCTCT GACTCTCTG GAAATCTCTC CAAGGCCAGA GCTATGCTTT AGGTCTCAAT 600
TTTGAATTT CAACACCAG CAAAAAATTG GAAATCGAGA TAGGTGCTG ACTTTTATTT 660

Seq ID NO: 16 Protein sequence:
Protein Accession #: NP_005969.1

1 11 21 31 41 51 60
MMCSSLEQAL AVLVTTFFHKY SQEGDKFKL SKGEMKELLH KELPSFVGEK VDEEGLKILM
GSLDENSQQ VDFQEYAVFL ALITVMCNDF FQGCPRDP

Seq ID NO: 17 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 939-2372

1 11 21 31 41 51 60
AAGACGGATT CTCAGACAAG GCTTGCAAAAT GCCCGCAGC CATCATTTAA CTGACCCGCG 60
AGAATAGTTA CGGTTTGTCA CCCGACCCCT CCGATCGCC TAATTGTGTC CTAGTGAGAC 120
CCGAGGGCTC TGCCCGGCGCC TGGCTTCTTC GTAGCTGGAT GCATATCGTG CTCGGGGCAG 180
CGCGGGCGCA GGGCAGCGGT TCGCGCACAC CCTAGCACAC ATGAACACGC GCAAGAGCTG 240
AACCAGCAC GGTTCATT TCAAAAAGGG AGACAGCCTC TACCGCGATT GTAGAAGAGA 300
CTGTGGTGTG AATTAGGGAC CGGAGGGCGT CGAACGGAGG AACGGTTCAT CTTAGAGACT 360
AATTTTCTGG AGTTTCTGCC CTTGCTCTGC GTCAGCCCTC ACCTCACTTC GCCAGCAGTA 420
GCAGAGGGCG CGGCGGGCGG TCCCGGAATT GGGTTGGAGC AGGAGCCTCG CTGGCTGCTT 480
CGCTCGCGCT CTACGCGCTC AGTCCCGGCG GGTAGCAGGA GCCTGGACCC AGGCGCGGCC 540
GGCGGGCGTG AGGCGCGGGA GCCCGCCCTC GAGGTGCATA CCGGACCCCT ATTCTGCATCT 600
AACAAGGAAT CTGCGCCCCA GAGAGTCCCG GGAGCGCGCG CGGTCTGCTC CCGCGCGGCC 660
GGGCCATGCA GCGACGGCGG CCGCGGAGCT CCGAGCAGCG GTAGCGCCCC CCTGTAAAGC 720
GGTTCTGCTAT GCGCGGGGCA TCTGTAACCC TGCCGCGCTG CGGAACACTC TTCGCTCCGG 780
ACGAGCTCAG CCTCTGATAA GCTGGAAGCT GCACGCGCGC AACAAACACC GAGGAGTTAA 840
GAGAGCCGCA TTTTCATCGCA AGCCCTCCCC GCACGGGTGG GGGAAAGCGG CCGGTGCAGC 900
GCGGGGACAG GCACCTCGGGC TGGCACTGGC TGCTAGGGAT GTGCTCTCG ATAAGGTGGC 960
ATGAGCCCGC CATGGCGCGG CTCTGGGGCT TCTGCTGGCT GGTGTGGGCT TTCTGGAGGG 1020
CCGCTTTTGG CTGTCCACAG TCCCTGCAAT GCAGTGCCTC TCGGATCTGG TGCAGCGACC 1080
CTTCTCCTGG CATCGTGGCA TTTCCGAGAT TGGAGCCTAA CAGTGTAGAT CCTGAGAAC 1140
TCACCGAAAT TTTTCATCGCA AGCCAGAAAG GGTAGAAAT CATCAACGAA GATGATGTTG 1200
AAGCTTATGT GGGACTGAGA AATCTGACAA TTGTGGATTG TGGATTAAAA TTGTGGCTC 1260
ATAAAGCATT TCTGAAAAAC AGCAACCTGC AGCAGATCAA TTTTACCGA AACAACTGA 1320
CGAGTTTGTG TAGGAAACAT TTCCGTACCC TTGACTTGTC TGAAGTATC CTGGTGGGCA 1380
ATCCATTATC ATGCTCTCTG GACATTATGT GGATCAAGAG TCTCCAGAG GCTAAATCCA 1440
GTCCAGACAG TCGAGATTGT TACTGCTGTA ATGAAGCAG CAAGAATATT CCCCTGGCAA 1500
ACCTGCAGAT ACCCAATTGT GGTTCGCCAT CTGCAATCT GGCAGCAGCT AACCTCACTG 1560
TGGAGGAAGG AAGCTCTATC CATTATCTCT GTAGTGTGGC AGGTGATCCG GTTCTAATA 1620
TGTATTGGGA GTTGGTAAAC CTGGTTTCCA AACATATGAA TGAACAAGC CACACACAGG 1680
GCTCCTTAAG GATAACTAAC ATTTCATCCG ATGACAGTGG GAAGCAGATC TCTTGTGTGG 1740
CGGAAATCTG TGTAGGAGAA GATCAAGATT CTGTCAACCT CACTGTGCAT TTTGCACCAA 1800
CTATCACATT TCTCGAATCT CCAACCTCAG ACCACCACTG GTGCATTCCA TTTACTGTGA 1860
AAGGCAACCC CAACACAGCG CTTCACTGGT TCTATAACGG GGCAATATTG AATGAGTCCA 1920
AATACATCTG TACTAAAAA CATGTTTACCA ATCACACGGA GTACCACGCG TGCCCTCCAGC 1980
TGGATAATCC CACTCACATG AACATGGGG ACTACACTCT AATAGCCAAG AATGAGTATG 2040
GGAAGGATGA GAAACAGATT TCTGCTCACT TCATGGGCTG GCCTGGAATT GACGATGGTG 2100
CAAAACCAAA TTAATCTGAT GTAATTTATG AAGATTATGG AACTGCAGCG AATGACATCG 2160
GGGACACAC GAAAGAGAGT AATGAAATCC CTTCCACAGA CGTCACTGAT AAAACCGGTC 2220
GGGAACATCT CTCGGTCTAT GCTGTGGTGG TGATTGGCTG TGTGGTGGGA TTTTGCCTTT 2280
TGGTAATGCT GTTCTGCTCT AAGTTGGCAA GACACTCCAA GTTGGCATG AAAGGTTTTG 2340
TTTTGTTTCA TAAGATCCCA CTGGATGGGT AGCTGAAATA AAGGAAAGA CAGAGAAAGG 2400
GGCTGTGGTG CTTGTGGTGT GATGCTGCCA TGTAAGCTGG ACTCCTGGGA CTGCTGTTGG 2460
CTTATCCCGG GAAGTGTCTG TTATCTGGGG TTTTCTGGTA GATGTGGGCG GTGTTGGAG 2520
GCTGTACTAT ATGAAGCCTG CATATACTGT GAGCTGTGAT TGGGGAACAC CAATGCAGAG 2580
GTAACCTCTA GGCAGCTAAG CAGCACCTCA AGAAAACATG TTAATTAAT GCTTCTCTTC 2640
TTACAGTAGT TCAAAATCAA AACTGAAATG AAATCCCAT TGGATTGACT TCTCTTCTGA 2700
AAAGTGTGCT TTTTGACCTT ACTGGACATT TATTGACTTA ATTGCTTCTG TTTATTAATA 2760
TTGACCTGCA AAGTTAAAAA AAAATTAAAG TTGAGAACAG GTATAAGTGC ACACCTGAATA 2820
GTCTAATCTA CATGTAACAC ATATTTTAGT GTGATTTTCT ATACTCTAAT CAGCACTGAA 2880
TTAGAGGGGT TTGACTTTTT CATCTATAAC ACAGTGACTA AAAGAGTTAA GGGTATATAT 2940
ACCATCACTT TGGGACTTGG TAGTATTATT AAAAGGTTAT TTCCTTCACT GTCATAAAAA 3000
GTCCAAATGT TTAGCTTAGG TCTGAGAGTC AAACAATGTT AAGGATTGTC TTAAGTTTCC 3060
TTAGCCAGCA AAACAAAACA AAACAAAACA AACAAATGAA AACCGTTTAA AAAGAAGAAG 3120
AAGAAAAAAA ACAAGAACAA GCAGCAACAG CTGTTTGTGT GGGGCTATAG ATTTAAGTTA 3180
GGCATAGTCA ATTTGAGAAT AACTAAGAGT GGAATATATG CATATGGTGA AATTATAACC 3240
TGGCCCTTTT TTATTTGCCC TCTGCGATCC ACCTGCTTTT TAGAAGTCTG CCGAGTGAGA 3300
AGGCCACAGT ATCTCATGCT GTTTCGATTA CAGAACTGCA GCTTTTCTAC TCTGAAAAGG 3360
CCTGGGAGCA GAATGGCTGG CTTGCTGTGA GCAGGAGAGG AGATTCTAAG AAGGATAGTC 3420
CCCCCTACAA CATACTGTCA TACTGCTGGG TTTTCATGGG TAGGAAAGCT TGTCTGACC 3480
CCAGCAGCAA AGAGGTGGCA GGTCTGTAAT GAATATATGC TTTATAATGT CCTTCTCAT 3540
TGCTGAGAGG CGAGCCTTAG AGCTGTGGAT TTCTGATCC CCCCTGAGTC TGACCCATGG 3600
ACACCTGTTT CATTCACTTT AGCATCACAG TGACCTTTGT ATGCTCTGTT CAGTCTGTGT 3660
CAGGCAGTAT GCTTGTCTCG AGAGAGGTT TGGCTATCCC CACCCCAACC CACCCCAACC 3720
TGTTCCCTTT TTATCAGGAG GACTTCAGAG CCAGCCCTGC AGCATTGTGT TTGAAACAC 3780
AATCAGCTCT GACAGTTAGA CATGCACACA GACGCCATAG CTGGATTGGA AACATTGATG 3840
TTTTAAAAAT TTATTTTTTT TGGAAATAGT TGCACAAATG CTGCAATTTA GCTTTAAGGT 3900
TCTATAGATT TTTAACTAGT CCAACACAGT CAGAAACATT GTTTTGAATC CTCTGTAAC 3960
CAAGGCATTA ATCTTAATAA ACCAGGATCC ATTTAGGTAC CACTTGATAT AAAAAGGATA 4020
TCCATAATGA ATATTTTATA CTGCATCCTT TACATTAGCC ACTAAATACG TTATTGCTTG 4080
ATGAAGACCT TTCACAGAAT CCTATGGATT GCAGCATTTT ACTTGCTTAC TTCATACCA 4140

5
10

```

TGCCTTAAAG AGGGGCAGTT TCTCAAAAGC AGAAACATGC CGCCAGTTCT CAAGTTTTCC 4200
TCCTAACTCC ATTTGAATGT AAGGGCAGCT GGGCCCCAAT GTGGGGAGGT CCGAACATTT 4260
TCTGAATTCG CATTTTCTTG TTCCGCGCTA AATGACAGTT TCTGTATTA CTTAGATTCC 4320
GATCTTTCCC AAAGGTGTTG ATTTACAAAG AGGCCAGCTA ATAGCAGAAA TCATGACCCT 4380
GAAAGAGAGA TGAATTCCTA GCTGTGAGCC AGGCAGGAGC TCAGTATGGC AAAGGTTCTT 4440
GAGAATCAGC CATTTGGTAC AAAAAAGATT TTTAAGCTT TTAGTTTATA CCATGGAGCC 4500
ATAGAAAGGC TATGGATTGT TTAAGAACTA TTTTAAAGTG TTCCAGACCC AAAAAGGAAA 4560
AATAAAAAAA AAGGAATATT TGTACCCAA AGCTAGAAGG ATTGCAAGGT AGATTTTTGT 4620
TTTAAATGG AGAGAAGTGG ACAGATAAGG CCATTTAATA TATCAAAGAT CAGTTGACAT 4680
CTCCTAGGGA ATGATGAAAA CAGCAGGCTA T

```

Seq ID NO: 18 Protein sequence:
Protein Accession #: CAA53571

15
20
25

```

1 11 21 31 41 51
MSSWIRWHGP AMARLWGFCH LVVGFWRFAF ACPTSCCKCSA SRIWCSDPSP GIVAPPRLEP 60
NSVDPENITE IFIANQKRLE IINEDDVEAY VGLRNLITVD SGLKFVAHKA FLKNSNLQHI 120
NFTRNKLTSL SRKHFRHLDL SBLILVGNFF TCSCDIMNIK TLQEAQSSPD TQDLYCLNES 180
SKNIPLANLQ IPNCGLPFSN LAAPNLTVEE GKSLTSLCSV AGDPVFNMYW DVGNLVSXHM 240
NETSHTQSSL RITNISSDDS GKQISCVAEV LVGEDQDSVN LTVHFAPTIT FLESPTSDDH 300
WCIPFTVKN PKPALQWFFN GAILNESKYI CTKIHTVNT HTYHGLQLDN PTHMNGDYT 360
LIAKNEYKGD EKQISAHFMG WPIIDGANGP NYPDVIYEDY GTAANDIGDT TNRSNEIPST 420
DVTDKTGREH LSVYAVVVIA SVVGFCLLVM LFLLKLARHS KFGMKGFVLF HKIPLDG

```

Seq ID NO: 19 DNA sequence
Nucleic Acid Accession #: NM_000228
Coding sequence: 82-3600

30
35
40
45
50
55
60
65
70
75
80
85

```

1 11 21 31 41 51
GCTTTCAGGC GATCTGGAGA AAGAACGGCA GAACACACAG CAAGGAAAGG TCCTTCTCTG 60
GGATCACCCC ATTTGGCTGAA GATGAGACCA TTCTTCCTCT TGTGTTTTGC CTGCTCTGGC 120
CTCCTGCATG CCAACAAGC CTGCTCCCGT GGGGCGCTGT ATCCACCTGT TGGGGACCTG 180
CTTGTGGGGA GGACCCGGTT TCTCCGAGCT TCATCTACCT GTGGACTGAC CAAGCCTGAG 240
ACCTACTGCA CCAAGTATGG CCAAGTGGCAG ATGAAATGCT GCAAGTGTGA CTCAGGCGAG 300
CCTCACAACT ACTACAGTCA CCGAGTAGAG AATGTGGCTT CATCTCCCG CCCCATGCGC 360
TGGTGGCAGT CCAAGATGA TGTGAACCTT GTCTCTCTGC AGCTGGACCT GGACAGGAGA 420
TTCCAGCTTC AAGAAGTCAT GATGGAGTTC CAGGGGCCCA TGCCCGCGG CATGCTGATT 480
GAGCGCTCCT CAGACTTCGG TAAGACCTGG CAGTGTGTACC AGTACCTGGC TGCCGACTGC 540
ACCTCCACTG TCCTCTGGGT CGGCCAGGGT CGGCTCAGA GCTGGCAGGA TGTTCGGTGC 600
CAGTCCCTGC CTCAGAGGCC TAATGCACGC CTAATGGGG GGAAGGTCCA ACTTAACTT 660
ATGGATTTAG TGTCTGGGAT TCCAGCAACT CAAAGTCAAA AAATTCAAGA GGTGGGGGAG 720
ATCACAAACT TGAGAGTCAA TTTCACCAAG CTGGCCCTGT TGCCCAAGG GGGCTACCA 780
CCTCCAGCGG CTTACTATGC TGTGTCCAG CTCCGTCTGC AGGGGAGCTG CTTCTGTAC 840
GGCCATGCTG ATGCTGGTGC ACCCAAGCCT GGGGCTCTG CAGGCCCTC CACCGCTGTG 900
CAGGTCCACG ATGTCTGTGT CTGCCAGCAC AACACTGCCG GCCCAATTG TGAGCGCTGT 960
GCACCTTCTT ACAACAAACG GCCCTGGAGA CCGGCGGAGG GCCAGGACGC CCATGAATGC 1020
CAAGAGTGCG ACTGCAATGG GCACTCAGAG ACATGTCACT TTGACCCCGG TGTGTTTGGC 1080
GCCAGCCAGG GGGCATATGG AGGTGTGTGT GACAATTGCC GGGACCAAC CGAAGGCAAG 1140
AACTGTGAGC GTGTCTCAGT GCACTATTTC CGGAACCGGC GCCCGGAGG TTCCATTGAG 1200
GAGACCTGCA TCTCCTGCGA GTGTGATCCG GATGGGGCAG TGCCAGGAGC TCCTGTGAC 1260
CCAGTGACCG GGCAGTGTGT GTGCAAGGAG CATGTGCAGG GAGAGCGCTG TGACCTATGC 1320
AAGCCGGGCT TCACTGGACT CACCTACGCC AACCGCAGG GCTGCCACCG CTGTGACTGC 1380
AACATCCTGG GGTCCCGGAG GGACATGCCG TGTGACGAGG AGAGTGGGCG CTGCTTTGT 1440
CTGCCAAGC GTGTGGGTCC CAAATGTGAC CAGTGTGCTC CTTACCACTG GAAGCTGGCC 1500
AGTGCCAGG GCTGTGAACC GTGTGCCTGC GACCCGCACA ACTCCCTCA GCCCACAGTG 1560
CAACCAGTTC ACAGGGCAGT GCCCTGTCCG GAAGGCTTGT GTGGCTGAT GTGACGCT 1620
GCAGCATCC GCAGTGTCC AGACCGGACC TATGGAGACG TGGCCACAGG ATGCCGAGCC 1680
TGTGACTGTG ATTTCCGGGG AACAGAGGGC CCGGCTGCGG ACAAGGCATC AGGCCGCTGC 1740
CTCTGCGCGC CTGGCTGAC CGGGCCCCGC TGTGACCACT GCCAGCGAGG CTAAGTCAAT 1800
CGCTACCGCG TGTGCTGGC CTGCCACCTT TGTCTCAGA CCTATGATGC GGACCTCCGG 1860
GAGCAGGCCC TGCCTTTGG TAGACTCCGC AATGCCACCG CCAGCTGTG GTGAGGCT 1920
GGGCTGGAGG ACCGTGGCCT GGCCTCCCG ATCTAGATG CAAAGAGTAA GATTGAGCAG 1980
ATCCGAGCAG TTCTCAGCAG CCCCGCAGT ACAGAGCAGG AGGTGGCTCA GGTGGCCAGT 2040
GCCATCCTCT CACTCAGCG AACTCTCCAG GGCCTGCAGC TGGATCTGCC CCGGAGGAG 2100
GAGACGTTGT CCCTCCGAG AGACCTGGAG AGTCTTGACA GAAGCTTCAA TGGTCTCCTT 2160
ACTATGTATC AGAGGAAGAG GGAGCAGTTT GAAAAAATAA GCAGTGTGTA TCCTTCAGGA 2220
GCCTTCCGGA TGTGAGCAC AGCCTACGAG CAGTCAGCCC AGGCTGCTCA GCAGTCTCC 2280
GACAGCTCGC GCCTTTTGGG CCAAGTCAGG GACAGCCGGA GAGAGGCGA GAGGCTGGTG 2340
CGGACGGCGG GAGGAGGAGG AGGCAACCGC AGCCCCAAGC TTGTGGCCCT GAGGCTGGAG 2400
ATGCTCTCGT TGCCTGACCT GACACCCACC TTCAACAAGC TCTGTGGCAA CTCCAGGCG 2460
ATGGCTTGCA CCCCAATATC ATGCCCTGGT GAGCTATGTC CCAAGACAA TGGCACAGCC 2520
TGTGGCTCCC GCTGACGGGG TGTCTTCCC AGGGCCGGTG GGGCTTCTT GATGGCGGG 2580
CAGGTGGCTG AGCAGCTGCG GGGCTTCAAT GCCCAGCTCC AGCGGACCG GCAGATGATT 2640
AGGGCAGCGG AGGAATCTGC CTCACAGATT CAATCCAGTG CCCAGCGCTT GGAGACCCAG 2700
GTGAGCGCCA GCGCTCCCA GATGGAGGAA GATGTGACAG GCACACGGCT CCTAATCCAG 2760
CAGGTCCGGG ACTTCTTAAC AGACCCGAC ACTGATGAC CCACTATCCA GGAGGTGAG 2820
GAGGCGGTGC TGGCCCTGTG GCTGCCACA GACTCAGCTA CTGTTCTGCA GAAGATGAAT 2880
GAGATCCAGC CCATTGCGAG CAGGCTCCCC AACGTGGACT TGGTGTGTC CCAGACCAAG 2940
CAGGACATTG CGCGTTGCGG GCTGAGGCTG AGGAAGCCAG GAGCCGAGCC 3000
CATGCAGTGG AGGGCCAGGT GGAAGATGTG GTTGGGAACC TGCGGCGAGG GACAGTGGCA 3060
CTGCAAGGAG CTCAGGACAC CATGCAAGGC ACCAGCGGCT CCCTTCGGCT TATCCAGGAC 3120
AGGGTGTGCT AGGTTTCAGCA GGTACTGCGG CCAGCAGAAA AGCTGGTGAC AAGCATGACC 3180
AAGCAGCTGG GTGACTTCTG GACACGGATG GAGGAGCTCC GCCACCAAGC CCGGCGAGCAG 3240
GGGGCAGAGC CATGCCAGC CCAGCAGCTT GCGGAAGGTG CCAGCGAGCA GGCATTGAGT 3300
GCCCCAGAGG GATTGAGAG AATAAAACAA AAGTATGCTG AGTTGAAGGA CCGGTGGGTT 3360

```

CAGAGTTCCA TGCTGGGTGA CGAGGGTGCC CGGATCCAGA GTGTGAAGAC AGAGGCAGAG 3420
 GAGCTGTTTG GGGAGACCAT GGAGATGATG GACAGGATGA AAGACATGGA GTTGGAGCTG 3480
 CTGCGGGGCA GCCAGGCCAT CATGCTGCGC TCGGCGGACC TGACAGGACT GGAGAAGCGT 3540
 GTGGAGCAGA TCCGTGACCA CATCAATGGG CGCGTGCTCT ACTATGCCAC CTGCAAGTGA 3600
 TGCTACAGCT TCCAGCCCGT TCGCCCACTC ATCTGCCGCC TTTGCTTTTG GTTGGGGGCA 3660
 GATTGGGTTG GAATGCTTTC CATCTCCAGG AGACTTTCAT GCAGCCTAAA GTACAGCCTG 3720
 GACCACCCCT GGTGTGTAGC TAGTAAGATT ACCCTGAGCT GCAGCTGAGC CTGAGCCAAT 3780
 GGGACAGTTA CACTTGACAG ACAAAGATGG TGGAGATTGG CATGCCATTG AAACCTAAGAG 3840
 CTCTCAAGTC AAGGAAGCTG GGCTGGGCAG TATCCCCGCG CTTTAGTTCT CCACTGGGGA 3900
 GGAATCCTGG ACCAAGCACA AAAACTTAAC AAAAGTGATG TAAAAATGAA AAGCCAAATA 3960
 AAAATCTTTG G

Seq ID NO: 20 Protein sequence:
 Protein Accession #: NP_000219

1 11 21 31 41 51
 MRPFLLCPA LPGLLHAQQA CSRGACYPPV GDLLVGRTRF LRASSTCGLT KPETYCTQYG 60
 EQMKCKCKD SRQPHNYSH RVENVASSSG PMRWWSQND VNPVSLQLDL DRRFQLQEVN 120
 MEFGQPMFAG MLIERSSDFG KTWVYQYLA ADCTSTFPRV RQGRPQSQWD VRCQSLPQRP 180
 NARLNGGKVG LNLMDLVSGI PATQSQKIQE VGEITNLRVN FTRLAPVPQR GYHPPSAYYA 240
 VSQRLRQGGC FCHGHADRC A PKPGASAGPS TAVQVHDVCV CQHNTAGPNC ERCAPFYNNR 300
 PWRPAEGQDA HECQRCDCNG HSETCHFDPA VFAASQGAAYG GVCNDCRDHT EGKNCERCQL 360
 HYFRNRRPGA SIQETCLSC E CDPDGAVPGA PCDPVTGQCV CKEHVQGERC DLCKPGFTGL 420
 TYANPOGCHR CDNCLGSRR DMPDDEESGR CLCLPNVVGK KCDQCAFYHW KLASGGQCEP 480
 CACDPHNSFG PTVQPVRRVA PCREGFGGLM CSAAAIROCP DRTYGDVATG CRACDCDFRG 540
 TEGPGCDKAS GRCLCRPLGT GPRCDQCQRG YCNRYFVCVA CHPCFQTYDA DLREQALRFG 600
 RLNRNATASLW SGPGLLEDRLG ASRILDASK IEQIRAVLSS PAVTEQVEVA VASAILSLRR 660
 TLQGLQLDLF LEEETLSLPR DLESLDRSFN GLLTMYQRKR EQFEKISSAD PSGAFRMLST 720
 AYEQSAQAQ QVSDSSRLLD QLRRDSRREAE RLVRQAGGGG GTGSPKLVAL RLEMSSSLPDL 780
 TPTFNKLKCN PTVMACPTIS CPGELCPQDN GTACGSRCRG VLPRAAGAFI MAGQVAEQLR 840
 GFNAQLQRT R QMIRAAEESA SIQSSAQRL ETQVSASRSQ MEEDVRTRL LIQQVRDLFT 900
 DPDTDAATIQ EVSEAVLALW LPTDSATVLQ KMNEIQAIAA RLPNVDLVLS QTKQDIARAR 960
 RLQAEAEER SRAHAEQGV EDVVGNLRRQ TVALQEAQDT MQGTSRSLRL IQDRVAEVQQ 1020
 VLRPAEKLV T SMTQLGDFW TRMEELRHQA RQQGAEEVQA QQLAEGASEQ ALSAQEGFER 1080
 IKQKYAELKD RLQSSMLGE QGARIQSVKT EAEELFGETM EMMDRMKDME LELLRGSQAI 1140
 MLRSADLTGL EKRVEQIRDH INGRVLYYAT CK

Seq ID NO: 21 DNA sequence
 Nucleic Acid Accession #: NM_003722
 Coding sequence: 145-1491

1 11 21 31 41 51
 TCGTTGATAT CAAAGACAGT TGAAGGAAAT GAATTTTGAA ACTTCACGGT GTGCCACCCT 60
 ACAGTACTGC CCTGACCCTT ACATCCAGCG TTTCTGTAGA ACCCAGCTCA TTTCTCTGG 120
 AAAGAAAGTT ATTACCGATC CACCATGTCC CAGAGCACAC AGACAAATGA ATTCTCTAGT 180
 CCAGAGGTTT TCCAGCATAT CTGGGATTTT CTGGAACAGC CTATATGTTC AGTTACAGCC 240
 ATTGACTTGA ACTTTGTGGA TGAACCATCA GAAGATGGTG CGACAAACAA GATTGAGATT 300
 AGCATGGACT GTATCCGACT GCAGGACTCG GACCTGAGTG ACCCCATGTG GCCACAGTAC 360
 ACGAACCTGG GGCTGCTGAA CAGCATGGAC CAGCAGATTG AGAACGGCTC CTCGTCCACC 420
 AGTCCCTATA ACACAGACCA CGCGCAGAAC AGCGTCACGG CGCCCTCGCC CTACGCACAG 480
 CCCAGCTCCA CCTTCGATCG TCTCTCTCCA TCACCCGCCA TCCCCTCCAA CACCGACTAC 540
 CCAGGCCCGC ACAGTTTCGA CGTGTCTCTC CAGCAGTCGA GCACCGCCAA GTCCGCCACC 600
 TGGAGCTATT CCAGTGAATC GAAGAAATCT TACTGCCAAA TTGCAAGAGC ATGCCCCATC 660
 CAGATCAAGG TGATGACCCC ACCTCCTCAG GGAGCTGTTA TCCGCGCCAT GCCTGTCTAC 720
 AAAAAAGCTG AGCAGCTCAC GGAGGTGGTG AAGCGGTGCC CCAACCATGA GCTGAGCCGT 780
 GAATTCAGC AGGACAGATG TGCCCTCTCT AGTCATTTGA TTCGAGTAGA GGGGAACAGC 840
 CATGCCAGT ATGTAGAAGA TCCCATCACA GGAAGACAGA GTGTGCTGGT ACCTTATGAG 900
 CCACCCAGG TTGGCACTGA ATTACAGACA GTCTGTGACA ATTTCTATGT TAACAGCAGT 960
 TGTGTGGAG GGTGGAACCG CGGTCCAATT TTAATCATTG TTAATCTGGA AACACAGAGT 1020
 GGGCAAGTCC TGGGCCACCG CTGCTTTGAG GCCCGGATCT GTGCTTGCCC AGGAAGAGAC 1080
 AGGAAGCGG ATGAAGATAG CATCAGAAAG CAGCAAGTTT CGGACAGTAC AAAGAACGGT 1140
 GATGGTACGA AGCCCGCGTT TCGTCAGAAC ACACATGGTA TCCAGATGAC ATCCATCAAG 1200
 AAACGAAGAT CCCAGATGA TGAATCTGTA TACTTACCAG TGAGGGGCCG TGAGACTTAT 1260
 GAAATGCTGT TGAAGATCAA AGAGTCCCTG GAATCTATGC AGTACTTCTC TCAGCACACA 1320
 ATTGAAACGT ACAGGCAACA GCAACAGCAG CAGCACCAGC ACTTACTTCA GAAACATCTC 1380
 CTTTCAGCCT GCTTCAGGAA TGAGCTTGTG GAGCCCCGGA GAGAAACTCC AAAACAATCT 1440
 GACGTCTTCT TTAGACATTC CAAGCCCCCA AACCGATCAG GTTACCCATA GAGCCCTATC 1500
 TCTATATTTT AAGTGTGTGT GTTGTATTTT CATGTGTATA TGTGAGTGTG TGTGTGTGTA 1560
 TGTGTGTGCG TGTGTATCTA GCCCTCATAA ACAGGACTTG AAGACACTTT GGCTCAGAGA 1620
 CCCAACTGCT CAAAGGCACA AAGCCACTAG TGAGAGAATC TTTTGAAGGG ACTCAAACTC 1680
 TTACAAGAAA GGATGTTTTC TGCAGATTTT GTATCCTTAG ACCGGCCATT GGTGGGTGAG 1740
 GAACCACTGT GTTGTCTCTG GAGCTTTCTG TTGTTTCTCT GGAGGGAGGG GTGAGGTGGG 1800
 GAAAGGGGCA TTAAGATGTT TATTGGAACC CTTTCTCTGT TTCTTCTGTT GTTTTCTTAA 1860
 AATTACAGG GAAGCTTTTG AGCAGGTCTC AAACCTAAGA TGCTTTTATA AGAAAAGGAG 1920
 AAAAAAGTTG TTATGTGCTG TGCATAAGTA AGTTGTAGGT GACTGAGAGA CTCAGTCAGA 1980
 CCGTTTAAAT GCTTGTCAATG TAATAATATT GCAAGTAGTA AGAAACGAGA GTGTCAAGTG 2040
 TACTGCTGGG CAGCGAGGTG ATCATTACCA AAAGTAATCA ACTTGTGGG TGGAGAGTTC 2100
 TTTGTGAGAA CTTCATTAT TGTGTCTCTC CCCTCATGTG TAGGTAGAAC ATTTCTTAA 2160
 GCTGTGTACC TGCCTCTGCC ACTGTATGTT GGCATCTGTT ATGTCTAAAG TTTTCTTGT 2220
 CATGAAACCT TGGAGAGACT ACTACAAAAA AACTGTGTGT TGGCCCCCAT AGCAGGTGAA 2280
 CTCATTTTGT GCTTTTAAAT GAAAGACAAA TCCACCCGAG TAATATTGGT CTTACGTAGT 2340
 TGTTTACCAT TATTCAAAGC TCAAAATAGA ATTTGAAGCC CTCTCAGAAA ATCTGTGATT 2400
 AATTGTCTTA ATTAGAGCTT CTATCCCTCA AGCCTACCTA CCATAAAACC AGCCATATTA 2460
 CTGATACTGT TCAGTGCATT TAGCCAGGAG ACTTACGTTT TGAGTAAGTG AGATCCAAGC 2520
 AGACGTGTTA AAATCAGCAC TCCTGGACTG GAAATTAAGG ATTGAAAGGG TAGACTACTT 2580

TTCTTTT TACTCAAAG TTTAGAGAAT CTCTGTTTCT TTCCATTTTA AAAACATATT 2640
 TTAAGATAAT AGCATAAAGA CTTTAAAAAT GTTCCTCCCC TCCATCTTCC CACACCCAGT 2700
 CACCAGCACT GTATTTTCTG TCACCAAGAC AATGATTTCT TGTATTATGAG GCTGTTGCTT 2760
 TGTGGATGT GTGATTTTAA TTTTCAATAA ACTTTTGCAT CTTGGTTTAA AAGAAA

Seq ID NO: 22 Protein sequence:
 Protein Accession #: NP_003713

1 11 21 31 41 51
 MSQSTQTNEF LSPEVFQHIW DFLEQPICSV QPIDLNFVDE PSEDGATNKI EISMDCIRMQ 60
 DSDLSDPMNP QYINLGLLNS MDQIQNGSS STSPYNTDHA QNSVTAPSPY AQPSSTFDAL 120
 SPSPAIPNT DYPGPHSFDV SFQSSSTAKS ATWTYSTELK KLYCQIAKTC PIQIKVMTFP 180
 PQGAVIRAMP VYKKAHVTE VVRCPCNHLE SREFNEGQIA PPSHLIRVEG NSHAQYVEDP 240
 ITGRQSVLVP YEPQVQTEF TTVLYNFMCN SSCVGMNRR PILIIVTLET RDGQVLGRRC 300
 FEARICACPG RDKADEDSI RKQVSDSTK NGDGTKRPFQ QNTHGIQMTS IKRRSPDDE 360
 LLYLPVRGRE TYEMLLIKE SLELMQYLPQ HTIETRYQQQ QQQHQHLLQK HLLSACFRNE 420
 LVEPRRETPEK QSDVFFRHSK PPNRSVYP

Seq ID NO: 23 DNA sequence
 Nucleic Acid Accession #: NM_001944.1
 Coding sequence: 84-3083

1 11 21 31 41 51
 TTTTCTTAGA CATTAACTGC AGACGGCTCG CAGGATAGAA GCACGGGCTC ACTTGGACTT 60
 TTTACACGAG GAAATCAGAG ACAATGATGG GGCTCTTCCC CAGAACTACA GGGGCTCTGG 120
 CCATCTTCGT GGTGGTCATA TTGGTTCATG GAGAATTGCG AATAGAGACT AAAGGTCAAT 180
 ATGATGAAGA AGAGATGACT ATGCAACAAG CTAAGAAGAG GCAAAACCGT GAATGGGTGA 240
 AATTGGCCAA ACCCTGCAGA GAAGGAGAAG ATAACCTCAA AAGAAACCCA ATTGCCAAGA 300
 TTAACCTCAGA TTACCAAGCA ACCCAGAAAA TCACCTACCG AATCTCTGGA GTGGGAATCG 360
 ATCAGCCGCC TTTTGGAAATC TTTGTTGTGG ACACAAACAC TGGAGATATT AACATAACAG 420
 CTATAGTCCA CCGGAGGAAA ACTCCAAGCT TCCTGATCAC ATGTGCGGCT CTAATGCCCC 480
 AAGGACTAGA TGTAGAGAAA CCACTTATAC TAAACGGTTAA AATTTTGGAT ATTAATGATA 540
 ATCTTCCAGT ATTTTCAAA CAAATTTTCA TGGGTGAAAT TGAAGAAAAT AGTGCCCTCA 600
 ACTCACTGGT GATGATACTA AATGCCACAG ATGCAGATGA ACCAAACAC TTGAATTTCTA 660
 AAATTCGCTT CAAAATTTGTC TCTCAGGAAC CAGCAGGCAC ACCCATGTTT CTCTTAAGCA 720
 GAAACACTGG GGAAGTCCGT ACTTTGACCA ATTCTCTTGA CCGAGAGCAA GCTAGCAGCT 780
 ATCGTCTGGT TGTGAGTGGT GCAGACAAAG ATGGAGAAAG ACTATCAACT CAATGTGAAT 840
 GTAATATTAA AGTAAAGAGT GTCAACGATA ACTTCCCAAT GTTTAGAGAC TCTCAGTATT 900
 CAGCACGAT TGAAGAAAAT ATTTTAAGTT CTGAATTACT TCGATTTCAA GTAAACAGATT 960
 TGGATGAAGA GTACACAGAT AATTGGCTTG CAGTATATTT CTTTACCTCT GGAATGAAG 1020
 GAAATTTGGT TGAATAACAA ACTGATCCTA GAACTAATGA AGGCATCTCT AAGTGGTGA 1080
 AGGCTCTAGA TTAAGAACAA CTACAAAGCG TGAACCTTAG TATTGCTGTC AAAACAAAG 1140
 CTGAATTTCA CCAATCAGTT ATCTCTCGAT ACCGAGTTCA GTCAACCCCA GTCACAATTC 1200
 AGGTAAATAA TGTAAAGAGG GGAATTGCAT TCCGTCCTGC TTCCAAGACA TTACTGTGTC 1260
 AAAAAGGCAT AAGTAGCAAA AAATTGGTGG ATTATATCCT GGAACATAT CAAGCCATCG 1320
 ATGAGGACAC TAACAAAGCT GCCTCAAATG TCAAAATATG CATGGGACGT AACGATGGTG 1380
 GATACCTAAT GATTGATTCA AAAACTGCTG AAATCAAATT TGTCAAAAT ATGAACCGAG 1440
 ATTCTACTTT GATCTTTAAC AAAACAATCA CAGCTGAGGT TCTGGCCATA GATGAATACA 1500
 CGGGTAAAC TTCTACAGGC ACGGTATATG TTAGAGTACC CGATTTCAAT GACAAATTGTC 1560
 CAACAGCTGT CCTGAAAAA GATGCAGTTT GCAGTCTTTC ACCTTCCGTG GTTGTCTCCG 1620
 CTAGAACACT GAATAATAGA TACACTGGCC CCTATACATT TGCACTGGAA GATCAACCTG 1680
 TAAAGTTGCC TGCCGTATGG AGTATCACAA CCCTCAATGC TACCTCGGCC CTCTCAGAG 1740
 CCCAGGAACA GATACCTCCT GGAGTATACC ACATCTCCCT GGTACTTACA GACAGTCAGA 1800
 ACNATCGGTG TGAGATGCCA CGCAGCTTGA CACTGGAAGT GTGTGAGTGT GACACAGGG 1860
 GCATCTGTGG AACTTCTTAC CCAACCACAA GCCCTGGGAC CAGGTATGGC AGGCCGCACT 1920
 CAGGAGGCT GGGGCTGCCC GCCATCGGCC TGCTGCTCCT TGGTCTCCTG CTGCTGCTGT 1980
 TGGCCCCCTT TCTGCTGTGT ACCTGTGACT GTGGGGCAGG TTCTACTGGG GGAGTGACAG 2040
 GTGGTTTTAT TCCAGTTCCT GATGGCTCAG AAGGAACAAT TCATCAGTGG GGAATTGAAG 2100
 GAGCCCATCC TGAAGACAAG GAAATCACAA ATATTGTGT GCCTCCTGTA ACAGCCAATG 2160
 GAGCCGATTT CATGGAAGT TCTGAAGTTT GTACAAATAC GTATGCCAGA GGCACAGCGG 2220
 TGAAGGCAC TTCAGGAATG GAAATGACCA CTAAGCTTGG AGCAGCCACT GAATCTGGAG 2280
 GTGCTGCAGG CTTTGCAACA GGGACAGTGT CAGGAGCTGC TTCAGGATTC GGAGCAGCCA 2340
 CTGGAGTTGG CATCTGTTCC TCAGGGCAGT CTGGAACCAT GAGAACCAAG CATTCACCTG 2400
 GAGGAACCAA TAAGGACTAC GCTGATGGGG CGATAAGCAT GAATTTTCTG GACTCCTACT 2460
 TTTCTCAGAA AGCATTTGCC TGTGCGGAGG AAGACGATGG CCAGGAAGCA AATGACTGCT 2520
 TGTGATCTA TGATAATGAA GGGCAGATG CCACTGGTTC TCCTGTGGGC TCCGTGGGTT 2580
 GTTGCAAGTT TATTGCTGAT GACCTGGATG ACAGCTTCTT GGACTCACTT GGACCCAAAT 2640
 TTAACAAACT TGCAAGATA AGCCTTGGTG TTGATGATGA AGGCAAGAAA GTTCAGCCAC 2700
 CCTCTAAAGA CAGCGTTAT GGGATTGAAT CCTGTGGCCA TCCCATAGAA GTCCAGCAGA 2760
 CAGGATTTGT TAAGTGCCAG ACTTTGTCAG GAAGTCAAGG AGCTTCTGCT TTGTCCGCCT 2820
 CTGGGTCTGT CCAGCCAGCT GTTTCATCC CTGACCCTCT GCAGCATGGT AACTATTTAG 2880
 TAAAGGAGAC TTACTCGGCT TCTGTTTCCC TCGTGCAACC TTCCACTGCA GGCTTTGATG 2940
 CACTTCTCAC ACAAAATGTG ATAGTGACAG AAAGGGTGTG CTGTCCCAT TCCAGTGTTC 3000
 CTGGCAACCT AGCTGGGCCA ACACAGCTAC GAGGGTCACA TACTATGCTC GTACAGAGG 3060
 ATCCTTGCTC CCGTCTAATA TGACCAAGAT GAGCTGGAAT ACCACACTGA CCAAACTCTG 3120
 ATCTTTGAC TAAAGTATTC AAAATAGCAT AGCAAAGCTC ACTGTATTGG GCTAATAATT 3180
 TGGCACTTAT TAGCTTCTCT CATAAACTGA TCACGATTAT AAATTAATG TTTGGGTTCA 3240
 TACCCCAAAA GCAATATGTT GTCACTCCTA ATTCTCAAGT ACTATTCAAA TTGTAGTAAA 3300
 TCTTAAAGTT TTTCAAAACC CTAATAATCAT ATTCGC

Seq ID NO: 24 Protein sequence:
 Protein Accession #: NP_001935.1

1 11 21 31 41 51

	MMGLFPRTTG	ALAIFVVVIL	VHGLRIETK	GOYDEEEMTM	QOAKRRQKRE	WVKFAKPCRE	60
	GEDNSKRNPI	AKITSDYQAT	QKITYRISGV	GIDQPPFGIF	VVDKNTGDIN	ITAIVDREET	120
5	PSFLITCRAL	NAQGLDVEKP	LILTVKILDI	NDNPPVVSQQ	IFMGEIEENS	ASNSLVMILN	180
	ATDADEPNHL	NSKIAFKIVS	QEPAGTSMFL	LSRNTGVEVRT	LTNSLDREQA	SSYRLVVSGA	240
	DKDGEGLSTQ	CECNIVKQDV	NDNPPMFRDS	QYSARIEENI	LSSELLRFQV	TDLDEEYTDN	300
	WLAVYFPTSG	NEGNWPEIQT	DPRTEGILK	VVKALDYBQL	QSVKLSIAVK	NKAEFHQSVI	360
	SRYRVQSTPV	TIQVINVREG	IAFRPASKTF	TVQKGISSEK	LVVDYILGTQ	AIDEDTNKAA	420
10	SNVKYVMGRN	DGGYLMIDSK	TAEIKFVKNM	NRDSTFIVNK	TITAEVLAI	ETGKTSTGT	480
	VYVRVPDFND	NCPTAVLEKD	AVCSSSPSVV	VSARTLNTRY	TGPTTFALD	QPVKLEPVNS	540
	ITTLNATSAL	LRAQEQIPPG	VYHISLVLT	SQNNRCMPR	SLTLEVCQCD	NRGICGTSYP	600
	TTSPGTRYGR	PHSGRLGPAA	IGLLLLGLLL	LLLAPELLLT	CDCAGSTGG	VTGGFIPVPD	660
	GSEGTIHQWG	IEGAHPEDKE	ITNICVFPVT	ANGADFMESS	EVCTNTYARG	TAVEGTSGME	720
15	MTTKLGAATE	SGGAAGPATG	TVSGAASGFG	AATGVGICSS	GQSGTMRTRH	STGGTNKDYA	780
	DGAISMNPLD	SYFQKAFAC	AEEDDGQEAN	DCLLIYDNEG	ADATGSPVGS	VGCCSFIADD	840
	LDDSPLDLSL	KPFKLAEIS	LGVDGEGKEV	QPPSKDSGYG	IESCGHPIEV	QQTGFVKCQT	900
	LSGSQGASAL	SASGSVQPAV	SIPDPLQHGN	YLVETETYSAS	GSLVQPSSTAG	FDPLLTQNV	960
	VERTICPIS	SVPGNLAGPT	QLRGSHTMLC	TEDPCSRLL			

Seq ID NO: 25 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 56-1642

25	1	11	21	31	41	51	
	AGTATCCCAG	GAGGAGCAAG	TGGCAGCTCT	TGGGACCTAG	GCTGCCCTTG	CCGTTCATGTC	60
	GCAAGGGGATC	CTTTCTCCGC	CAGCGGGCTT	GCTGTCCGAT	GACGATGTCG	TAGTTTCTCC	120
	CATGTTTGAG	TCCACAGCTG	CAGATTGGGG	GTCGTGGGTA	CGCAAGAACC	TGCTATCAGA	180
30	CTGCTCTCTG	GTCTCTACCT	CCCTAGAGGA	CAAGCAGCAG	TTCCATCTCT	AGGACAGTAT	240
	GGAGAAGGTG	GAATATATCT	TGAGGGTTAG	GCCCTTGTTA	CCTTCAGAGT	TGGAACGACA	300
	GGAGATCAG	GGTGTGTCTC	GTATTGAGAA	TGTGGAGACC	CTTGTTCTAC	AAGCACCCAA	360
	GGACTCTTTT	GCCCTGAAGA	GCAATGAACG	GGGAATTGGC	CAAGCCACAC	ACAGTTTAC	420
	CTTTTCCCAG	ATCTTTGGGC	CAGAAGTGGG	ACAGGCATCC	TTCTTCAACC	TAACTGTGAA	480
35	GGAGATGGTA	TAGATTGATC	TCAAAGGGCA	GAACCTGGCTC	ATCTATACAT	ATGGAGTCAC	540
	TAACTCAGGG	AAAACCCACA	CGATTCAAGG	TACCATCAAG	GATGGAGGGA	TTCTCCCCCG	600
	GTCCCTGGCG	CTGATCTTCA	ATAGCCTCCA	AGGCCAACTT	CATCCAACAC	CTGATCTGAA	660
	GCCCTTGCTC	TCCAATGAGG	TAATCTGGCT	AGACAGCAAG	CAGATCCGAC	AGGAGGAAAT	720
	GAAGAAGCTG	TCCCTGCTAA	ATGGAGGCTT	CCAAGAGGAG	GAGCTGTCCA	CTTCTTGAA	780
40	GAGGAGTGTG	TACATCGAAA	GTGGATAGG	TACCAGCACC	AGCTTCGACA	GTGGCATTCG	840
	TGGGCTCTCT	TCTATCAGTC	AGTGATACAG	CAGTAGCCAG	CTGGATGAAA	CAAGTCATCG	900
	ATGGGCACAG	CCAGCAGTCG	CCCCACTACC	TGTCCCGGCA	AACATTGCTG	TCTCCATCTG	960
	GATCTCATTC	TTTGAGATCT	ACAACGAACT	GCTTTATGAC	CTATTAGAAC	CGCCTAGCCA	1020
	ACAGCGCAAG	AGGCAGACTT	TGCGGCTATG	CGAGGATCAA	AATGGCAATC	CCTATGTGAA	1080
45	AGATCTCAAC	TAGATTCAATG	TGCAAGATGC	TGAGGAGGCC	TGGAAGCTCC	TAAAGTGGG	1140
	TGTAAGAAAC	CAGAGCTTTG	CCAGCACCCA	CCTCAACAGG	AACTCCAGCC	GCAGTCACAG	1200
	CATCTTCTCA	ATCAGGATCT	TACACCTTCA	GGGGGAAGGA	GATATAGTCC	CCAAGATCAG	1260
	CGAGCTGTCA	CTCTGTGATC	TGCTGTGCTC	AGAGCGCTGC	AAAGATCAGA	AGAGTGGTGA	1320
	ACGGTTGAAG	GAAGCAGGAA	ACATTAAACAC	CTCTCTACAC	ACCCCTGGCC	GCTGTATTGC	1380
50	TGCCCTTCGT	CAAAACCGGC	AGAACCAGTC	AAAGCAGAAC	CTGGTTCCCT	TCCGTGACAG	1440
	CAAGTTGACT	CGAGTGTTC	AAGGTTTCTT	CACAGGCCGA	GGCCGTTCCT	GCATGATTGT	1500
	CAATGTGAA	CCCTGTGATC	CTACCTATGA	TGAAACTCTT	CATGTGGCCA	AGTTCTCAGC	1560
	CATTGCTAGC	CAGGTGACTT	GTGCATGCCC	CACCTATGCA	ACTGGGATTC	CCATCCCTGC	1620
	ACTCGTTCAT	CAAGGAACAT	AGTCTTCAGG	TATCCCCAGC	CTTAGAGAAA	GGGGCTAAGG	1680
55	CAGACACAGG	CCTTGATGAT	GATATTGAAA	ATGAAGCTGA	CATCTCCATG	TATGGCAAAG	1740
	AGGAGCTCCT	ACAAGTTGTG	GAAGCCATGA	AGACACTGCT	TTTGAAGGAA	CGACAGGAAA	1800
	AGCTACAGCT	GGAGATGCAT	CTCCGAGATG	AAATTGCAAA	TGAGATGGTA	GAACAGATGC	1860
	AACAGCGGGA	ACAGTGTGTC	AGTGAACATT	TGGACACCCA	AAAGGAACCT	TTGGAGGAAA	1920
	TGTATGAAGA	AAAACATAAT	ATCCTCAAGG	AGTCACTGAC	AAGTTTTTAC	CAAGAAGAGA	1980
60	TTCAGGAGCG	GGATGAAAAG	ATTGAAGAGC	TAGAAGCTCT	CTTCGAGGAA	GCCAGACAAC	2040
	AGTCAGTGGC	CCATCAGCAA	TCAGGGTCTG	AATTGGCCCT	ACGGCGGTCA	CAAAGGTTGG	2100
	CAGCTTCTGC	CTCCACCCAG	CAGCTTCAGG	AGGTTAAAGC	TAAATTACAG	CAGTGCAAG	2160
	CAGAGCTAAA	CTCTACCACT	GAAGAGTTGC	ATAAGTATCA	GAAATGTGTA	GAACCAACAC	2220
	CCTCAGCCAA	GCCCTTCACC	ATTGATGTGG	ACAAGAAGTT	AGAAGAGGGC	CAGAAGAATA	2280
65	TAAGGCTGTT	GCGGACAGAG	CTTCAGAAAC	TTGGTGAGTC	TCTCCAATCA	GCAGAGAGAG	2340
	CTTGTGTTCA	CAGCACTGGG	GCAGGAAAAC	TTGCTCAAGC	CTTGACCACT	TGTGATGACA	2400
	TCCTTAATCAA	ACAGGACCCAG	ACTCTGGCTG	AACTGCAGAA	CAACATGGTG	CTAGTGAAAC	2460
	TGGACCTTCG	GAAGAAGGCA	GCATGTATTG	CTGAGCAGTA	TCATACCTGT	TTGAAACTCC	2520
	AAGGCCAGGT	TTCTGCAAAA	AAGCGCCTTG	GTACCAACCA	GGAAAATCAG	CAACCAAAACC	2580
70	AACAACCAAC	AGGGAAGAAA	CCATTCTTTC	GAAATTTACT	TCCCGGAACA	CCAACCTGCC	2640
	AAAGCTCAAC	AGACTGCAGC	CCTTATGCCC	GGATCCTACG	CTCACGGCGT	TCCCTTTTAC	2700
	TCAAATCTGG	GCCTTTGGC	AAAAAGTACT	AAGGCTGTGG	GGAAAGAGAA	GAGCAGTCAT	2760
	GGCCCTGAGG	TGGGTGAGCT	ACTCTCCTGA	AGAAATAGGT	CTCTTTTATG	CTTTACCATA	2820
	TATCAGGAAT	TATATCCAGG	ATGCAATACT	CAGACACTAG	CTTTTCTCTC	ACTTTTGTAT	2880
75	TATAACCACC	TATGTAATCT	CATGTTGTTG	TTTTTTTTTA	TTTACTTATA	TGATTCTTAT	2940
	GCACACAAAA	ACAGTTATAT	TAAAGATATT	ATTGTTTACA	TTTTTTTATTG	AATTCCAAAT	3000
	GTAGCAAAAAT	CATTAAAAACA	AATTATAAAA	GGGACAGAAA	AA		

Seq ID NO: 26 Protein sequence:
Protein Accession #: Eos sequence

80	1	11	21	31	41	51	
	MSQGLSPPA	GLLSDDDDVV	SPMFESTAAD	LGSVVRKNLL	SDCSVVSTSL	EDKQVPSSE	60
85	SMEKVKVYL	VRPLLPSELE	RQEDQGCVR	ENVETLVLQA	PKDSFALKSN	ERIGIQATHR	120
	FTFSQIFGPE	VQASFFNL	VKEMVKDVLK	QGNWLYTYG	VTNSGKTHTI	QGTIKDGGIL	180
	PRSLALIFNS	LQGLHPPTD	LKPLLSNEVI	WLDKSKIRQE	EMKLSLLNG	GLQEELSTS	240
	LKRSVYIESR	IGTSTSPDSG	IAGLSSISQC	TSSSQLDETS	HRWAQPTAP	LPVPANIRFS	300

INISPFPEIYN ELLYDLLEPP SQQRKRQTLR LCEDQNGNPF VKDLNWIHVQ DAEBAWKLLK 360
 VGRKNQSPAS THLNQNSSRS HSIFSRILH LQEGDIVPK ISELSLCDLA GSERCKDQKS 420
 GERLKEAGNI NTSLHTLGRG IALRQNNQN RSKQNLVPR DSKLTRVFGQ FFTGRGRSCM 480
 IVNVNPCAST YDETLHVAKF SAIASQVTCA CPTYATGIPI PALVHQGT

Seq ID NO: 27 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 13-1424

10 1 11 21 31 41 51
 TAGAAGTTTA CAATGAAGTT TCTTCTAATA CTGCTCCTGC AGGCCACTGC TTCTGGAGCT 60
 CTTCCTCTGA ACAGCTCTAC AAGCCTGGAA AAAAATAATG TGCTATTGG TGAAGATAC 120
 15 TTAGAAAAAT TTATGGCCT TGAGATAAAC AAACCTCCAG TGACAAAAAT GAAATATAGT 180
 GGAAACTTAA TGAAGGAAAA AATCCAAGAA ATGCAGCACT TCTTGGGTCT GAAAGTGACC 240
 GGGCAACTGG ACACATCTAC CCTGGAGATG ATGCACGCAC CTCGATGTGG AGTCCCGGAT 300
 GTCCATCATT TCAGGGAAT GCCAGGGGGG CCCGTATGGA GGAACATTA TATCACCCTAC 360
 AGAATCAATA ATTACACACC TGACATGAAC CGTGAGGATG TTGACTACGC AATCCGAAA 420
 20 GCTTTCCAAAG TGAAGATTA TGTACCCCTC TTGAAATTCA GCAAGATTAA CACAGGCATG 480
 GGTGACATTT TGGTGGTTTT TGCCCGTGGA GCTCATGGAG ACTTCCATGC TTTTGATGGC 540
 AAAGGTGGAA TCCTAGCCCA TGCTTTTGGA CTGGATCTG GCATTGGAGG GGATGCACAT 600
 TTCGATGAGG ACGAATTCTG GACTACACAT TCAGGAGGCA CAAACTTGT CTCTACTGCT 660
 GTTCACGAGA TTGGCCATTC CTTAGGTCTT GGCCATTCTA GTGATCCAAA GGCCGTAATG 720
 25 TTCCCCACCT ACAATATGT TGACATCAAC ACATTTCGCC TCTCTGCTGA TGACATACGT 780
 GGCAATCAGT CCCTGTATGG AGACCCAAA GAGAACCAAC GCTTGCCAAA TCCTGACAA 840
 TCAGAACCAG TCTCTCTGTA CCCCAATTG AGTTTGTATG CTGTCACTAC CGTGGGAAAT 900
 AAGATCTTTT TCTTCAAGA CAGGTTCTTC TGGCTGAAGG TTTCTGAGAG ACCAAAGACC 960
 AGTGTATATT TAATTTCTTC CTTATGGCCA ACCTTGCCAT CTGGCATTTA AGCTGCTTAT 1020
 30 GAAATGGAAG CCAAGATCA AGTTTTCTT TTTAAAGATG ACAAATCTG GTTAATTAGC 1080
 AATTTAAGAC CAGAGCCAAA TTAATCCCAAG AGCATACATT CTTTGTGTT TCCTAACTTT 1140
 GTGAAAAAAA TTGATGAGC TGTTTTTAAC CCAAGTTTTT ATAGGACCTA CTTCTTTGTA 1200
 GATAACCACT ATTGGAGGTA TGATGAAAG AGACAGATGA TGGACCCCTG TTATCCCAA 1260
 CTGATTACCA AGAATTTCCA AGGAATCGGG CCTAAAATTG ATGCAGTCTT CTACTCTAAA 1320
 35 AACAAATACT ACTATTTCTT CCAAGGATCT AACCAATTG AATATGACT CTACTCTCAA 1380
 CGTATCACA AAACACTGAA AAGCAATAGC TGGTTTGGTT GTTGAAAATG GTGTAATTAA 1440
 TGGTTTTTGT TAGTTCAGCT CAGCTTAATA AGTATTATAT GCATATTGTC TATGTCCTCA 1500
 GTGTACCACT ACTTAGAGAT ATGTATCATA AAAATAAAAT CTGTAAACCA TAGGTAATGA 1560
 TTATATAAAA TACATAATAT TTTTCAATT TGAAAACTCT AATTGTCCAT TCTTGCTTGA 1620
 40 CTCTACTATT AAGTTTGA AAATAGTTACCT TCAAAGCAAG ATAATTCTAT TTGAAGCATG 1680
 CTCTGTAAGT TGCTTCCTAA CATCCTTGGA CTGAGAAATT ATACTTACTT CTGGCATAAC 1740
 TAAATTAAG TATATATATT TTGGCTCAA TAAAAATTG

Seq ID NO: 28 Protein sequence:
 Protein Accession #: Eos sequence

45 1 11 21 31 41 51
 MKFLILLILQ ATASGALPLN SSTSLKNNV LFGERYLEKF YGLEINKLPV TKMKVSGNLM 60
 50 KEKIQEMQHF LGLKVTQQLD TSTLEMMHAP RCGVPDVHHP REMPGGPVWR KHYITYRINN 120
 YTPDMNREDV YGAIKRFQV WSNVTPPKFS KINTGMADIL VVPARGAHGD PHAFDGGGGI 180
 LAHAFPGSGG IGGDAHFDDE EFWTHSGGT NLPLTAVHEI GHSLGLGHSS DPKAVMFPDY 240
 KYVDINTFRL SADDIRGIQS LYGDPKENQR LPNPDNSEPA LCDENLSFDA VTTVGNKIFF 300
 FKDRPFWLKV SERPKTSVNL ISSLWPTLPS GIEAAVEIEA RNQVFLPKDD KYWLISNLRP 360
 55 EPNYPKSIHS GFPPNFVKKI DAAVFNPRFY RYTFVFDNQY WRYDERRQMM DPGYPKLITK 420
 NFQGGIPKID AVFYSKNKYY YFFQGSNQPE YDFLLQRITK TLKSNWFFGC

Seq ID NO: 29 DNA sequence
 Nucleic Acid Accession #: NM_006115.1
 Coding sequence: 236..1765

60 1 11 21 31 41 51
 GCTTCAGGGT ACAGCTCCCC CGCAGCCAGA AGCGGGGCTC GCAGCCCTC AGCACCGCTC 60
 65 CGGGACACCC CACCCGCTTC CCAGGCGTGA CCTGTCAACA GCAACTTCGC GGTGTGGTGA 120
 ACTCTCTGAG GAAAAACCAT TTTGATTATT ACTCTCAGAC GTGCGTGGCA ACAAGTGACT 180
 GAGACCTAGA AATCCAAGCG TTGGAGGTCC TGAGGCCAGC CTAAGTCGCT TCAAAATGGA 240
 ACGAAGCGGT TTTGGGGGTT CCATTAGAG CCGATACATC AGCATGAGTG TGTGGACAAG 300
 CCCACGGAGA CTTGTGGAGG TGGCAGGCA GAGCCTGCTG AAGGATGAGG CCCTGGCCAT 360
 70 TGCCCGCCCTG GAGTTGCTGC CCAGGGAGCT CTTCGCCCA CTCTTCATGG CAGCCTTTGA 420
 CGGGAGACAC AGCCAGACCC TGAAGGCAAT GGTGCAGGCC TGGCCCTTCA CTGCTCTCCC 480
 TCTGGGAGTG CTGATGAAGG GACACATCT TCACTGGAG ACCTTCAAAG CTGTGCTTGA 540
 TGGACTTGAT GTGCTCTGT CCCAGGAGGT TCGCCCCAGG AGGTGGAAC TTCAAGTGCT 600
 GGATTTACGG AAGAACTCTC ATCAGGACTT CTGGACTGTA TGGTCTGGAA ACAGGGCCAG 660
 75 TCTGTACTCA TTTCCAGAGC CAGAAGCAGC TCAGCCCATG ACRAAGAAGC GAAAAGTAGA 720
 TGGTTTGAGC ACAGAGGCAG AGCAGCCCTT CATTCCAGTA GAGGTGCTCG TAGACCTGTT 780
 CCTCAAGGAA GGTCCCTGTG ATGAATTGTT CTCCTACCTC ATTGAGAAAG TGAAGCGAAA 840
 GAAAAATGTA CTACGCTGT GCTGTAAGAA GCTGAAGATT TTTGCAATGC CCATGCACGA 900
 TATCAAGATG ATCCTGAAAA TGGTGCAAGT GGAATCTATT GAAGATTGG AAGTGACTTG 960
 TACCTGGAAG CTACCCACCT TGGCGAAATT TTCTCCTTAC CTGGGCCAGA TGATTAATCT 1020
 80 GCGTAGACTC CTCCTCTCCC ACATCCATGC ATCTTCCTAC ATTTCCCGG AGAAGGAAGA 1080
 CGAGTATATC GCCCAGTCTA CCTCTCAGTT CACTCAGTCT CAGTGCCTGC AGGCTCTCTA 1140
 TGTGGACTCT TTATTTTTC TTAGAGGCCG CCTGGATCAG TTGCTCAGGC ACGTGATGAA 1200
 CCCTTGGA AACCCTCTCA TAACTAACTG CCGGCTTTG GAAGGGGATG TGATGCATCT 1260
 GTCCCAAGAT CCCAGCCTCA GTCAGCTAAG TGTCTGAGT CTAAGTGGGG TCATGCTGAC 1320
 85 CGATGTAAGT CCCGAGCCCC TCCAAGCTCT GCTGGAGAGA GCCTCTGCCA CCCTCCAGGA 1380
 CCTGGTCTTT GATGAGTGTG GGATCAGCTC CTTGCCCTCC TGCCTTCCCT 1440
 GAGCCACTGC TCCAGCTTA CAACCTTAAG CTTCTACGGG AATTCCATCT CCATATCTGC 1500

CTTGCAGAGT CTCTGCAGC ACCTCATCGG GCTGAGCAAT CTGACCCACG TGCTGTATCC 1560
 TGTCCCCCTG GAGAGTTATG AGGACATCCA TGGTACCCCT CACCTGGAGA GGCTTGCCCTA 1620
 TCTGCATGCC AGGCTCAGGG AGTTGCTGTG TGAGTTGGGG CGGCCACAGC TGGTCTGGCT 1680
 TAGTGCCAAAC CCTGTCTCTC ACTGTGGGGA CAGAACTTTC TATGACCCGG AGCCCATCCT 1740
 GTGCCCTGT TTTATGCCCTA ACTAGCTGGG TGACATATC AAATGCTTCA TTCTGCATAC 1800
 TTGGACACTA AAGCCAGGAT GTGCATGCAT CTTGAAGCAA CAAAGCAGCC ACAGTTTCAG 1860
 ACAAATGTTT AGTGTGAGTG AGGAAACAT GTTCAGTGAG GAAAAACAT TCAGACAAAT 1920
 GTTCAGTGAG GAAAAAAGG GGAAGTTGGG GATAGGCAGA TGTGTACTTG AGGAGTTAAT 1980
 GTGATCTTTG GGGAGATACA TCTTATAGAG TTAGAAATAG AATCTGAATT TCTAAAGGGA 2040
 GATTCTGGCT TGGGAAGTAC ATGTAGGAGT TAATCCCTGT GTAGACTGTT GTAAAGAAAC 2100
 TGTGAAAAT AAAGAGAAGC AATGTGAAGC AAAAAA AAAAAA

Seq ID NO: 30 Protein sequence:
 Protein Accession #: NP_006106.1

1 11 21 31 41 51
 | | | | |
 GCTTCAGGGT ACAGCTCCCC CGCAGCCAGA AGCCGGGGCT GCAGCGCCTC AGCACCCTC 60
 CGGACACCCC CACCCCTCTC CCAGGCGTGA CCTGTCAACA GCAACTTCGC GGTGTGGTGA 120
 ACTCTCTGAG GAAAAACCAT TTTGATTATT ACTCTCAGAC GTGCGTGGCA ACAAGTGAAT 180
 GAGACCTAGA AATCCAAGCG TTGGAGGTCC TGAGGCCAGC CTAAGTCGCT TCAAAATGGA 240
 ACGAAGGGCT TTTGGGGT CCATTAGAG CCGATACATC AGCATGAGTG TGTGGACAAG 300
 CCCACGGAGA CTTGTGGAGC TGGCAGGGCA GAGCCTGCTG AAGGATGAGG CCCTGGCCAT 360
 TGCCGCGCTG GAGTTCTGTC CCAGGAGCT CTTCCGCCA CTCTTCATGG CAGCCTTTGA 420
 CGGGAGACAC AGGCAGACCC TGAAGGCAAT GGTGCAGGCC TGGCCCTTCA CCTGCCTCCC 480
 TCTGGGAGTG TGTGAGAGG GACACATCT TCACCTGGAG ACCTTCAAAG CTGTGCTTGA 540
 TGGACTTGAT GTGCTCCTTG CCCAGGAGT TCGCCCCAGG AGGTGGAAAC TTCAGTGCT 600
 GGAATTTACG AAGAATCTCT ATCAGGACTT CTGGAAGTGA TGGTCTGGAA ACAGGGCCAG 660
 TCTGTACTCA TTTCCAGAGC CAGAAGCAGC TCAGCCCATG ACAAAGAAGC GAAAAGTAGA 720
 TGGTTTGAAC ACAGAGGCA AGCAGCCCTT CATTCAGSTA GAGGTGCTCG TAGACCTGTT 780
 CCTCAAGGAA GGTGCGTGTG ATGAATTGTT CTCCTACCTC ATTGAGAAAG TGAAGCGAAA 840
 GAAAAATGTA CTACGCTCTG GCTGTAAGAA GCTGAAGATT TTTGCAATGC CCATGCAGGA 900
 TATCAAGATG ATCTGAAAA TGGTGCAGCT GGACTCTATT GAAGATTGG AAGTCACTTG 960
 TACCTGGAAG ATCCCACTT TGGCGAAATT TTCTCCTTAC CTGGGCCAGA TGATTAACT 1020
 GCGTAGACTC CTCTCTCCC ACATCCATGC ATCTCTCTAC ATTTCCCGG AGAAGGAAGA 1080
 GCAGTATATC GCCGTCTTCA CCTCTCAGTT CCTCAGTCTG CAGTGCCTGC AGGCTCTCTA 1140
 TGTGGACTCT TTATTTTCC TTAGAGGCGG CCTGGATCAG TTGCTCAGGC ACGTGATGAA 1200
 CCCCTTGGA ACCCTCTCA TAACTAAGT CCGGCTTTCC GAAGGGGATG TGATGCATCT 1260
 GTCCAGAGT CCAGAGCTCA CTCAGCTAAG TGTCTGAGT CTAAGTGGGG TCATGCTGAC 1320
 CGATGTAAGT CCGAGCCCC TCAGAGCTCT GCTGGAGAGA GCCTCTGCCA CCCTCCAGGA 1380
 CCTGGTCTTT GGTGAGTGTG GATCACGGA TGATCAGCTC CTTGCCCTCC TGCCTTCCCT 1440
 GAGCCACTGC TCCAGCTTA CAACCTAAG CTTCTACGGG AATTCATCT CCATATCTGC 1500
 CTTGCAGAGT CTCTGAGC ACCTCATCGG GCTGAGCAAT CTGACCCACG TGCTGTATCC 1560
 TGTCCCCCTG GAGAGTTATG AGGACATCCA TGGTACCCCT CACCTGGAGA GGCTTGCCCTA 1620
 TCTGCATGCC AGGCTCAGGG AGTTGCTGTG TGAGTTGGGG CGGCCACAGC TGGTCTGGCT 1680
 TAGTGCCAAAC CCTGTCTCTC ACTGTGGGGA CAGAACTTTC TATGACCCGG AGCCCATCCT 1740
 GTGCCCTGT TTTATGCCCTA ACTAGCTGGG TGACATATC AAATGCTTCA TTCTGCATAC 1800
 TTGGACACTA AAGCCAGGAT GTGCATGCAT CTTGAAGCAA CAAAGCAGCC ACAGTTTCAG 1860
 ACAAATGTTT AGTGTGAGTG AGGAAACAT GTTCAGTGAG GAAAAACAT TCAGACAAAT 1920
 GTTCAGTGAG GAAAAAAGG GGAAGTTGGG GATAGGCAGA TGTGTACTTG AGGAGTTAAT 1980
 GTGATCTTTG GGGAGATACA TCTTATAGAG TTAGAAATAG AATCTGAATT TCTAAAGGGA 2040
 GATTCTGGCT TGGGAAGTAC ATGTAGGAGT TAATCCCTGT GTAGACTGTT GTAAAGAAAC 2100
 TGTGAAAAT AAAGAGAAGC AATGTGAAGC AAAAAA AAAAAA

Seq ID NO: 31 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 64-2754

1 11 21 31 41 51
 | | | | |
 GGCAGGTCTC GCTCTCGGCA CCCTCCCGGC GCCCGCGTTC TCCTGGCCCT GCCCGGCATC 60
 CCGATGGCCG CCGCTGGGCC CCGGCGCTCC GTGCGCGGAG CCGTCTGCCT GCATCTGCTG 120
 CTGACCCCTG TGATCTTCAG TCGTGATGGT GAAGCCTGCA AAAAGGTGAT ACTTAATGTA 180
 CCTTCTAAAC TAGAGGCAGA CAAAATAATT GGCAGAGTTA ATTTGGAAGA GTGCTTCAGG 240
 TCTGCAGACC TCATCCGGTC AAGTGATCCT GATTTAGAG TTCTAAATGA TGGGTCACTG 300
 TACACAGCCA GGGCTGTTGC GCTGTCTGAT AAGAAAAGAT CATTTACCAT ATGGCTTTCT 360
 GACAAAAGGA AACAGACACA GAAAGAGGTT ACTGTGCTGC TAGAACATCA GAAGAAGGTA 420
 TCGAAGACAA GACACACTAG AGAACTGTT CTCAGGCGTG CCAAGAGGAG ATGGGCACCT 480
 ATTCCTTGCT CTATGCAAGA GAATTCCTTG GGCCTTTCC CATTTGTTCT TCAACAAGTT 540
 GAATCTGATG CAGCAGAGAA CTATCTGTC TTCTACTCAA TAAGTGGAGC TGGAGTTGAT 600
 AAAGAACCTT TAAATTTGTT TTATATAGAA AGAGACACTG GAAATCTATT TTGCACTCGG 660
 CCTGTGGATC GTGAAGAATA TGATGTTTTT GATTGATTG CTTATGCGTC AACTGCAGAT 720
 GGATATTGAG CAGATCTGCC CCTCCACTA CCCATCAGGG TAGAGGATGA AAATGACAAC 780
 CACCTCTGTT TCACAGAAGC AATTTATAAT TTTGAAGTTT TGGAAAGTAG TAGACCTGGT 840
 ACTACAGTGG GGGTGGTTTG TGCCACAGAC AGAGATGAAC CGGACACAAT GCATACGCGC 900
 CTGAAATACA GCATTTTGCA GCAGACACCA AGGTCACTG GGTCTTTTC TGTGCATCCC 960
 AGCAGAGCG TAATCCACAC AGTCTCTCAT TATTTGGACA GAGAGGTTGT AGACAAGTAC 1020
 TCATTGATAA TGAAGTACA AGACATGGAT GGCCAGTTTT TTGGATTGAT AGGCACATCA 1080
 ACTTGTATCA TAACAGTAAC AGATTCAAT GATAATGCAC CCACCTTCAG ACAAATGCT 1140
 TATGAAGCAT TTGTAGAGGA AATGTCATT AATGTGGAAA TCTTACGAAT ACCTATAGAA 1200
 GATAAGGATT TAATTAACAC TGCCAAATTG AGAGTCAATT TTACCATTTT AAAGGGAAT 1260
 GAAAATGGAC ATTTCAAAAT CAGCAGAC AAAGAACTA ATGAAGGTGT TCTTTCTGTT 1320
 GTAAAGCCAC TGAATATGA AGAAACCGT CAAGTGAACC TGGAAATGG AGTAAACAAT 1380
 GAAGCGCCAT TTGCTAGAGA TATTTCCAGA GTGACAGCCT TGAACAGAGC CTTGGTTACA 1440
 GTTCATGTGA GGGATCTGGA TGAGGGGCT GAATGCACCT CTGCAGCCCA ATATGTGCGG 1500
 ATTAAGAAA ACTTAGCAGT GGGGTCAAAG ATCAACGGCT ATAAGGCATA TGACCCCGAA 1560

	AATAGAAATG	GCAATGGTTT	AAGGTACAAA	AAATTGCATG	ATCCTAAAGG	TTGGATCACC	1620
	ATTGATGAAA	TTTCAGGGTC	AATCATAACT	TCCAAAATCC	TGGATAGGGA	GGTTGAAACT	1680
	CCCAAAAAAT	AGTTGTATAA	TATTACAGTC	CTGGCAATAG	ACAAAGATGA	TAGATCATGT	1740
5	ACTGGAAACAC	TTGCTGTGAA	CATTGAAGAT	GTAAATGATA	ATCCACCAGA	AATACTTCAA	1800
	GAATATGTAG	TCATTTGCAA	ACCAAAAAATG	GGGTATACCG	ACATTTTAGC	TGTTGATCCT	1860
	GATGAACCTG	TCCATGGAGC	TCCATTTTAT	TTCACTTTGC	CCAATACTTC	TCCAGAAATC	1920
	AGTAGACTGT	GGAGCCTCAC	CAAAAGTTAAT	GATACAGCTG	CCCGTCTTTC	ATATCAGAAA	1980
	AATGCTGGAT	TTCAAGAATA	TACCATTCTC	ATTACTGTAA	AAGACAGGGC	CGGCCAAGCT	2040
10	GCAACAAAAT	TATTGAGAGT	TAATCTGTGT	GAATGTACTC	ATCCAACTCA	GTGTCGTGGG	2100
	ACTTCAAGGA	GTACAGGAGT	AATACTTGGA	AAATGGGCAA	TCCTTGCAAT	ATTACTGGGT	2160
	ATAGCACTGC	TCTTTTCTGT	ATTGCTAACT	TTAGTATGTG	GAGTTTTTGG	TGCAACTAAA	2220
	GGGAAACGTT	TTCTGAAGA	TTTAGCACAG	CAAAACTTAA	TTATATCAAA	CACAGAAGCA	2280
	CCTGGAGAGC	ATAGAGTTGT	CTCTGCCAAT	GGATTTATGA	CCCAAACTAC	CAACAACTCT	2340
	AGCCCAAGGT	TTTGTGGTAC	TATGGGATCA	GGAATGAAAA	ATGGAGGGCA	GGAAACCAT	2400
15	GAAATGATGA	AAGGAGGAAA	CCAGACCTTG	GAATCCTGCC	GGGGGGCTGG	GCATCATCAT	2460
	ACCCTGAGCT	CCTGCAGGGG	AGGACACACG	GAGGTGGACA	ACTGCAGATA	CACCTACTCG	2520
	GAGTGGCACA	GTTTTACTCA	ACCCCGTCTC	GGTGA AAAAT	TGCATCGATG	TAATCAGAA	2580
	GAAGACCGCA	TGCCATCCCA	AGATTATGTC	CTCACTTATA	ACTATGAGGG	AAGAGGATCT	2640
	CCAGCTGGTT	CTGCTGGCTG	CTGCAGTGAA	AAGCAGGAAG	AAGATGGCCT	TGACTTTTTA	2700
20	AATAATTGGG	AACCCAAAT	TATTACATTA	GCAGAAGCAT	GCACAAAGAG	ATAATGTCAC	2760
	AGTGCTACAA	TATGGTCTTT	CTCAGACATT	CTGGAGGTTT	CCAAAAATAA	TATTGTAAAG	2820
	TTCAATTTC	ACATGTATGT	ATATGATGAT	TTTTTTCTCA	ATTTTGAATT	ATGCTACTCA	2880
	CCAATTATTA	TTTTTAAAGC	CAGTTGTTCG	TTATCTTTTC	CAAAAAGTGA	AAAATGTTAA	2940
25	AACAGACAAC	TGGTAAATCT	CAAACTCCAG	CACCTGGAAT	AAGGTCTCTA	AAGCATCTGC	3000
	TCTTTTTTTT	TTTTAGCGAT	ATTTTAGTAA	TAAATATGCT	GGATAAATAT	TAGTCCAACA	3060
	ATAGCTAAGT	TATGCTAATA	TACATTATT	ATGTATTAC	TTTAAGTGAT	AGTTTAAAAA	3120
	ATAAACAAAG	AATATTGAGT	ATCACTATGT	GAAGAAAGTT	TTGGA AAAAG	AACAATGAAG	3180
	ACTGAATTAA	ATTAAAAAATG	TTGCAGCTCA	TAAAGAAATG	GGACTCACCC	CTACTGCACT	3240
30	ACCAAAATTA	TTTTGACTTG	GAGGCAAAAT	GTGTTGAAGT	GCCCTATGAA	GTAGCAATTT	3300
	TCTATAGGAA	TATAGTTGGA	AATAAATGTG	TGTTGTGATA	TTATTATTA	TCAATGCAAT	3360
	ATTTAAAAAT	AAATGAGAAC	AAGAGGAAA	ATGGTAAAAA	CTTGAATGA	GGCTGGGGTA	3420
	TAGTTTGCTC	TACAATAGAA	AAAAGAGAGA	GCTTCCCTAGG	CCTGGGCTCT	TAAATGCTGC	3480
	ATTATAACTG	AGTCTATGAG	GAAATAGTTC	CTGTCCAATT	TGTGTAATTT	GTTTAAAAAT	3540
35	GTAAATAAAT	TAAACTTTTC	TGGTTTCTGT	GGGAAGGAAA	TAGGGAAATCC	AATGGAACAG	3600
	TAGCTTTGCT	TTGCAGTCTG	TTTCAAGATT	TCTGCATCCA	CAAGTTAGTA	GCAAACTGGG	3660
	GAATACTCGC	TGCAGCTGGG	TTTCCCTGCT	TTTTGGTAGC	AAGGGTCCAG	AGATGAGGTG	3720
	TTTTTTTTCG	GGAGCTAATA	ACAAAAACAT	TTTAAAACTT	ACCTTTACTG	AAGTTAAATC	3780
	CTCTATTGCT	GTCTTATTC	TCTCTATAG	TGACCAACAT	CTTTTAAAT	TAGATCCAAA	3840
40	TAACCATGTC	CTCCTAGAGT	TAGAGGGCTA	GAGGGAGCTG	AGGGGAGGAT	CTTACTGAAA	3900
	GCACCTGGG	GAGATTGATT	GTCCCTAAAC	CTAAGCCCCA	CAAACTTGAC	ACCTGATCAG	3960
	GTCTGGGAGC	TACAAAAATT	CATTTTCTC	CTCACTGCCC	TTCTTCTGAG	TGGCATGGC	4020
	CTGAATCAAG	GAAAGCCAGG	CCTTGTGGGC	CCCCTTCTTT	CGGCTTCTG	CTAAGCAAC	4080
	ACCTCCAGCA	GAGATTCCCT	TAAAGTACTC	CAGGTTTTCC	ACCATCCTTC	AGCGTGAATT	4140
45	AATTTTAAAT	CAGTTTGTCT	TCTCCAGAGA	AATTTTAAAA	TAATAGAAGA	AATAGAAAT	4200
	TTGAATGTAT	AAAAGAAAAA	GATCAAGTTG	TCATTTTAGA	ACAGAGGGAA	CTTTGGGAGA	4260
	AAGCAGCCCA	AGTCAAGTTT	TTGTACAGTC	AGAGGGCAAC	AGGAAGATGC	AGGCCTTCAA	4320
	GGGCAAGGAG	AGGCCACAAG	GAATATGGGT	GGGAGTAAAA	GCAACATCGT	CTGCTTCATA	4380
	CTTTTCTCTA	GGCTTGGCAC	TGCCTTTTCC	TTTCTCAGGC	CAATGGCAAC	TGCCATTGTA	4440
50	GTCCGGTGAG	GGATCAGCCA	ACCTCTTCTC	TATGGCTCAC	CTTATTGGA	GTGAGAAATC	4500
	AAGGAGACAG	AGCTGACTGC	ATGATGAGTC	TGAAGGCATT	TGCAGGATGA	GCCTGAACTG	4560
	GTGTGTCAGA	ACAAACAAAG	CATTCAATGG	AATTGTTGTA	TTCCCTCTGC	AGCCCTCCTT	4620
	CTGGGCACCTA	AGAAGGTCTA	TGAATTAAT	GCCTATCTAA	AATTCGTATT	TATTCCTACA	4680
	TTTTCTGTTT	TCTAATTTGA	CCTAAAAATC	TATGTGTTTT	AGACTTAGAC	TTTTTATTGC	4740
55	CCCCCCCCCT	TTTTTTTTTG	AGACGGAGTC	TCGCTCTGAC	GCACAGGCTG	GAGTGCAGTG	4800
	GCTCCGATCT	CTGCTCACTG	AAAGCTCCGC	CTCCCGGGTT	CATGCCATTG	TCCTGCCTCA	4860
	GCCTCCTGAG	TAGCTGGGAC	TACAGGCGCC	CACCACCAAG	CCCGGCTAAT	TTTTTGTATT	4920
	TTTAATAGAG	ACGGGGTTTC	ACTGTGTTAG	CCAGGATGGT	CTCGATCTCC	TGACCTCGTG	4980
	ATCCGCCCTGC	CTCGGCTCC	CAAGTGCTG	GGATTACAGG	CATGACCAC	CGCTCCCGGC	5040
	CTTGTTTTTCC	GTTTAAAGTC	GTCTTCTTTT	AATGTAATCA	TTTTGAACAT	GTGTGAAAGT	5100
60	TGATCATACG	AATTGGATCA	ATCTTGAAAT	ACTCAACCAA	AAGACAGTCG	AGAAGCCAGG	5160
	GGGAGAAAAG	ACTCAGGGCA	CAAAATATTG	GTCTGAGAA	GGAATTCCTC	GTAAGCCTAG	5220
	TTGCTGAAAT	TTCTGCTGT	AACCAGAAGC	CAGTTTATATC	TAACGGCTAC	TGAAACACCC	5280
	ACTGTGTTTT	GCTCACTCCC	TCACTCACCG	ATCAAAACCT	GCTACCTCCC	CAAGACTTTA	5340
65	CTAGTGCCGA	TAACTTTCT	CAAAGAGCAA	CCAGTATCAC	TTCCCTGTTT	ATAAAACCTC	5400
	TAACCATCTC	TTTGTCTTT	GAACATGCTG	AAAACCACTT	GGTCTGCATG	TATGCCCGAA	5460
	TTTGAATTC	TTTTCTCTCA	AATGAAAAAT	TAATTTTAGG	GATTCATTTT	TATATTTTCA	5520
	CATATGTAGT	ATTATTATTT	CCTTATATGT	GTAAGGTGAA	ATTTATGGTA	TTTGAGTGTG	5580
	CAAGAAAATA	TATTTTAAAA	GCTTTCAATT	TTCCCCAGT	GAATGATTGA	GAATTTTFTA	5640
70	TGTAAATATA	CAGAATGTTT	TTTCTTACTT	TTATAAGGAA	GCAGCTGTCT	AAAATGCAAT	5700
	GGGGTTTGT	TTGCAATGTT	TTAAACAGAG	TTTTAGTATT	GCTATTAAAA	GAAGTTACTT	5760
	TGCTTTTAAA	GAAACTTGGC	TGCTTAAAAAT	AAGCAAAAAAT	TGGATGCATA	AAGTAATATT	5820
	TACAGATGTG	GGGAGATGTA	ATAAAACAAT	ATTAACCTGG	TTTCTTGTTT	TTGCTGTATT	5880
	TAGAGATTAA	ATAATTCTAA	GATGATCACT	TTGCAAAATT	ATGCTTATGG	CTGGCATGGA	5940
75	AATAGAAATA	CTCAATTATG	TCTTTGTTGT	ATTAATGGGG	AATATTTTGG	ACAATGTTTC	6000
	ATTATCAAA	TGTCGACATC	ATTAATATAT	ATTGTAATGT	TGGGAAGAGA	TCACTATTTT	6060
	GAAGCACAGC	TTTACAGATG	AGTATCTATG	ATACATATGT	ATAATAAAT	TTGATCGGGT	6120
	ATTAAAAATA	TTAGAAGGTG	GTTATAATTG	CAGAGTATTC	CATGAATAGT	ACACTGACAC	6180
	AGGGGTTTTA	CTTTGAGGAC	CAGTGTAGTC	AAGGGA AAAAC	ATGAGTTAAA	AAGAAAAGCA	6240
80	GGCAATATTG	CAGTCTTGAT	TCTGCCACTT	ACAGGATAGA	TAATGCCTGA	ACTTTAATGA	6300
	CAAGATGATC	CAACCAATAA	GGTGCTCTGT	GCTTCACAGT	GAATCTTTTC	CCCATGCAGG	6360
	AGTGTGCTCC	CCTACAAACG	TTAAGACTGA	TCATTTCAAA	AATCTATTAG	CTATATCAAA	6420
	AGCCTTACAT	TTTAATATAG	GTTGAACCAA	AATTTCAATT	CCAGTAACTT	CTATTGTAAC	6480
	CATTATTTTT	GTGATGTCT	TCAAGAAATG	TCATTGGATT	TTTGTGTTGA	ATAGTAAAA	6540
85	ACCGGATACA	TTTCAAGTGT	CCTTCAGTAT	TGATTGGGTT	GAATATTGGG	TCATAATGGT	6600
	TGAGAAGCAT	GGACACTAGA	GCCAGAATGC	TTGGATATGA	ATCCTGGATC	TGTCACTTAC	6660
	TTCTGTGTGA	CCTTTGAAAG	GCTACTTATT	TCCTCTCTTA	GCTTTCTCAT	TAAAAATCAAT	6720
	GAACAAATGCC	AGCCTCATGG	GGTGTGTGAA	TGATTAAATT	AGTTAATATA	CCTAAAGTAC	6780

ATAGAACACT GCCTGCACAT AGTAAAGAA TTATAAGTGT GAGGTAGTTG GTAAATATAT 6840
 GTAGTTGGAT ATACTACCGA ACAATATCTA ATCTCTTTTT AGGGAAATAA AGTTTGTGCA 6900
 TATATATAAT CCCGAAACAT G

5 Seq ID NO: 32 Protein sequence:
 Protein Accession #: NP_001932.1

1	11	21	31	41	51	
MAAAGPRRSV	RGAVCLHLLL	TLVIFSRDGE	ACKKVILNVP	SKLEADKIIG	RVNLEECFRS	60
ADLIRSSDPD	FRVLNDGSVY	TARAVALSDK	KRSFTIWLSD	KRKQTQKEVT	VLLHQQKKVS	120
KTRHTRETVL	RRAKRRWAPI	PCSMQENSLG	PFPLFLQQVE	SDAAQNYTVF	YSISGRGVDK	180
EPLNLFYIER	DTGNLFCTRP	VDREEDYDVF	LIAYASTADG	YSADLPLPLP	IRVEDENDNH	240
PVFTEAIYNF	EVLESSRPGT	TGVVVCATDR	DEPDTMHTRL	KYSILQQTFR	SPGLFSVHPS	300
TGVITTVSHY	LDREVVVDKYS	LIMKVQDMDG	QFFGLIGTST	CIITVTSND	NAPTRQONAY	360
EAFFEENAFN	VELLRIBIED	KDLINTANWR	VNFTILKGNE	NGHFKISTDK	ETNEGVLVV	420
KPLNYEENRQ	VNLEIGVNNE	APFARDIPRV	TALNRALVTV	HVRDLDEGPE	CTPAAQYVRI	480
KENLAVGSKI	NGYKAYDPEN	RNGNGLRYKK	LHDPKGWITI	DEISGSIITS	KILDREVETP	540
KNELYNITVL	AIIDKDRSCT	GLAVNIEDV	NDNPPEILQE	YVVICPKPMG	YTDILAVDPD	600
EPVHGAPFPY	SLPNTSPEIS	RWSLTKVND	TAARLSYQKN	AGFQETIPI	TVKDRAGQAA	660
TKLLRVNLCE	CTHPTQCRAT	SRTGVILGK	WAILAILGI	ALLFSVLLTL	VCGVFGATGK	720
KRFPPDLAQQ	NLIISNTEAP	GDDRVCSANG	FMTQTNNSS	QGFCGTMSGG	MKNQGGQETIE	780
MMKGNGQTL	SCRGAGHHHT	LDSCRGGHTE	VDNCRYTYSE	WHSFTQPRLG	EKLHRCNQNE	840
DRMPSQDYVL	TYNIEGRGSP	AGSVGCCSEK	QBEDGLDPLN	NLEPKFITLA	EACTKR	

Seq ID NO: 33 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 64-2583

1	11	21	31	41	51	
GGCAGGTCTC	GCTCTCGGCA	CCCTCCCGGC	GCCCGCGTTC	TCCTGGCCCT	GCCCGGCATC	60
CCGATGGCCG	CCGCTGGGCC	CCGCGCGTCC	GTGCGCGGAG	COGTCTGCCT	GCACTCTGCTG	120
CTGACCCCTCG	TGATCTTCAG	TGCTGATGGT	GAAGCCTGCA	AAAAGGTGAT	ACTTAATGTA	180
CCTTGTAATV	TAGAGGCAGA	CAAAATAATT	GGCAGAGTTA	ATTGGAAGA	GTGCTTCAGG	240
TCTGCAGACC	TCATCCGCTC	AAGTGATCCT	GATTTCAGAG	TTCTAAATGA	TGGGTCAGTG	300
TACACAGCCA	GGGCTGTGTC	GCTGTCTGAT	AAGAAAAGAT	CATTTACCAT	ATGGCTTTCT	360
GACAAAAGGA	AACAGACACA	GAAAGAGGTT	ACTGTGCTGC	TAGAACATCA	GAAGAAGGTA	420
TGGAAGACAA	GACACACTAG	AGAAACTGTT	CTCAGGCGTG	CCAAGAGGAG	ATGGGCACCT	480
ATTCCTTGCT	CTATGCAAGA	GAATTCCTTG	GGCCCTTTCC	CATTGTTTCT	TCAACAAGTT	540
GAATCTGATG	CAGCACAGAA	CTATACTGTC	TCTACTCAA	TAAGTGGACG	TGGAGTTGAT	600
AAAGAACCTT	TAAATTTGTT	TTATATAGAA	AGAGACACTG	GAAATCTATT	TTGCACTCGG	660
CCTGTGGATC	GTGAAGAATA	TGATGTTTTT	GATTGTATGG	CTTATGCGTC	AAGTGCAGAT	720
GGATATTTCAG	CAGATCTGCC	CCTCCCACTA	CCCATCAGGG	TAGAGGATGA	AAATGACAAAC	780
CACCCCTGTT	TCCAGGAAGC	AATTTATAAT	TTTGAAGTTT	TGGAAGTAG	TAGACCTGGT	840
ACTACAGTGG	GGGTGGTTTG	TGCCACAGAC	AGAGATGAAC	CGGACACAAT	GCATACGCGC	900
CTGAATACA	GCAATTTGCA	CGACACACCA	AGGTCACTG	GGCTCTTTTC	TGTGCATCCC	960
AGCACAGGCG	TAATCACACC	AGTCTCTCAT	TATTTGGACA	GAGAGGTTGT	AGACAAGTAC	1020
TCATTGATAA	TGAAGTACA	AGACATGGAT	GGCCAGTTTT	TTGGATTGAT	AGGCACATCA	1080
ACTTGATATC	AGTTGTAAC	GAATTCAAAT	GATAATGCAC	CCACTTTTCA	ACAAAATGCT	1140
TATGAAGCAT	TTGTGAGGA	AAATGCATT	AATGTGAAA	TCTTACGAAT	ACCTATAGAA	1200
GATAAGGATT	TAATTAACAC	TGCCAATTGG	AGAGTCAATT	TTACCATTTT	AAAGGGAAT	1260
GAAAATGGAC	ATTTTCAAAT	CGCACACAGC	AAAGAACTA	ATGAAGGTGT	TCTTTCTGTT	1320
GTAAAGCCAT	TGAATTATGA	AGAAAACCGT	CAAGTGAACC	TGGAAATTTG	AGTAAACAAT	1380
GAAGCGCCAT	TTGCTGAGGA	TATTTCCAGA	GTGACAGCCT	TGAACAGAGC	CTTGTTTACA	1440
GTTTATGTGA	GGGATCTGGA	TGAGGGGCTC	GAATGCACCT	CTGCAGCCCA	ATATGTGCGG	1500
ATTAAGAA	ACTTAGCAGT	GGGTCAAAG	ATCAACGGCT	ATAAGGCATA	TGACCCCGAA	1560
AATAGAAATG	GCAATGGTTT	AAGGTACAAA	AAATTCGATG	ATCCTAAAGG	TTGGATCACC	1620
ATTGATGAAA	TTTCAGGGTC	AATCATAACT	TCCAAAATCC	TGGATAGGGA	GGTTGAAACT	1680
CCCAAAAATG	AGTTGTATAA	TATTACAGTC	CTGGCAATAG	ACAAAGATGA	TAGATCATGT	1740
ACTGGAACAG	TTGCTGTGAA	CATTGAAGAT	GTAATGATA	ATCCACCAGA	AATACTTCAA	1800
GAATATGTAG	TCATTTGCAA	ACCAAAAATG	GGGTATACCG	ACATTTTAGC	TGTTGATCCT	1860
GATGAACCTG	TCCATGGAGC	TCCATTTTAT	TTCAGTTTGC	CCAATACTTC	TCCAGAAATC	1920
AGTAGACTGT	GGAGCCTCAC	CAAAGTTAAT	GATACAGCTG	CCCGTCTTTC	ATATCAGAAA	1980
AATGCTGGAT	TTCAAGAATA	TACCATTCCT	ATTACTGTAA	AAGACAGGGC	CGGCCAAGCT	2040
GCAACAAAAT	TATTGAGAGT	TAATCTGTGT	GAATGTACTC	ATCCAACTCA	GTGTCGTGCG	2100
ACTTCAAGGA	GTACAGGAGT	AATACTTGA	AAATGGGCAA	TCCTTGCAAT	ATTACTGGGT	2160
ATAGCACTGC	TCTTTTCTGT	ATTGCTAACT	TTAGTATGTG	GAGTTTITGG	TGCAACTAAA	2220
GGGAAACGTT	TTCTTGAAGA	TTTAGCACAG	CAAAACTTAA	TTATATCAAA	CACAGAAGCA	2280
CCTGGAGACG	ATAGAGTGTG	CTCTGCCAAT	GGATTATGA	CCCAACTAC	CAACAACTCT	2340
AGCCAAGGTT	TTTGTGGTAC	TATGGGATCA	GGATGAAAA	ATGGAGGGCA	GGAAACCATT	2400
GAAATGATGA	AAGGAGGAAA	CCAGACCTTG	GAATCCTGCC	GGGGGGCTGG	GCATCATCAT	2460
ACCTGGAGCT	CCTGCAGGGG	AGGACACACG	GAGGTGGACA	ACTGCAGATA	CACCTACTCG	2520
GAGTGGCACA	GTTTTACTCA	ACCCCGTCTC	GGTGAAGAAT	CCATTAGAGG	ACACACTGGT	2580
TAAAAATTAA	ATCAAAAAGA	AATTCATCG	ATGTAATCAG	AATGAAGACC	GCATGCCATC	2640
CCAAGATTAT	GTCTCTCACT	ATAACTATGA	GGGAAGAGGA	TCTCCAGCTG	GTCTGTGGG	2700
CTGCTGCAGT	GAAGAAGCAG	CCTTGACTTT	TTAAATAAAT	TGGAACCCAA		2760
ATTTATTACA	TTAGCAGAAG	CATGCACAAA	GAGATAATGT	CACAGTGCTA	CAATTAGGTC	2820
TTTGTGAGAC	ATTCTGGAGG	TTTCAAAAA	TAATATTGTA	AAGTTCAATT	TCAACATGTA	2880
TGTATATGAT	GATTTTITTC	TCAATTTTGA	ATTATGCTAC	TCACCAATTT	ATATTTTATA	2940
AGCCAGTTGT	TGCTTATCTT	TTCCAAAAAG	TGAAAAATGT	TAAAAAGAC	AACTGGTAAA	3000
TCTCAAACTC	CAGCATGGA	ATTAAAGTCT	CTAAAGCATC	TGCTCTTTT	TTTTTTTACG	3060
GATATTTTAG	TAATAATAT	GCTGGATAAA	TATTAGTCCA	ACAATAGCTA	AGTTATGCTA	3120
ATATCACATT	ATTATGTATT	CACTTTAAGT	GATAGTTTAA	AAAATAAACA	AGAAATATTG	3180
AGTATCATA	TGTGAAGAAA	GTTTTTGAAA	AGAAACAATG	AAGACTGAAT	TAAATTAATA	3240
ATGTTGCAGC	TCATAAGAAA	TTGGGACTCA	CCCCTACTGC	ACTACCAAA	TCATTTGACT	3300

	TTGGAGGCAA	AATGTGTTGA	AGTGCCCTAT	GAAGTAGCAA	TTTTCTATAG	GAATATAGTT	3360
	GGAAATAAAT	GTGTGTGTGT	ATATTATTAT	TAATCAATGC	AATATTAAAA	ATGAAATGAG	3420
	AACAAAGAGG	AAAATGGTAA	AAACTTGAAA	TGAGGCTGGG	GTATAGTTTG	TCCTACAAATA	3480
5	GAAAAAAGAG	AGAGCTTCCT	AGGCTGGGCG	TCCTAAATGC	TGCATTATAA	CTGAGTCTAT	3540
	GAGGAAATAG	TTCTCTGCCA	ATTGTGTGTA	TTTGTTTAAA	ATTGTAATAA	AATTAACCTT	3600
	TTCTGTGTTT	TGTGGGAAGG	AAATAGGGAA	TCCAATGGAA	CAGTAGCTTT	GCTTTGCAGT	3660
	CTGTTTCAAG	ATTTCTGCAT	CCACAAGTTA	GTAGCAAAC	GGGGAATACT	CGCTGCAGCT	3720
	GGGGTTCCTT	GCTTTTGTGT	AGCAAGGGTC	CAGAGATGAG	GTGTTTTTTT	CGGGGAGCTA	3780
10	ATAACAAAAA	CATTTTAAAA	CTTACCTTTA	CTGAAGTTAA	ATCCTCTATT	GCTGTTTCTA	3840
	TTCTCTCTTA	TAGTGACCAA	CATCTTTTAA	ATTAGATGCC	AAATAACCAT	GTCCTCCTAG	3900
	AGTTTAGAGG	CTAGAGGGAG	CTGAGGGGAG	GATCTTACTG	AAAGCACCTT	GGGGAGATTG	3960
	ATTGTCCTTA	AACCTAAGCC	CCACAACTT	GACACCTGAT	CAGGTCTGGG	AGCTACAAAA	4020
	TTTCATTTTT	CTCTCTCACTG	CCCTTCTTCT	GAGTGGCATT	GGCCTGAATC	AAGGAAAGCC	4080
	AGGCTTGTGT	GGCCCTCTTC	TTTCGGCTTT	CTGCTAAAGC	AACACCTCCA	GCAGAGATTG	4140
15	CCTTAAGTGA	CTCCAGGTTT	TCCACCATCC	TTACGCGTGA	ATTAATTTTT	AATCAGTTTG	4200
	CTTTCTCCAG	AGAAATTTTA	AAATAATAGA	AGAAATAGAA	ATTTTGAATG	TATAAAGAA	4260
	AAAGATCAAG	TTGTCAATTT	AGAACAGAGG	GAACCTTGGG	AGAAAGCAGC	CCAAGTAGGT	4320
	TATTTGTACA	CTCAGAGGGC	AACAGGAAGA	TGCAGGCCTT	CAAGGGCAAG	GAGAGGCCAC	4380
20	AAGGAATATG	GGTGGGAGTA	AAAGCAACAT	CGTCTGCTTC	ATACTTTTTC	CTAGGCTTGG	4440
	CACTGCCTTT	TCCTTTCTCA	GGCCCAATGGC	AACCTGCCAT	TGAGTCCGGT	GAGGGATCAG	4500
	CCAACCTCTT	CTGTAGGGCT	CACCTTATTT	GGAGTGAGAA	ATCAAGGAGA	CAGAGCTGAG	4560
	TGCATGATGA	GTCTGAAGGC	ATTTGCAGGA	TGAGCCTGAA	CTGGTGTGTC	AGAACAAACA	4620
	AGGCATTCAT	GGGAATTTGT	GTATTCTTCT	TGCAGCCCTC	CTTCTGGGCA	CTAAGAAAGT	4680
25	CTATGAATTA	AATGCAATATC	TAAAATTCTG	ATTATTCCCT	ACATTTTCTG	TTTTCTAATT	4740
	TGACCCCTAA	ATCTATGTGT	TTTAGACTTA	GACTTTTTAT	TGCCCCCCCC	CCCTTTTTTT	4800
	TTGAGACCGA	GTCTGCTCTT	GACGCACAGG	CTGGAGTGCA	GTGGCTCCGA	TCTCTGCTCA	4860
	CTGAAAGCTC	CGCCTCCCGG	GTTCATGCCA	TTCTCCTGCC	TCAGCCTCCT	GAGTAGCTGG	4920
	GACTACAGGC	GCCCAACACC	ACGCCCGGCT	AAATTTTTGT	ATTTTAAATA	GAGACGGGGT	4980
30	TTACTGTGT	TAGCCAGGAT	GGCTCTCGATC	TCCTGACCTC	TGATCTCCGC	TGCCTCGGCC	5040
	TCCCAAGTGT	CTGGGATTAC	AGGCATGACC	CACGCTCCCG	GGCCTTGTTT	TCCGTTTAAA	5100
	GTCGTCTTCT	TTTAATGTGA	TCATTTTGAA	CATGTGTGAA	AGTTGATCAT	ACGAATTGGA	5160
	TCAATCTTGA	AATACTCAAC	CAAAAGACAG	TCGAGAAGCC	AGGGGGAGAA	AGAACTCAGG	5220
	GCACAAATAA	TTGGTCTGAG	AATGGAATTC	TCTGTAAAGC	TAGTTGCTGA	AATTTCTGTC	5280
35	TGTAAACAGA	AGCCAGTTTT	ATCTAACCGC	TACTGAAACA	CCCCTGTGT	TTTGCTCACT	5340
	CCCCTCACC	GATCAAAACC	TGCTACCTCC	CCAAGACTTT	ACTAGTGCCG	ATAAACTTTC	5400
	TCAAAGAGCA	ACCAGTATCA	CTTCCCTGTT	TATAAAACCT	CTAACCATCT	CTTTGTTCTT	5460
	TGAACATGCT	GAAAAACCAC	TGGTCTGCAT	GTATGCCCGA	ATTTGTAAAT	CTTTTCTCTC	5520
	AAATGAAAT	TTAATTTTAG	GGATTCAATT	CTATATTTTC	ACATATGTAG	TATTATTATT	5580
40	TCCTTATATG	TGTAAAGTGA	AATTTATGGT	ATTGAGTGT	GCAAGAAAT	ATATTTTAA	5640
	AGCTTTCAAT	TTTCCCCAG	TGAATGATTT	AGAATTTTTT	ATGTAATAT	ACAGAAATGT	5700
	TTTTCTTACT	TTTATAAGGA	AGCAGCTGTC	TAAATGCAG	TGGGGTTTGT	TTTGCAATGT	5760
	TTTAAACAGA	GTTTTAGTAT	TGCTATTAAA	AGAAATTAAT	TTGCTTTTAA	AGAAACTTGG	5820
	CTGCTTAAAA	TAAACAAAAA	TTGGATGCAT	AAAGTAATAT	TTACAGATGT	GGGGAGATGT	5880
45	AATAAAACAA	TATTAACCTG	GCTGCTTAAA	ATAAGCAAAA	ATTGGATGCA	TAAAGTAATA	5940
	TTTACAGATG	TGGGGAGATG	TAAATAAACA	ATATTAACTT	GGTTTCTTGT	TTTTGCTGTA	6000
	TTTAGAGATT	AAATAGATCT	AAGATGATCA	CTTTGCAAAA	TTATGCTTAT	GGCTGGCATG	6060
	GAAATAGAAA	TACTCAATTA	TGCTTTTGT	GTATTAAATG	GGAAATTTTT	GGACAATGTT	6120
	TCATTATCAA	ATTGTGACCA	TCATTAATAT	ATATTGTAAT	GTGGGAAGA	GATCACTATT	6180
50	TTGAAGCACA	GCTTTACAGA	TGAGTATCTA	TGATACATAT	GTATAATAAA	TTTTGATCGG	6240
	GTATTAAAG	TATTAGAAGG	TGGTTATAAT	TGCAGAGTAT	TCCATGAATA	GTACACTGAC	6300
	ACAGGGGTTT	TACTTTGAGG	ACCACTGTAG	TCAAGGGAAA	ACATGAGTTA	AAAAGAAAAA	6360
	CAGGCAATAT	TGCAGTCTTG	ATTCTGCCAC	TTACAGGATA	GATAATGCC	GAACTTTAAT	6420
	GACAAGATGA	TCCAACCAT	AAGGTGCTCT	GTGCTTCA	GTGAATCTTT	TCCCATGCA	6480
55	GGAGTGTGCT	CCCCTACAAA	CGTTAAGACT	GATCATTTCA	AAAATCTATT	AGCTATATCA	6540
	AAAGCCTTAC	ATTTTAAAT	AGGTTGAACC	AAAATTTCAA	TTCCAGTAA	TTCTATTGTA	6600
	ACCATTATTT	TTGTGATATG	CTTCAAGAA	GTTCAATGGA	TTTTTGTGTT	TAATAGTAAA	6660
	ATACCGGATA	CATTTCACGT	GTCCTTCAGT	ATTGATTGG	TTGAATATTG	GGTCATAATG	6720
	GTTGGAAGC	ATGGAGACTA	GAGCCAGAA	GCTTGGATAT	GAATCCTGGA	TCTGTCACTT	6780
60	ACTTCTGTGT	GACCTTTGAA	AGGCTACTTA	TTTCTCTCT	TAGCTTTCTC	ATTAAATCA	6840
	ATGAACAATG	CCAGCCTCAT	GGGGTTGTTG	AATGATTA	TTAGTTAATA	TACCTAAAGT	6900
	ACATAGAAC	CTGCCCTGAC	ATAGTAAAG	AATTATAAGT	GTGAGGTAGT	TGGTAAATTT	6960
	ATGTAGTTGG	ATATACTACC	GAACAATATC	TAATCTCTTT	TTAGGGAAT	AAAGTTTGTG	7020
	CATATATATA	ATCCCCAAAC	ATG				

Seq ID NO: 34 Protein sequence:
Protein Accession #: NP_077741.1

	1	11	21	31	41	51	
70	MAAAGPRRSV	RGAVCLHLLL	TLVIFSRDGE	ACKKVILNVP	SKLEADKIIG	RVNLEECFRS	60
	ADLIRSSDPD	FRVLNDGSVY	TARAVALSDK	KRSPTIWLSD	KRKQTQKEVT	VLLHQKKVS	120
	KTRHTRFVTL	RRAKRRWAPI	PCSMQENSLG	PFPLFLQQVE	SDAAQNYTVF	YSISGRGVDK	180
	EPLNLFYIER	DTGNLFCSTR	VDREYDVFD	LIAYASTADG	YSADLPLPLP	IRVEDENDNH	240
75	PVFTEAIYNF	EVLESSRPGT	TVGVVCASTR	DEPDTHMTRL	KYSILQQTFR	SPGLFSVHPS	300
	TGVITTVSHY	LDREVVDKYS	LIMKVDMDG	QFGLIGTST	CIITVDSND	NAPTFRQNAV	360
	EAPVEENAFN	VEILRIPIED	KDLINTANWR	VNFTILKONE	NGHFKISTDK	ETNBSVLSVV	420
	KPLNYENNRQ	VNLEIGVNNE	APFARDIPRV	TALNRALVTV	HVRDLDEGPE	CTFAAQYVRI	480
	KENLAVGSKI	NGKAYDPEN	RNGNGLRYKK	LHDPKGNWIT	DEISGSIITS	KILDREVEPT	540
80	KNELNYITVL	AIDKDRSCT	GTFLAVNIEDV	NDNPPEILQE	YVVIKPKPMG	YTDILAVDPD	600
	EPVHGAPPFY	SLPNTSPFIS	RLWSLTKVND	TAARLSYOKN	AGFQETIPI	TVKDRAGQAA	660
	TKLLRVNLCE	CTHPTQCRAT	SRSTGVILCK	WAILAILLGI	ALLFSVLLTL	VCGVFGATKG	720
	KRFPEDLAQQ	NLIISNTEAF	GDGDRVCSANG	FMTQTTNNS	QGFCGTMGSG	MKNGGQETIE	780
	MMKGGNQTL	SCRAGHHHT	LDSCRGGHTE	VDNCRYTYS	WHSFTQPRLG	EESIRGHTG	

Seq ID NO: 35 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 146-1273.

	1	11	21	31	41	51	
5	GGGAGTGGGC	GTGGCGGTGC	TGCCCAGGTG	AGCCACCGCT	GCTTCTGCCC	AGACACGGTC	60
	GCCTCCACAT	CCAGGTCTTT	GTGCTCCTCG	CTTGCTGTGT	CCTTTTCAC	GCAITTTCCA	120
	GGATAACTGT	GACTCCAGGC	CGCAATGGA	TGCCCTGCAA	CTAGCAAATT	CGGCTTTTGC	180
	CGTTGATCTG	TTCAAACAAC	TATGTGAAAA	GGAGCCACTG	GGCAATGTCC	TCTTCTCTCC	240
	AATCTGTCTC	TCCACCTCTC	TGTCACTTGC	TCAAGTGGGT	GCTAAAGGTG	ACACTGCAAA	300
10	TGAAATTGGA	CAGGTTCTTC	ATTTTGAAAA	TGTCAAAGAT	ATACCCCTTG	GATTTCAAAC	360
	AGTAACATCG	GATGTAAACA	AACTTAGTTC	CTTTTACTCA	CTGAAACTAA	TCAAGCGGCT	420
	CTACGTAGAC	AAATCTCTGA	ATCTTTCTAC	AGAGTTCATC	AGCTCTACGA	AGAGACCCTA	480
	TGCAAAAGGAA	TTGAAAACTG	TTGACTTCAA	AGATAAATG	GAAGAAACGA	AAGGTCAGAT	540
	CAACAACATCA	ATTAAGGATC	TCACAGATGG	CCACTTTGAG	AACATTTTAG	CTGACAACAG	600
	TGTGAACGAC	CAGACCAAAA	TCCTTGTTGT	TAATGCTGCC	TACTTTGTTG	GCAAGTGGAT	660
15	GAAGAAATTT	CCTGAATCAG	AAACAAAAGA	ATGTCCTTTC	AGACTCAACA	AGACAGACAC	720
	CAAAACCAATG	CAGATGATGA	ACATGGAGGC	CACGTTCTGT	ATGGGAAACA	TTGACAGTAT	780
	CAATTGTAAG	ATCATAGAGC	TTCTTTTTC	AAATAAGCAT	CTCAGCATGT	TCATCCTACT	840
	ACCAAGGAT	GTGGAGGATG	AGTCCACAGG	CTTGGAGGAG	ATTGAAAAAC	AACTCAACTC	900
20	AGAGTCACTG	TCACAGTGGG	CTAATCCCG	CACCATGGCC	AATGCCAAGG	TCAAACCTC	960
	CATTCCAAAA	TTTAAGGTGG	AAAAGATGAT	TGATCCCAAG	GCTTGTCTGG	AAAACTAGG	1020
	GCTGAAACAT	ATCTTCAGTG	AAGACACATC	TGATTTCTCT	GGAATGTCAG	AGACCAAGGG	1080
	AGTGGCCCTA	TCAAATGTTA	TCCACAAAGT	GTGCTTAGAA	ATAACTGAAG	ATGGTGGGGA	1140
	TTCCATAGAG	GTGCCAGGAG	CAGCGATCCT	GCAGCACAAAG	GATGAATTGA	ATGCTGACCA	1200
25	TCCCTTTATT	TACATCATCA	GGCACAACAA	AACTCGAAAC	ATCATTCTCT	TTGGCAAAAT	1260
	CTGTTCTCCT	TAGTGGCATC	AGCCCATGTT	AAGTCTCTCC	TGACTTTTCT	GTGGATGCCG	1320
	ATTTCTGTAA	ACTCTGCATC	CAGAGATTCA	TTTTCTAGAT	ACAATAAATT	GCTAATGTTG	1380
	CTGGATCAGG	AAGCCGCCAG	TACTTGTCT	ATGTAGCCTT	CACACAGATA	GACCTTTTTT	1440
	TTTTTCCAAAT	TCTATCTTTT	GTTCCTTTT	TTCCCAATAG	ACAATGACAT	ACGCTTTTAA	1500
30	TGAAAAGGAA	TCACGTTAGA	GGAAAAATAT	TTATTCATTA	TTTGTCAAAT	TGTCGGGGGT	1560
	AGTTGGCAGA	AATACAGTCT	TCCACAAAGA	AAATTCCTAT	AAGGAAGATT	TGGAAGCTCT	1620
	TCTTCCAGC	ACTATGCTTT	CCTTCTTGG	GATAGAGAAT	GTTCAGACA	TTCTCGCTTC	1680
	CCTGAAAGAC	TGAAGAAAGT	GTAGTGCATG	GGACCCACGA	AACTGCCCTG	GCTCCAGTGA	1740
	AACTTGGGCA	CATGCTCAGG	CTACTATAGG	TCCAGAAGTC	CTTATGTTAA	GCCCTGGCAG	1800
35	GCAGGTGTTT	ATTAAAAATC	TGAATTTTGG	GGATTTTCAA	AAGATAATAT	TTTACATACA	1860
	CTGTATGTGA	TAGAACTTCA	TGGATCAGAT	CTGGGGCAGC	AACCTATAAA	TCAACACCTT	1920
	AATATGCTGC	ACAAAAATGT	AGAAATTCCA	GACAAAAATG	ATACATAAAG	ACTAAGTAGC	1980
	CCATAAGGGG	TCAAAATTTG	CTGCCAAATG	CGTATGCCAC	CAACTTACAA	AAACACTTCG	2040
	TTCCGAGAGC	TTTTTCAGATT	GTGGAATGTT	GGATAAGGAA	TTATAGACCT	CTAGTAGCTG	2100
40	AAATGCAAGA	CCCCAAGAGG	AAGTTCAGAT	CTTAATATAA	ATTCACCTTC	ATTTTGTATA	2160
	GCTGTCCCAT	CTGGTCATGT	GGTTGGCACT	AGACTGGTGG	CAGGGGCTTC	TAGCTGACTC	2220
	GCACAGGGAT	TCTCAACAAT	CCCGATATCA	GAATTTGTGT	TGAAGGAAC	TGTCTCTTCA	2280
	TCTAATATGA	TAGCGGAAAA	AGGAGAGGAA	ACTACTGCCT	TTAGAAAATA	TAAGTAAAGT	2340
	GATTAAAGTG	CTCACGTTAC	CTTGACACAT	AGTTTTCAG	TCTATGGGTT	TAGTTACTTT	2400
45	AGATGGCAAG	CATGTAACCT	ATATTAATAG	TAATTTGTAA	AGTTGGGTGG	ATAAGCTATC	2460
	CCTGTTGCCG	GTTCATGGAT	TACTTCTCTA	TAAAAAATAT	ATATTACCA	AAAAATTTTG	2520
	TGACATTCTC	TCTCCATCT	CTTCTTGAC	ATGCATTGTA	AATAGGTTCT	TCTTGTCTCG	2580
	AGATTCAATA	TTGAATTTCT	CCTATGCTAT	TGACATAAAA	ATATTATTGA	ACTACC	

Seq ID NO: 36 Protein sequence:
Protein Accession #: NP_002630.1

	1	11	21	31	41	51	
55	MDALQLANSA	FAVDLPKQLC	EKEPLGNVLF	SPICLSTSL	LAQVGAKGDT	ANEIGQVLHF	60
	ENVKIDIPFG	QTVTSVNVKL	SSFYSKLKIK	RLYVDKSLNL	STFPISTKR	PYAKELETVD	120
	FKDKLESTKG	QINNSIKDLT	DGHFENILAD	NSVNDQTKIL	VVNAAYFVGK	WMKKFPESET	180
	KECPRLNKNT	DTKPVQMMNM	EATPCMGNID	SINCKIIELP	FONKHLBMFI	LLPKDVEDES	240
	TGLEKIEKQL	NSEBSLSQWTN	PSTMANAKVK	LSIPKFKVEK	MIDPKACLEN	LGLKHIFSED	300
60	TSPSGMSET	KVGLNSNVIIH	KVCLEITEBG	GDSIEVPGAR	ILQHKDELNA	DHPFIYIIRH	360
	NKTRNIIFFG	KFCSP					

Seq ID NO: 37 DNA sequence
Nucleic Acid Accession #: NM_0168583
Coding sequence: 72-842

	1	11	21	31	41	51	
70	GGAGTGGGGG	AGAGAGAGGA	GACCAGGACA	GCTGCTGAGA	CCTCTAAGAA	GTCCAGATAC	60
	TAAGAGCAAA	GATGTTTCAA	ACTGGGGGCC	TCATGTCTTT	CTACGGGCTG	TTAGCCGAGA	120
	CCATGGCCCA	GTTTGGAGGC	CTGCCGTGTC	CCCTGGACCA	GACCCCTGCK	TTGAATGTGA	180
	ATCCAGCCCT	GCCCTTGAGT	CCACACAGTC	TTGCAGGAAG	CTTGACAAAT	GCCCTCAGCA	240
	ATGGCTGTCT	GTCCTGGGGC	CTGTTGGGCA	TTCTGGAAAA	CCTTCCGCTC	CTGGACATCC	300
75	TGAAGCCTGG	AGGAGTACT	TCTGGTGGCC	TCCTTGGGGG	ACTGCTTGGA	AAAGTGACGT	360
	CAGTGATTCC	TGGCCTGAAC	AAACATCATT	ACATAAAGGT	CACTGACCCC	CAGCTGCTGG	420
	AACTTGGCCT	TGTGCAAGGC	CCTGATGGCC	ACCGTCTCTA	TGTCAACCAT	CCTCTCGGCA	480
	TAAAGCTCCA	AGTGAATACG	CCCTGGTTCG	GTGCAAGTCT	GTTGAGGCTG	GCTGTGAAGC	540
	TGGACATCAC	TGTGCAAAATC	TTAGCTGTGA	GAGATAAGCA	GGAGAGGATC	CACCTGGTCC	600
80	TTGGTGACTG	CACCCATTCC	CCTGGAAGCC	TGCAAAATTC	TCTGCTTGAT	GGACTTGGCC	660
	CCCTCCCAT	TCAAGGCTCT	CTGGACAGCC	TCACAGGGAT	CTTGAATAAA	GTCCTGCTCG	720
	AGTTGGTTCA	GGGCAACGTG	TGCCCTCTGG	TCAATGAGGT	TCTCAGAGGG	TTGGACATCA	780
	CCCTGGTGCA	TGACATTGTT	AACATGCTGA	TCCACGAGCT	ACAGTTTGTG	ATCAAGGTCT	840
	AAGCCTTCCA	GGAAGGGGCT	GGCCTCTGCT	GAGCTGCTTC	CAGTGTCTCA	CAGATGGGCT	900
	GCCCATGTGC	TGGAAGATGA	CACAGTTGCT	TTCTCTCCGA	GGAACCTGCC	CCCTCTCCTT	960
85	TCCCACCAGG	CGTGTGTAAC	ATCCCATGTG	CCTCACCTAA	TAAATGGCT	CTTCTTCTGC	1020
	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA				

WO 02/086443

Seq ID NO: 38 Protein sequence:
Protein Accession #: NP_057667

PCT/US02/12476

5 1 11 21 31 41 51 60
MFQTGGGLIVF YGLLAQMTMAQ FGGLEVPVLDQ TLPLNVNPAI PLSPTGLAGS LTNALSNGLL 120
SGGLLGILEN LPLLDILKPG GGTSGGGLLG LLGKVTSVIP GLNNIIDIIV TDPQLLELGL 180
VQSPDGHRLY VTIPLEGKILQ VNTPLVGASL LRLAVKLDIT AEILAVRDQ ERIHLVLGDC 240
10 THSPGSLQIS LLDLGLPLPI QGLDLSLTGI LNKVLPVLVQ GNVCPLVNEV LRGLDITLVH
DIVNMLIHGL QFVIKV

Seq ID NO: 39 DNA sequence
Nucleic Acid Accession #: NM_004363.1
Coding sequence: 115-2223

15 1 11 21 31 41 51 60
CTCAGGGCAG AGGGAGGAAG GACAGCAGAC CAGACAGTCA CAGCAGCCTT GACAAAACGT 120
TCCTGGAACCT CAAGCTCTTC TCACAGAGG AGGACAGAGC AGACAGCAGA GACCATGGAG 180
TCTCCCTCGG CCCCTCCCCA CAGATGGTGC ATCCCTTGGC AGAGGCTCCT GCTCACAGCC 240
TCACTTCTAA CCTTCTGGAA CCCGCCACC ACTGCCAAGC TCACTATTGA ATCCACGCCG 300
TTCAATGTCC CAGAGGGGAA GGAGGTGCTT CTACTTGTC ACAATCTGCC CCAGCATCTT 360
TTTGGCTACA GCTGGTACAA AGGTGAAAGA GTGGATGGCA ACCGTCAAAT TATAGGATAT 420
GTAATAGGAA CTCAACAAGC TACCCAGGG CCCGCATACA GTGGTCGAGA GATAATATAC 480
CCCAATGCAT CCTGTCTGAT CCAGAACATC ATCCAGAATG ACACAGGATT CTACACCCTA 540
CACGTCATAA AGTCAGATCT TGTGAATGAA GAAGCAACTG GCCAGTCCG GGTATACCCG 600
GAGCTGCCCA AGCCCTCCAT CTCCAGCAAC AACTCCAAAC CCGTGAGGA CAAGGATGCT 660
GTGGCCTTCA CCTGTGAACC TGAGACTCAG GACGCAACCT ACCTGTGGTG GGTAAACAAAT 720
CAGAGCCTCC CGTGCAGTCC CAGGCTGCAG CTGTCCAATG GCAACAGGAC CCTCACTCTA 780
TTCAATGTCA CAGAAATGA CACAGCAAGC TACAAATGTG AAACCCAGAA CCCAGTGAGT 840
GCCAGGCGCA GTGATTCACT CATCTGAAT GTCCTCTATG GCCCGATGCG CCCCACTATT 900
TCCCTCTAA ACACATCTTA CAGATCAGGG GAAAATCTGA ACCTCTCCTG CCACGCAGCC 960
TCTAACCCAC GTCCACAGTA CTCTTGGTTT GTCAATGGGA CTTTCCAGCA ATCCACCCAA 1020
GAGCTCTTTA TCCCCAACAT CACTGTGAAT AATAGTGGAT CCTATACGTG CCAAGCCCAT 1080
AACTCAGACA CTGGCCTCAA TAGGACCACA GTCACGACGA TCACAGTCTA TGCAGAGCCA 1140
CCCAAACCTT TCATCACCAG CAACAACCTC AACCCCGTGG AGGATGAGGA TGCTGTAGCC 1200
TTAAGCTGTG AACCTGAGAT TCAGAACACA ACCTACCTGT GGTGGGTAA TAATCAGAGC 1260
CTCCCGGTCA GTCCAGGCT CAGACTGTCC AATGACRACA GGACCTCAC TCTACTCAGT 1320
GTCACAAGGA ATGATGTAGG ACCCTATGAG TGTGGAATCC AGAAGCAAT AAGTGTGAC 1380
CACAGCGACC CAGTCTCCTT GAATGTCCTT TATGGCCAG ACACCCCACT CATTTCCTCC 1440
TCATACACCT ATTACCGTCC AGGGGTGAAC CTCAGCCTCT CCGCATGCG AGCCTCTAAC 1500
CCACCTGCAC AGTATTCTTG GCTGATTGAT GGAACATCC AGCAACACAC ACAAGAGCTC 1560
TTTATCTCCA ACATCACTGA GAAGAACAGC GGACTCTATA CCGCCAGGC CAATAACTCA 1620
GCCAGTGCC ACAGCAGGAC TACAGTCAAG ACAATCAGAG TCTCTGCGGA GCTGCCCAAG 1680
CCCTCCATCT CCAGCAACAA CTCGAAACCC GTGGAGGACA AGGATGCTGT GGCCTTCACT 1740
TGTGAACCTG AGGCTCAGAA CACAACCTAC CTGTGGTGGG TAAATGGTCA GAGCCTCCCA 1800
GTCAGTCCCA GGCTGCAGCT GTCCAATGGC AACAGSACCC TCACTCTATT CAATGTCA 1860
AGAAATGACG CAGAGGCTTA TGTATGTGGA ATCCAGAACT CAGTGAGTGC AAACCGCAGT 1920
GACCCAGTCA CCTTGGATGT CCTCTATGGG CCGGACACCC CCATCTATT CCCCCCAGAC 1980
TCGTCTTACC TTTCGGGAGC GAACCTCAAC CTCTCCTGCC ACTCGGCCTC TAACCCATCC 2040
CCGCACTATT CTGGCGGTAT CAATGGGATA CCGCAGCAAC ACACACAAGT TCTCTTTATC 2100
GCCAAATCA CGCCAAATAA TAACGGGACC TATGCCTGTT TTGTCTCTAA CTGGCTACT 2160
GGCGCAATA ATTCCATAGT CAGAGCATC ACAGTCTCTG CATCTGGAAC TTCTCTGGT 2220
CTCTCAGCTG GGGCCACTGT CGGCATCATG ATTGGAGTGC TGTTTGGGGT TGCTCTGATA 2280
TAGCAGCCTT GGTGTAGTTT CTTCATTTCA GGAAGACTGA CAGTTGTGTT GCTTCTTCT 2340
TAAAGCATTT GCAACAGCTA CAGTCTAAAA TTGCTTCTT ACCAAGGATA TTACAGAAA 2400
AGACTCTGAC CAGAGATCGA GACCATCCTA GCCAACATCG TGAAACCCCA TCTCTACTAA 2460
AAATACAAAA ATGAGCTGGG CTGTGTGGCG CGCACCTGTA GTCCAGTTA CTGGGAGGC 2520
TGAGGAGGAA GAATCGCTTG AACCCGGGAG GTGGAGATTG CAGTGAGCCC AGATCGCACC 2580
ACTGCACCTC AGTCTGGCAA CAGAGCAAGA CTCATCTCA AAAAGAAAAG AAAAGAAAGC 2640
TCTGACCTGT ACTCTGAAT ACAAGTTTCT GATACCACTG CACTGTCTGA GAATTTCAA 2700
AACTTTAATG AACTAAGTGA CAGCTTCATG AAACGTGTTA CCAAGATCAA GCAGAGAAA 2760
TAATTAATTT CATGGGACTA AATGAACATA TGAGGATTGC TGATCTTTA AATGTCTGT 2820
TTCCAGATT TCAGGAAACT TTTTCTTT TAAGCTATCC ACTCTACAG CAATTTGATA 2880
AAATATACCT TTGTGAACAA AAATTGAGAC ATTTACATTT TCTCCCTATG TGGTCGCTCC 2940
AGACTTGGGA AACTATTTCAT GAATATTTAT ATTGTATGTT AATATAGTTA TTGCACAACT
TCAATAAAAA TCTGCTCTTT GTATAACAGA AAAA

Seq ID NO: 40 Protein sequence:
Protein Accession #: NP_004354.1

75 1 11 21 31 41 51 60
MESPSAPPHR WCIPQRLLL TASLLTFWNP PTTAKLTIES TPFNVAEKKE VILLVHNLQ 120
HLFGYSWKYK ERVDGNRII GYVIGTQQAT PGPAYSGREI IYPNASLLIQ NIIQNDTGFY 180
TLHVIKSLDV NEEATGQFRV YPELPKPSIS SNNSKPFVDEK DAVAFTEPE TQDATYLMWV 240
NNQSLPVSPR LQLSNVTRND TLFNVTRNDT ASYKCEQNP VSARRSDSVI LNVLYGPDAP 300
TISPLNTSYR SGENLNLSCH AASNPPAQYS WFNVTGFPQS TOELFIPNIT VNNSGSYTCQ 360
AHNSDTGLNR TTVTTITVYA EPPKPFITSN NSNPVEDEDA VALTCEPEIQ NITYLWVNN 420
QSLPVPFRLQ LSNDRRLTL LSVTRNDVGF YECGIQNELS VDHSDPVILN VLYGDDPTI 480
SPSYTYRREG VNLSLSCHAA SNPPAQYSWL IDGNIQHQHT ELFI SNITEK NSGLYTCQAN 540
NSAGHSRTT KLTITVSABL PKPSSISNNS KPVEDKDAVA FTCEPEAQNT TYLWVNGQS 600
LPVSPRLQLS NGNRTLTLFN VTRNDARAYV CGIQNSVSN RSDFVTLVDL YGPDPTIISP 660
85 PDSSYLSGAN LNLSCBASN PSPQYSWRIN GIPOQHTQVL FIAKITPNNN GTYACFVSNL
ATGRNNSIVK SITVSAGTS PGLSAGATVG IMIGVLVGA LI

Seq ID NO: 41 DNA sequence
Nucleic Acid Accession #: NM_006952.1
Coding sequence: 11-793

5
10
15
20

1	11	21	31	41	51	
AATCCCGACA	ATGGCGAAAG	ACAACTCAAC	TGTTGCTTGC	TTCCAGGGCC	TGCTGATTTT	60
TGGAATGTG	ATTATTGGTT	GTTCGGCAT	TGCCCTGACT	GCGGAGTGCA	TCTTCTTTGT	120
ATCTGACCAA	CACAGCCTCT	ACCCACTGCT	TGAAGCCACC	GACAAAGATG	ACATCTATGG	180
GGCTGCCTGG	ATCGGCATAT	TTGTGGGCAT	CTGCCTCTTC	TGCTGTCTG	TICTAGGCAT	240
TGTAGGCATC	ATGAAGTCCA	GCAGGAAAT	TCTTCTGGCG	TATTTTCATTC	TGATGTTTAT	300
AGTATATGCC	TTTGAAGTGG	CATCTTGTAT	CACAGCAGCA	ACACAACGAG	ACTTTTTCAC	360
ACCCAACTCT	TTCTGGAAGC	AGATGCTAGA	GAGGTACCAA	AACAACAGCC	CTCCAAACAA	420
TGATGACCAG	TGGAATAACA	ATGGAGTCAC	CAAAACCTGG	GACAGGCTCA	TGCTCCAGGA	480
CAATTGCTGT	GGCGTAAATG	GTCCATCAGA	CTGGCAAAAA	TACACATCTG	CCTTCCGGAC	540
TGAGAATAAT	GATGCTGACT	ATCCCTGGCC	TCGTCAATGC	TGTGTTATGA	ACAATCTTAA	600
AGAACCTCTC	AACCTGAGG	CTTGTAAACT	AGGCGTGCTT	GGTTTTTATC	ACAATCAGGG	660
CTGCTATGAA	CTGATCTCTG	GTCCAATGAA	CCGACACGCC	TGGGGGGTTG	CCTGGTTTGG	720
ATTTGCCATT	CTCTGCTGGA	CTTTTGGGGT	TCTCTGGGT	ACCATGTTCT	ACTGAGCAG	780
AATTGAATAT	TAAGAA					

Seq ID NO: 42 Protein sequence:
Protein Accession #: NP_008883.1

25
30

1	11	21	31	41	51	
MAKDNSTVRC	FQGLLIFGNV	IIGCCGIALT	AECIFFVSDQ	HSLYPLLEAT	DNDDIYGAAW	60
IGIFVGLCLF	CLSVLGIIVG	MKSSRKILLA	YFILMFIVYA	FEVASCITAA	TQRDFPTPNL	120
FLKQMLERYQ	NNSPFNDDQ	WKNNGVTKTW	DRLMLQDNCC	GVNGPSDWQK	YTSAPRTENN	180
DADYFPWRQC	KVMNMLEPL	NLEACKLGVP	GFYHNQGCYE	LISGPMNRHA	WGVANFGFAI	240
LCWTFWVLLG	TMFYWSRIEY					

Seq ID NO: 43 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 83-2605

35
40
45
50
55
60
65
70
75
80
85

1	11	21	31	41	51	
GCCGGACAGA	TCTGCGGTA	TCCTGGAGCC	GGCCCAAGTTG	TGAAGTAGGA	GAGCTTTGGG	60
ACCTCTGTCC	CAAGCAAGAG	AGATGAATGG	AGAGTATAGA	GGCAGAGGAT	TTGGACGAGG	120
AAGATTTCAA	AGCTGGAAAA	GGGGAAGAGG	TGGTGGGAAC	TTCTCAGGAA	AATGGAGAGA	180
AAGAGAACAC	AGACCTGATC	TGAGTAAAC	CACAGGAAAA	CGTACTTCTG	AACAAACCCC	240
ACAGTTTTTG	CTTTCAACAA	AGACCCCA	GTCATGTCAG	TCAACATTGG	ATCGATTTCAT	300
ACCATATAAA	GGCTGGGAAG	TTTATTTCTC	TGAAGTTTAC	AGCGATAGCT	CTCCTTTGAT	360
TGAGAAGATT	CAAGCATTTG	AAAAATTTT	CACAAGGCAT	ATTGATTTGT	ATGACAAGGA	420
TGAAATAGAA	AGAAAGGGAA	GTATTTTGGT	AGATTTTAAA	GAAGTGACAG	AAGGTGGTGA	480
AGTAACAAAC	TTGATACCA	ATATAGCAAC	TGAAGTAAAG	GATGCACCTG	AGAAAACTTT	540
GGCTTGCAAT	GGTTTGCAAA	TACATCAGGT	GTTAACTAAG	GACCTTGAAA	GGCATGCAAG	600
TGAGTTACAA	GCCCAAGGAG	GATTGTCTAA	TGATGGAGAA	ACAATGGTAA	ATGTGCCACA	660
TATTCATGCA	AGGATGTACA	ACTATGAGCC	TTTGACACAG	CTCAAGAAAT	TCAGAGCAAA	720
TTACTATGGA	AAATACATTG	CTCTAAGAGG	GACAGTGGTT	CGTGTCACTA	ATATAAGGCC	780
TCTTTGCACC	AAGATGGCTT	TTCTTTGTGC	TGCACTGTGA	GAAATTCAGA	GCTTTCTCTC	840
TCCAGATGGA	AAATACAGTC	TTCCCAACAA	GTGTCTCTGT	CCTGTGTGTC	GAGGCAGGTC	900
ATTTACTGCT	CTCCGAGGCT	CTCCTCTCAC	AGTTACGATG	GACTGGCAGT	CAATCAAAAT	960
CCAGGAATTG	ATGTCATGAT	ATCAGAGAGA	AGCAGGTCGG	ATTCCACGAA	CAATGAAATG	1020
TGAGCTTGTT	CATGATCTTG	TGGATAGCTG	TGTCCCGGGA	GACACAGTGA	CTATTACTGG	1080
AATTGTCAAA	GTCTCAAAAT	CGGAAGAAGG	TTCTCGAAAT	AAGAATGACA	AGTGTATGTT	1140
CCTTTTGTAT	ATTGAAGCAA	ATTCTATTAG	TAATAGCAAA	GGACAGAAAA	CAAGAGTTTC	1200
TGAGGATGGG	TGTAAGCATG	GAATGTTGAT	GGAGTTCTCA	CTTAAAGACC	TTTATGCCAT	1260
CCAAGAGATT	CAAGCTGAAG	AAAACCTGTT	TAAACTCATT	GTCAACTGCG	TTTGCCCTGT	1320
CATTTTGTGT	CATGAACCTG	TTAAAGCAGG	TTTGGCATT	GCACTCTTTG	GAGGAAGCCA	1380
GAAATACGCA	GATGACAAAA	ACAGAATTCC	AATTGCGGGA	GACCCCAACA	TCCTTGTTGT	1440
TGGAGATCCA	GGCCTAGGAA	AAAGTCAAAT	GCTACAGGCA	GCGTGCAATG	TTGCCCCACG	1500
TGGCGTGAT	GTTTGTGGTA	ACACCACGAC	CACCTCTGGT	CTGACGGTAA	CTCTTTCAAA	1560
AGATAGTTCC	TCTGGAGATT	TTGCTTTGGA	AGCTGGTGCC	CTGGTACTTG	GTGATCAAGG	1620
TATTTGTGGA	ATCGATGAAT	TTGATAAGAT	GGGGAATCAA	CATCAAGCCT	TGTTGGAAGC	1680
CATGGAGCAG	CAAAGTATTA	GTCTTGCTAA	GGCTGGTGTG	GTTTGTAGCC	TTCTTGCAAG	1740
AACCTTCCATT	ATTGCTGCTG	CAAATCCAGT	TGGAGGACAT	TACAATAAAG	CCAAAACAGT	1800
TTCTGAGAA	TTAAAAATGG	GGAGTGCACT	ACTATCCAGA	TTTGATTGTT	TCTTTATCCT	1860
GTTAGATACT	CCAAATGAGC	ATCATGATCA	CTTACTCTCT	GAACATGTGA	TTGCAATAAG	1920
AGCTGGAAAG	CAGAGAACCA	TTAGCAGTGC	CACAGTAGCT	CGTATGAATA	GTCAAGATTG	1980
AAATACTTCC	GTACTTGAAG	TAGTTTCTGA	GAAGCCATTA	TCAGAAAGAC	TAAAGGTGGT	2040
TCCTGGAGAA	ACAATAGATC	CCATTCCCCA	CCAGCTATTG	AGAAAGTACA	TTGGCTATGC	2100
TGGGAGATAT	TGTATGCCAA	GGCTATCCAC	AGAAGCTGCT	CGAGTTCTTC	AAGATTTTTA	2160
CCTTGAGCTC	CGGAAACAGA	GCCAGAGGTT	AAATAGCTCA	CCAATCACTA	CCAGGCAGCT	2220
GGAATCTTTG	ATTCTGTCTG	CAGAGGCACG	AGCAAGGTTG	GAATTGAGAG	AGGAAGCAAC	2280
CAAAGAAGAC	GCTGAGGATA	TAGTGGAAAT	TATGAAATAT	AGCATGCTAG	GAACCTACTC	2340
TGATGAATTT	GGGAACCTAG	ATTTTGAGCG	ATCCAGCAT	GGTCTGGA	TGAGCAACAG	2400
GTCAACAGCG	AAAAGATTTA	TTTCTGCTCT	CAACAACGTT	GCTGAAAGAA	CTTATAATAA	2460
TATATTTCAA	TTTCATCAAC	TTGCGCAGAT	TGCCAAAGAA	CTAAACATTC	AGGTTGCTGA	2520
TTTTGAAAT	TTTATTTGAT	CACATAAATG	CCAGGTTTAC	CTCTTGAAAA	AAGGCCAAAA	2580
AGTTTACCAG	CTTCAAACTA	TGTAAAGGA	CTTCAACAG	TTAGGGCTCT	CTGGGTTTAT	2640
TGCAGATTAA	AGCCATCTCA	GTGAAGATAT	GCSTGCACGC	ACAGACAGAC	AGACACACAC	2700
ACACACACAC	ACACACACAC	ACACACACAC	AAATACTGTT	CTCTGAAAAA		2760
TGATGTCCCA	AAAGTATTAT	AATAGGAAAA	AAGCATTA	TATAATAAAC	TAATTTAAGA	2820

AGTGATAAAG TCTCCAGATG CAGTAGCTCA CACTGTAATC ACAGTGACTC AGGAGGCTGA 2880
 GGTGAGAGGA TTCCTTGAGG CCAGGGTTTG AGACCAACCT TGGGCAACAT AGCAAGACCC 2940
 CATTTCCTAA AAAAAAATAA AAAAAATTTA AACTTAGCTG GGTATGGTGG CACATGCCTA 3000
 TAGTCTCAGC TACTTGTGAG GCTGAGGCGAG GAGGATTCTT TGAGCCGAGG AGTTTGAGGT 3060
 TACAGTGAGC CACAATCACA CCAATCACTG CACTCCAGCC TGGGCAATAA AGTAACTCTT 3120
 GACTCAAAAA AATAAAAAAA ATTGTAGTGG TAGCCATGTG TTAATTGTTA AATAAATTCT 3180
 CCAAAGGGCT AAAAGTAAAT TACTTATAAA TTTTATTATG TTGTATTTTT GACCTGCCTT 3240
 TTATATGTAT GAATATTTC A TAGTTTTGCA TATCAGATGT AGGCATACAG ACAAAATACAT 3300
 AAACCAATGA ATATATTACA TATTCTGTGT TCCAATAAAA CTTTATTAT GGACACTAAA 3360
 ATTTGAATTT CATAAATTT TCCTATGTCA AGAATACAAA ATACTTGAGT TTTGTTTTTA 3420
 GCTATTTAAT AATAGGCTCT ATTTATTCCA CAGGCTGTAG TTTGTAGTCT TGCTTGAAC 3480
 AATAGAAACA GACTGATTAA GCAGGAGAAG TTTTGTGAAA GAATTTTGTG TGGCTCACGG 3540
 AATTATTAGA AGGCAGGTGA ACCAGGAGGG TAAGCTTCCA GCAGCAATTT GTAAAAACCT 3600
 GCCTTAGAAT TGGAGCTTGC AAGAAGCTGC TGACACTCCA CTGCCACACA GGGCACTGGA 3660
 AGAAAGTGCT GCTGCCTCCC TGCCCCACCT TTGCCACTTC TCAGCAGGGA ATAGGTAGAA 3720
 GAATGCCCCC ACCGCAACG GAACAGCAAC AAAAGGATTC TGCATGAGAT GCCTCCCTAA 3780
 ATTGCTGAAT TCAAAAAAGA AGTTGCATAC AAAGACATCT GATTGAAAAA GGGTATGTTA 3840
 TATGCCCTCT TCATAGGCTG CTAGGGAGTT TTCTTGGTTC TACTTTCAGG TGGTGGGATC 3900
 AATAAGACGA GAATTTCTCA TATGTTGTGA GAGGATTCAA ATGTTACAGG GTTGGCAGCC 3960
 AAACATCAAA TCATGTATAA ATCCAACAAA CACTTTGTAA CATAACAGAA CTCAGGAAAT 4020
 GTGAACCAAT GTTGGAGAAT TACTAAAAAT ACGGCTTCCC GCAACGGAAG ATGAATGGAA 4080
 AATGTAAATA AAAAGAAGCT GCAGTGTATA TCAGATGTTT AACTATAGGA CCAGAACTAA 4140
 GATGTGGAGA CTATTGTCAT AGACCAACAAT GTAAATTTTT AAGTGAGGAA GGAAAAATCA 4200
 GGAATCAAAA GGGGCCAGGT GCAGTGGCTC ACATCTATAA TCCCAGAGCT TTGGGAGTTC 4260
 GAGGCAGGAG GATCACTTGA AGCCAGTTTT GAGACCAGCC TATGCAACAC ATTGAGACCC 4320
 TATCTCTACA AAAATGAGTA TAGCTGGGCA CGGTGGTGCA TGCCTATTGT CCTACCTACT 4380
 GTGGAGGCTG AAGTAGGAAA TCACITGAGC CCGAGAGTTT GAGGTTACAG TGAGCTATGA 4440
 TTATACCACT GCACCTCAGC CTGGGCAAGA GAGCAAGACC TTGTCCTCT

Seq ID NO: 44 Protein sequence:
 Protein Accession #: CAB55276.2

1 11 21 31 41 51
 MNGEYRGRGF GRGRFQSWKR GRGGGNFSGK WREREHRPDL SKTTGKRTSE QTPQFLLSTK 60
 TPQSMQSTLD RFIPYKGWKL YFSEVYSDSS PLIEKIQAFE KFFTRHIDLY DKDEIERKGS 120
 ILVDFKELTE GGEVTNLIPD IATELRDAPE KTLACMGLAI HQVLTKDLER HAAELQAQEG 180
 LSNDETGMVN VPHIHARVYN YEPLTQLKNV RANYYGKYIA LRGTVVVRVN IKPLCTKMAP 240
 LCAACGEQGS FPLPDGKYSL PTKCPVPVPCR GRSFTALRSS PLVTMTDWQS IKIQLMSDD 300
 QREAGRIPT IECBLVEDLV DSCVPGDVT ITGIVKVSNA BEGSRNKNK CMFLLYIEAN 360
 SISNSKGQKT KSSEDGCKHG MMEFSLKDL YAIQEIQABE NLFKILVNSL CPVIFGHELV 420
 KAGLALALFG GSQKYADDKN RPIRGDPHI LVVGDPLGLK SMLQAACNV APRGVVYCGN 480
 TTTTSGLTVT LSKDSSSGDF ALEAGALVLG DQICIGIDEF DKMGNQHQAL LEAMEQQSIS 540
 LAKAGVVCSL PARTSIIAAA NPVGGHYNKA KTVSENLMKG SALLSRFDLV FILLDTFNEH 600
 HDHLLSEHVI AIRAGKQRTI SSATVARMNS QDSNTSVLEV VSEKPLSERL KVPGETIDP 660
 IPHQLLRKYI GYARQVYPR LSTEARVLQ DFYLELRKQS QRLNSSPIT RQLESILRLT 720
 BARARLEIRE EATKEDAEI VEIMKYSLG TYSDEFNLD FERSQHGSGM SNRSTAKRFI 780
 SALNNVAERT YNNIFQPHQL RQIAKELNIQ VADFENFIGS LNDQGYLLKK GPKVYQLQTM

Seq ID NO: 45 DNA sequence
 Nucleic Acid Accession #: NM_005416.1
 Coding sequence: 149..658

1 11 21 31 41 51
 ACCAGATCCC AGAGGCTGAA CACCTCGACC TTCTCTGCAC AGCAGATGAT CCCTGAGCAG 60
 CTGAAGACCA GAAAAGCTTC TAAGACTTTC TGCTTAATTC AGGAGCTTAG AGGATTCTTC 120
 AAAGAGTGTG TCCACGATCC TTTGAAGCAT GAGTTCTTAC CAGCAGAAGC AGACCTTTAC 180
 CCCACCACCT CAGCTTCAAC AGCAGCAGGT GAAACAACCC AGCCAGCCTC CACCTCAGGA 240
 AATATTGTGT CCCACAACCA AGGAGCCATG CCACTCAAAG GTTCCACAAC CTGGAAACAC 300
 AAAGATTCCA GAGCCAGGCT GTACCAAGGT CCCTGAGCCA GGCTGTACCA AGGTCCCTGA 360
 GCCAGGCTGT ACCAAGGTCC CTGAGCCAGG TTGTACCAAG GTCCCTGAGC CAGGCTGTAC 420
 CAAGGTCCCT GAGCCAGGTT GTACCAAGGT CCCTGAGCCA GGCTACACCA AGGTCCCTGA 480
 ACCAGGCGAC ATCAAGGTCC CTGACCAAGG CTTTCATCAAG TTTCTGAGC CAGGTGCCAT 540
 CAAAGTTTCT GAGCAAGGAT ACACCAAGT TCCTGTGCCA GGCTACACAA AGCTACACGA 600
 GCCATGTCTT TCAACGGTCA CTCCAGGCCC AGCTCAGCAG AAGACCAAGC AGAAGTAATT 660
 TGGTGCACAG ACAAGCCCTT GAGAAGCCAA CCACCAGATG CTGGACACCC TCTTCCCATC 720
 TGTTCCTGTG TCTTAATTGT CTGTAGACCT TGTAATCAGC ACATTGTAC CCACAGCCAT 780
 AGTCTCTCTC TTATTGTAT CCTAAAAATA CGTACTATAA AGCTTTTGTG CACACACACT 840
 CTGAAGAATC CTGTAAGCCC CTGAATTAAG CAGAAAGTCT TCATGGCTTT TCTGGTCTTC 900
 GGCTGCTCAG GGTTCATCTG AAGATTCGAA TGAAAGAAA TGCAATGTTT CTGCTCTTCC 960
 CTCATTAAAT TGCTTTAAT TECA

Seq ID NO: 46 Protein sequence:
 Protein Accession #: NP_005407.1

1 11 21 31 41 51
 MSSYQKQTF TPPPQLQQQ VKQPSQPPQ EIFVPTTKEP CHSKVPQKVP TKIPEPGCTK 60
 VPEPGCTKVP EPGCTKVPEP GCTKVPEPG TKVPEPGCTK VPEPGYTKVP EPGSIKVPDQ 120
 GFIKFPEPGA IKVPEQGYTK VVPVGYTKLP EPCPSTVTPG PAQQKTKQK

Seq ID NO: 47 DNA sequence
 Nucleic Acid Accession #: Eos sequence

1 11 21 31 41 51
 5 GCGTCGTGTG CAGGCGTCCC CGGGCTGTGG ATAATTAGAC ACGTTCCTCC CTCATTGCC 60
 AAGGCTCGTT AGAATTCGCC CTAGAGCTGT ATCATGTATT TTCTTTCAAA TTAACCTTGC 120
 TTGCAATTAA GCTTAGGGAA CCAGCAACAA AAGCAAACCT GGCCCGAGGT CGTTCACCGC 180
 GAAAATGGAT TAGAGAACT TCTTCCCGA TTTAAGGGGA AAGATTCTCTG CGGCCAGCGC 240
 TTTGGGGAAA GTGCCCGAC CGCAGAGGCG ACGACAGGGG AGCAGGAAGC TGCTCACGGT 300
 AGTCGGCGTT GGCGGCAGCG GTGGCCCTTC TCATCTGGGC GATGTGGGCT CCTAGAAGAG 360
 10 TAAGGATAAC ATCTTGAAA TGACTTCTGT ACGGTTTGAG CCCAACTGCA CACTCATGAC 420
 TTGGAGCTGC CCTGTGGAGT TACAGTTTAC CAAACACATT CATGAACATA ATCTCATTTA 480
 CTA AAAACTT TGTGAGAAAT TTCTTTTACT AAAATTTTCT CTTATTACAA A

Seq ID NO: 48 DNA sequence:
 Nucleic Acid Accession #: CAT cluster

1 11 21 31 41 51
 20 TTCCAAATTT TTTTCTTGT AATAAGAAAA AATTTTAGTA AAAGAAAATT CTCACAAAGT 60
 TTTTAGTAAA TGAGATTATG TTCATGAATG TGTTTGGTAA ACTGTAACCT CACAGGGCAG 120
 CTCCAAGTCA TGAGTGTGCA GTTGGGCTCA AACCGTACAG AAGTCATTTC CAGGATGTTA 180
 TCCTTACTCT TCTGGAGGCC CACATCGCCC AGATGAGGAA GGCCACCGCT GCCGCCAACG 240
 CGGACTACCG TGAGCAGCTT CCTGCTCCCC TGTCGCTGCC TCTGCGGTGC GGGCAGTTTC 300
 25 CCCAAAGCGC TGGCCGAGG AATCTTTCCC CTTAAATCGG GGAAGAAAGT TCTCTAATCC 360
 ATTTTCGGGG TGAACGACCT CGGGCCAAAG TTGCTTTTGT TGCTGTGTCC CTAAGCTTAA 420
 TTGCAAGCAA AGTTAAATTTG AAAGAAAATA CATGATACAG CTCTAGGGCG AATTCTAACG 480
 AGCCTTGGGC AATGAGGGAA GAACGTGTCT AGTTATCCAC AGCCCGGGGA CGCCTGCACA 540
 CGACGCT

Seq ID NO: 49 DNA sequence
 Nucleic Acid Accession #: CAT cluster

1 11 21 31 41 51
 35 TCTTCTTCTT GCTGCTCGTT TGCTCTCTCT GTGCTCTTCT TCTTCTTCTT CCTCGCCGCT 60
 CCTGCGGAGC TCTGTGTCTT CTCTCTGAT GCGCGGGGCG GGGAGAAAGT GACCGGTGAG 120
 ACCGTAGACC CGAAACCAT GGGTGTGACA AGCCGGTGGC CGGCTTTTTT GGGAGAACCC 180
 GACACATGCA GACCAGTTT CTGGAACNG CATGACCATG TTATTACTAT GGGCCGCTTC 240
 40 CCCAACCAA GTGTTTAAAA CTTTTTAGGG CACCCCAAAT ATTTTCTTTT TTTTCTTTT 300
 TTCAATTAAA AACTCTAAT ATTTATATTA AATACAAAGA TACCACAAAC CTTTATGCTT 360
 TCTTCTGTA TCTGTGCTT TTTCTTTGA CAGCATCTCC ATTTTCTTTC TGCTGCTTCA 420
 TCGCTGTAGC CATGGGAATC CGTTTCATTA TTATGGTAGC AATATGGAGT GCTGTATTCC 480
 TAAAGAAACT GACACAGGAG AATCACTTGA ACTTGGGAGG CAGAGTTTGC AGTGAGCCGA 540
 45 GATTGAACCA GTGCACTCCA GCCTTGGCAG CGGAGCAAGA TTCTGTGACA GTTCTGTAAG 600
 TGCTGGTATC GTCCGTGAGC CCCATCCTCG GTTCCATTGC GCTGCCAGGC AGGGTGCTGG 660
 GACGTGGGGA GAGCTGGTCT ATATATCCGG GTGAAGCTCA GCTGTGGCAC ACCTTGGATG 720
 CCGGTGCTCT CCTGGCCCGG GGAACCTAGT ATTTTGTCCA CGAGTGTACA CCAACCAAAG 780
 GAGACAGCAT CATTTATGAG CCTGCAGCAT CCACCCCTACT GCTGTATCCA GTTTCATTG 840
 ACTG

Seq ID NO: 50 DNA sequence
 Nucleic Acid Accession #: L05187
 Coding sequence: 1991..2260

1 11 21 31 41 51
 55 CTGCAGGGAG GCAGGTAGAA AAGGCTTTTG GGTTTTCAGG TGGGGGGCAG TCTAGCCTGA 60
 TCAGAAAGGA GGAAGAGGCC AGGCGAGATG TCTGGGTGGA GTGAAGGGAA AAAGTGATCC 120
 60 CAGAAAGAAG ATTAGCCCTT GAAAGTCCCT GAAAGTAGGAG AAGGGTAAAG GTGTGGTTGG 180
 TGAAGGAAG CAGGTTTTTC CAGATTAGCA ACCAGTCAGG GGGAGGAAGG TGAGAGTGGG 240
 AGAGTCATAA GTAATATTAT CTGAATGTGT GTAGTTTAAAT GGAATTGGGA AAAAGATGGG 300
 GGAATGGAT GGAAGGTCTT GGAATCTGAG ACAAGGGGTC TATAATCAGT CCATTTCATT 360
 ATTTCTAGCT TCCACCTTCA CCAAGGCAGA CAAGGAGGCG CCACCTCAGC TCTCTGCTC 420
 65 CCCCCTCCCT TCCCACCTAT TCATGTGTGC AAGAGTGCCC TGTCCCACAG AACACGGGGA 480
 ACAACCATCT CAATGACAAG GACAGCAGGT GGCAGGGCTC AACAGGACTC AGATGTCCCC 540
 CCAGGGTTAA CTCATGAAAC CCTCCATGAA GCCTGCTGCT CACCCCTCCC TCAAGGCAG 600
 CCCTGCACCT GGGTCTGAGG ATGAGGGTGG CAGTGAAAAT TAGGCCAGTG ACATCATTTT 660
 CAGCCAGCTA GTGCCAAAAA ATATCAGGTG GTGTTTCATCA AATAAGCCGA GCCAACCGGT 720
 70 GATGAGGATG GTAGTGTGAG TCATGTGTGA CAGGTGAGGA ATGAAAACAG AGTGCCCGAG 780
 AGCTTCTATT TCCTTAGGCG AGGGCTCATI CATCTTATAA AAGCCAGCTG GCCATTGCCT 840
 TCACACCAA CCCAAGGGAC CACACAGCCC ATTTCTGCTCC GTATACCAGG TAAGTCTCTG 900
 ATTGCAACAA ACTGGCAATT CTAGTGTACT TTTTCATTAT TAGAAATTAG CTAAGGGCAA 960
 75 ATATGTGTAA GCAGGTAAAT CCAGGTTTTC AATGGGAGAT AGAGAATAGT GGAATATCTT 1020
 TATTTTAAGT TAAATTACAG TCTGGATTTC AAAGGACCTT AGAGATGGTT AGGCTCCCA 1080
 CCTCAGTAGA TAGTCATTGA ACTGGGAGTC CTGGAGAAGA TTGTTCAAAAT GCCCATGGGA 1140
 AGTTCATAGC AGAAGTAGAA CTCAGGCCAG AGCACTCTCA GTAAACACTGC AATTTCCCCC 1200
 TGACAAGATA TTTATAGAAA TTTTAATTTA TTAGATGGAT CTCTACTGAG CATTTATTCC 1260
 ATTTAAGGCA TGAATGTAGG CACTTTGGAC AAATCAATGC CCTAACGTAC TTACTTAACA 1320
 80 AACATAAAC CTAGCAGGAA GGTAAATACAT ATATATAAAT AATGAAATG CAAAGTAGAT 1380
 AGTAATTGGC ATGACGGAGA TGGGCAGAGA AGGGCTGTGC ACTTTGGGA GACTTGCTCA 1440
 AGGAGACCTC TAGGGTGTCA AGTGATGTGA GCTATGATGG AGGGGTATTT GGACAAGCAG 1500
 AGATGGGAAG AAAAGCATTT GGAAGGGACT GTGTAAAGCAC AGACCAGAAAG CAAAACCATTA 1560
 GAGGCTTAGA TGAATGTAAA GCCATCCTAT AAGTCACAGG CTTTCTACAT GGTACTAGGA 1620
 85 GAGGAAAGTG GTCTGATGCC ATTTTCCAAA AGACCTAATA TGCGGACCTC ATGTCCCTCA 1680
 GAAGCCAGCT TTAGTAGGGC ATTTTCCAG AACAGATATA AGGTGCTTGT GGTAGGAAGG 1740
 GAGCCAGAAA GAGCAACTCCA ATAAATTTGA GCAGAAGAAA TTGCTTTTAA GCTCCTCTCT 1800
 TTCAAAGGGC CTGAAAATTA TCCAAGCTTA TTTCTTTTAA AATGTAAATG GGGGAGCTAA 1860

GGGAGATGAA AGGCTTTCTC TTCTAAAGGG TCCTGAAATA AAATCTGTTT GGCATTGAAT 1920
TGTATATCCAT CTTTCTTTAA TTGAATCACT GTGTGAGCTT TCTGTCTCTA GAAAAAACA 1980
CATTTTGAAGC ATGAATTTCTC AGCAGCAGAA GCAGCCTTGC ACCCCACCCC CTCAGCCTCA 2040
GCAGCAGCAG GTGAAACAAC CTTGCCAGCC TCCACCCAG GAACCATGCA TCCCCAARAC 2100
CAAGGAGCCC TGCCAAACCA AGGTGCCTGA GCCCTGCCAC CCCAAAGTGC CTGAGCCCTG 2160
CCAGCCCAAG ATTCCAGAGC CCTGCCAGCC CAAGGTGCCT GAGCCCTGCC CTTCAACGGT 2220
CACTCCAGCA CCAGCCAGC AGAAGACCAA GCAGAAATA TGTGGTCCAC AGCCATGCCC 2280
TTGAGGAGCT GGCACCTGGA TACTGAACAC CCTACTCCAT TCTGCTTATG AATCCCATT 2340
GCCTATTGAC CCTGCAGTTA GCATGCTGTC ACCCTGAATC ATAATCGCTC CTTGACCT 2400
CTAAAAAGAT GTCCCTTACC CTCACTCTGG AGGCTCCTGA GCCTCTGCGT AAGGCTGAAC 2460
GTCTCACTGA CTGAGCTAGT CTTCTTGTG CTCGGGTGCA TTTGAGGATG GATTGGGGA 2520
AGGTCAAGTG ACCATCCCTA G

Seq ID NO: 51 Protein sequence:
Protein Accession #: AAC26838

1 11 21 31 41 51
MNSQQKQKPC TPPPQPQQQQ VKQPQPQQPQ EPCIPKTKEP CQPKVPEPCH PKVPEPCQPK 60
IPEPCQPKVP EPCPSTVTPA PAQKQTKQK

Seq ID NO: 52 DNA sequence
Nucleic Acid Accession #: NM_002638.1
Coding sequence: 120-473

1 11 21 31 41 51
CAATACAGCT AAGGAATTAT CCCTTGTAAT TACCACAGAC CCGCCCTGGA GCCAGGCCAA 60
GCTGGAGTGC ATAAAGATTG GTATGGCCTT AGCTCTTAGC CAAACACCTT CCTGACACCA 120
TGAGGGCCAG CAGCTTCTTG ATCGTGGTGG TGTTCCTCAT CGCTGGGACG CTGGTTCTAG 180
AGGCAGCTGT CACGGGAGTT CCTGTAAAG GTCAAGACAC TGTCAAAGGC CGTGTCCAT 240
TCAATGGACA AGATCCCGTT AAAGGACAAG TTTCAAGTAA AGGTCAAGAT AAAGTCAAAG 300
CGCAAGAGCC AGTCAAAGGT CCAGTCTCCA CTAAGCCTGG CTCTGCCCC ATTATCTTGA 360
TCCGGTGGGC CATGTTGAAT CCCCTAACCC GCTGCTTAA AGATACTGAC TGCCACAGGA 420
TCAAGAAAGT CTGTGAAGGC TCTTGGCGGA TGGCCTGTT CGTTCCCGC TGAAGGGAGC 480
CGGTCTTGGC TGACCTGTG CCGTCCCCAG AGCTACAGGC CCGATCTGGT CCTAAGTCCC 540
TGCTGCCCTT CCCCTTCCCA CACTGTCCAT TCTTCTCTCC ATTCAAGATG CCCACGGCTG 600
GAGCTGCCCT TCTCATCCAC TTTCCAATAA A

Seq ID NO: 53 Protein sequence:
Protein Accession #: NP_002629.1

1 11 21 31 41 51
MRASSFLIVV VFLIAGTLVL EAAVTGVFVK GQDTVKGKRP FNGQDPVKQ VSVKGQDKVK 60
AQEPVKGPVS TKPSCPIIL IRCAMLNPPN RCLKDTCDFG IKKCCGSCG MACFVPQ

Seq ID NO: 54 DNA sequence
Nucleic Acid Accession #: NM_019618
Coding sequence: 75-584

1 11 21 31 41 51
GGCACGAGCC ACATTTCAGT CCCCTGGACT GTAGATAAAG ACCCTTCTT GCCAGGTGCT 60
GAGACAAACA CACTATGAGA GGCACCTCCAG GAGACGCTGA TGGTGGAGGA AGGGCCGTCT 120
ATCAATCAAT GTGTAAACCT ATTAAGTGGG CAATTAATGA TTTGAATCAG CAAGTGTGGA 180
CCCTTCAGGG TCAGAACCTT GTGGCAGTTC CACGAAGTGA CAGTGTGACC CCAATCACTG 240
TTGCTGTTAT CACATGCAAG TATCCAGAGG CTCTTGAGCA AGGCAGAGGG GATCCCATTT 300
ATTTGGGAAT CCAGAATCCA GAAATGTGTT TGTATTGTGA GAAGGTGGA GAACAGCCCA 360
CAATGCAGCT AAAGAGCAG AAGATCATGG ATCTGTATGG CCAACCCGAG CCCGTGAAAC 420
CCTTCTCTTT CTACCGTGCC AAGACTGGTA GGACCTCCAC CCTTGAGTCT GTGGCCTTCC 480
CGGACTGGTT CATTGCCCTC TCCAAGAGAG ACCAGCCCAT CATTCTGACT TCAGAACTTG 540
GGAAGTCATA CAACACTGCC TTTGAATTAA ATATAAATGA CTGAAGTCA CAGTAGAGTG 600
GCAGCTTGGT CTTTGTCTTA AAGTTTCTGG TTCCCAATGT GTTTTCGTCT ACATTTCTT 660
AGTGTCAAT TCACGCTGGT GCTGAGACAG GGGCAAGGCT GCTGTTATCA TCTCATTTTA 720
TAATGAAGAA GAAGCAATTA CTTATAGCA ACTGAAGAAC AGGATGTGGC CTCAGAAGCA 780
GGAGAGCTGG GTGATATAAG GCTGCTCTCT CAAGCTGGTG CTGTGTAGGC CACAAGGCA 840
CTGCATGAGT GACTTTAAGA CTCAAAGACC AAACACTGAG CTTTCTTCTA GGGGTGGGTA 900
TGAAGATGCT TCAGAGCTCA TGCGGTTTAC CCACGATGGC ATGACTAGCA CAGAGCTGAT 960
CTCTGTTTCT GTTTTGTCTT ATTCCCTCTT GGGATGATAT CATCCAGTCT TTATATGTTG 1020
CCAATATACC TCATTGTGTG TAATAGAAC TTTCTAGCAT TAAGACCTTG TAAACAAAA 1080
TAATCTTGT GTTAAGTTAA ATCATTTTGT TCCTAATGT AATGTGTAAT CTTAAGTTA 1140
AATAAACTTT GTGTATTAT ATAATAAAAA AAAAAAAAA AAA

Seq ID NO: 55 Protein sequence:
Protein Accession #: NP_062564

1 11 21 31 41 51
MRGTPGDADG GGRAVYQSMC KPITGTINDL NQQVWTLQGG NLVAVPRSDS VTPVTVAVIT 60
CKYPEALEQG RGPFIYLIQ NPMECLYCEK VGEQPTLQK EQKIMDLVYQ PEPVKPFLFY 120
RAKTGRTSTL ESWAFPDWFI ASSKRDQPII LTSELGKSYN TAFELNIND

Seq ID NO: 56 DNA sequence
Nucleic Acid Accession #: NM_003125
Coding sequence: 65-334

1 11 21 31 41 51
 5 AGCAGTTCTA AGGGACCATA CAGAGTATTC CTCTCTTCAC ACCAGGACCA GCCACTGTTG 60
 CAGCATGAGT TCCAGCAGC AGAAGCAGCC CTGCATCCCA CCCCCTCAGC TTCAGCAGCA 120
 GCAGGTGAAA CAGCCTTGCC AGCCTCCACC TCAGGAACCA TGCAATCCCA AAACCAAGGA 180
 GCCCTGCCAC CCCAAGGTGC CTGAGCCCTG CCACCCCAAA GTGCCGTGAGC CCTGCCAGCC 240
 CAAGCTTCCA GAGCCATGCC ACCCCAAGGT GCCTGAGCCC TGCCCTTCAA TAGTCACTCC 300
 10 AGACCCAGCC CAGCAGAAGA CCAAGCAGAA GTAATGTGGT CCACAGCCAT GCCCTTGAGG 360
 AGCCGGCCAC CAGATGCTGA ATCCCTATC CATCTCTGTG TATGAGTCCC ATTTGCGCTG 420
 CAATTAGCAT TCTGTCTCCC CCAAAAAGA ATGTGCTATG AAGCTTCTT TCCTACACAC 480
 TCTGAGTCTC TGAATGAAGC TGAAGTCTT AGTACCAGAG CTAGTTTCA GCTGCTCAGA 540
 ATTCACTGTA AGAGAGACTT AAGATGAAAG CAAATGATTG AGCTCCCTTA TACCCCAATT 600
 15 AAATTCATT TCAATTCCA

Seq ID NO: 57 Protein sequence:
 Protein Accession #: NP_003116

1 11 21 31 41 51
 20 MSSQQQKQPC IPPPQLQQQQ VKQPCQPPPP EPCIPKTKEP CHPKVPEPCH PKVPEPCQPK 60
 25 LPEPCHPKVP EPCPSIVTPA PAQKTKQK

Seq ID NO: 58 DNA sequence
 Nucleic Acid Accession #: NM_001793.2
 Coding sequence: 71-2560

1 11 21 31 41 51
 30 AAAGGGGCAA GAGCTGAGCG GAACACCGGC CCGCCGTGCG GGCAGCTGCT TCACCCCTCT 60
 CTCTGCAGCC ATGGGGCTCC CTGCTGAGCC TCTGCGCTCT CTCTCTCTTC TCCAGGTTTG 120
 CTGGCTGCAG TCGCGCGCCT CCGAGCCGTG CCGGGCGGTC TTCAGGAGG CTGAAGTGAC 180
 35 CTGGAGGCGG GAGGCGCGCG AGCAGGAGCC CGGCCAGCGC CTGGGGAAAG TATTTCATGGG 240
 CTGCCCTGGG CAAGAGCCAG CTCTGTTTAG CACTGATAAT GATGACTTCA CTGTGCGGAA 300
 TGGCGAGACA GTCCAGGAAA GAAGGTCACT GAAGGAAAGG AATCCATTGA AGATCTTCCC 360
 ATCCAAACGT ATCTTACGAA GACACAAGAG AGATTGGGTG GTTGCTCCAA TATCTGTCCC 420
 TGAAAATGGC AAGGGTCCCT TCCCCAGAG ACTGAATCAG CTCAAGTCTA ATAAAGATAG 480
 40 AGACACCAAG ATTTTCTACA GCATCAACGGG GCGGGGGGCA GACAGCCCCC CTGAGGGTGT 540
 CTTCGCTGTA GAGAAGGAGA CAGGCTGGTT GTTGTGAAT AAGCCACTGG ACCGGGAGGA 600
 GATTGCCAAG TATGAGCTCT TTGGCCACGC TGTGTCAGAG AATGGTGCCT CAGTGGAGGA 660
 CCCATGAAAC ATCTCCATCA TCGTGACCGA CCAGAATGAC CACAAGCCCA AGTTTACCCA 720
 45 GGACACCTTC CGAGGGAGTG TCTTAGAGGG AGTCTTACCA GGTACTTCTG TGATGCAGGT 780
 GACAGCCACG GATGAGGATG ATGCCATCTA CACCTACAA TGGGTGGTTG CTTACTCCAT 840
 CCATAGCCAA GAGGTGCGTG ACCCAACAGA CCTCATGTTT ACCATTCAAC GGAGCACAGG 900
 CACCATCAGC GTCATCTCCA GTGGCTGGA CCGGGAAAAA GTCCCTGAGT ACACACTGAC 960
 CATCCAGGCC ACAGACATGG ATGGGACCGG CTCACACACC ACGGCAGTGG CAGTAGTGA 1020
 50 GATCCTTGAT GCCAATGACA ATGCTCCCAT GTTTGACCCC CAGAAGTACG AGGCCCATGT 1080
 GCCTGAGAA TGCAGTGGGCC ATGAGGTGCA GAGGCTGACG GTCACTGATC TGGACGCCCC 1140
 CAACCTACCA CCGTGGCGTG CACCTACCT TATCATGGGC GGTGACGACG GGGACCAATT 1200
 TACCATCACC ACCCAACCTG AGAGCAACCA GGGCATCCTG ACAACAGGAG AGGGTTTGA 1260
 TTTTGGGCCC AAAAACCCAG ACACCCTGTA CGTTGAAGTG ACCAAGGAG CCCCTTTTGT 1320
 55 GCTGAAGCTC CCAACCTCCA CAGCCACCAT AGTGGTCCAC GTGGAGGATG TGAATGAGGC 1380
 ACCTGTGTT GTCCCCCCT CCAAGTCTGT TGAGGTCCAG GAGGGCATCC CCACTGGGG 1440
 GCCTGTGTT GTCTACACTG CAGAAGACCC TGACAAGGAG AATCAAAAGA TCAGTACCG 1500
 CATCTGAGA GACCCAGCAG GGTGGCTAGC CATGACCCCA GACAGTGGGC AGGTCAACGC 1560
 TGTGGGCACC CTCGACGCTG AGGATGAGCA GTTTGTGAGG AACAACATCT ATGAAGTCAT 1620
 60 GGTCTTGGCC ATGGACAATG GAAGCCCTCC CACCACTGGC ACGGGAACCC TTCTGCTAAC 1680
 ACTGATTGAT GTCAATGACC ATGGCCCACT CCCTGAGCCC CGTCAGATCA CCATCTGCAA 1740
 CCAAAGCCCT GTGCGCCAGG TGCTGAACAT CACGGAACAAG GACCTGTCTC CCCACACCTC 1800
 CCCTTTCCAG GCCCAGTCTA CAGATGACTC AGACATCTAC TGGACGGCAG AGGTCAACGA 1860
 65 GGAAGGTGAC ACAGTGGTCT GTTCCCTGAA GAAGTTCTCT AAGCAGGATA CATATGACGT 1920
 GCACCTTTCT CTGTCTGACC ATGGCAACAA AGAGCAGCTG ACGGTGATCA GGGCCACTGT 1980
 GTGCGACTGC CATGGCCATG TCGAAACCTG CCCTGGACCC TGGAGGGAG GTTTCATCCT 2040
 CCCTGTGCTG GGGGCTGTCC TGGCTCTGCT GTTCTCTCTG CTGGTGTCTG TTTTGTGTT 2100
 GAGAAAGAA CCGAAGATCA AGGAGCCCCC CTACTCCCA GAAGATGACA CCCGTGACAA 2160
 70 CBTCTTCTA TATGGCGAAG AGGGGGTGG CGAAGAGGAC CAGGACTATG ACATCACCCA 2220
 GCTCCACCGA GGTCTGGAGG CCAGGCCGGA GGTGGTCTC CGCAATGACG TGGCACCAAC 2280
 CATCATCCCG ACACCCATGT ACCGTCTCTG GCCAGCCAAC CCAGATGAAA TCGGCAACTT 2340
 TATAATTGAG AACCTGAAGG CGGCTAACAC AGACCCCA CA GCGCCGCCCT ACGACACCTT 2400
 CTGTGTTCT GACTATGAGG GCAGCGGCTC CGACGCCGCG TCCCTGAGCT CCCTCACCTC 2460
 75 CTCCGCTCC ACCCAAGACC AAGATTACGA TTATCTGAAC GAGTGGGGCA GCGCTTCAA 2520
 GAAGCTGGCA GACATGTACG GTGGCGGGGA GGAAGACTAG GCGGCCCTGC TGCAGGGCTG 2580
 GGGACCAAC GTCAAGGCCAC AGAGCATCTC CAAGGGGTCT CAGTTCCTCC TTCAGCTGAG 2640
 GACTTCGAGG CTTGTCAAGG AGTGGCCGTA GCAACTTGGC GGAGACAGCG TATGAGTCTG 2700
 ACGTTAGAGT GGTGTCTTCC TTAGCCTTTC AGGATGGAGG AATGTGGGCA GTTTGACTTC 2760
 80 AGCACTGAAA ACCTCTCCAC CTGGGCCAGG GTTGCCTCAG AGGCCAAGTT TCCAGAAGCC 2820
 TCTTACCTGC CGTAAATGTC TCAACCTGT GTCTGGGCC TGGGCCCTGT GTGACTGACC 2880
 TACAGTGAC TTTCTCTCTG GAATGGAACC TTCTTAGGCC TCCTGTGCA ACTTAATTTT 2940
 TTTTTTTAA GCTATCTTCA AAACGTTTGA GAAAGTTCTT CAAAAGTGCA GCGCAGAGCT 3000
 GCTGGGCCCA CTGGCCGTCC TGCAATTCTG GTTCCAGAC CCAATGCGCT CCCATTCCGA 3060
 85 TGGATCTCTG CGTTTTTATA CTAGTGTGTC CTAGTTGCC CTTATTTTTT TATTTTCCCT 3120
 GTTGGGTGTC TATAGATGAA GGGTGAGGAC AATCGTGTAT ATGTACTAGA ACTTTTTTAT 3180
 TAAAGAACT TTTCCAGAA AAAAA

Seq ID NO: 59 Protein sequence:

Protein Accession #: NP_001784.2

	1	11	21	31	41	51	
5	MGLPRGPLAS	LLLLQVCWLQ	CAASEPCRAV	FREAETVLEA	GGAEQEPGQA	LGKVFMGCPG	60
	QEPALFSTDN	DDFTVRNGET	VQERRSLKER	NPLKIFPSKR	ILRRHKRDWV	VAPISVPENG	120
	KGPFFPQRLNQ	LKSNKDRDTK	IFYSITGPGA	DSPPEGVFAV	EKETGWLLLN	KPLDREEIAK	180
	YELFGHAYSE	NGASVEDPMN	ISIIIVTDQND	HKPKFTQDTF	RGSVLEGVLP	GTSVMQVTAT	240
10	DEDDAIYTYN	GVVAYSISHSQ	EPKDPHDLMF	TIHRSTGTIS	VISGLDREK	VPEYTLTIQA	300
	TDMGDGSGTT	TAVAVVEILD	ANDNAPMDFP	QKYEAHVPEN	AVGHEVQRLT	VTDLDAPNSP	360
	AWRATYILMG	GDDGDHFTIT	THPESNOGIL	TRKGLDFEA	KNQHTLYVEV	TNEAPFVLKL	420
	PTSTATIVVH	VEDVNEAPVF	VPPSKVVEVQ	EGIPTGEPVC	VYTAEDPDKE	NQKISYRILR	480
	DPAGWLAMP	DSGQVTAVGT	LDREDEQFVR	NNIYEVMLA	MDNGSPPTTG	TGTLTLLTLD	540
	VNDHGPVPEP	RQITICNQSP	VRQVLNITDK	DLSPHTSPFQ	AQLTDDSDIY	WTAEVNEEGD	600
15	TVVLSLKKFL	KQDTYDVHLS	LSDHGNKEQL	TVIRATVCDC	HGHVETCPGP	WKGGFILPVL	660
	GAVLALLPLL	LVLVLLVRKK	RKIKEPLLLP	EDDTRDNVFP	YGEEGGGEED	QDYDITQLHR	720
	GLEARPEVVL	RNDVAPTIIIP	TPMYRPRPAN	PDEIGNFIE	NLKAANTDPT	APPYDTLLVF	780
	DYEGSGSDAA	SLSLTSSAS	DQDQDYDYLN	EWGSRFKKLA	DMYGGGEDD		

Seq ID NO: 60 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 162-428

	1	11	21	31	41	51	
25	GCGTTCGGTT	GGCGGCGGAT	TCGAACGTTT	GGACTGAGGT	TTTTCTGCCT	GAAGAAGCGT	60
	CATACGGACC	GGATTGTTTT	CGCTGGCCCA	GTGTCCCGCG	AGCTTGTGTG	CGATACAGAG	120
	AGCACCCTCG	AAGCTGAGGC	AGCTGGTACT	TGACAGAGAG	GATGGCGCTG	TCGACCATAG	180
	TCTCCCAAG	GAACGAGATA	AAGCGGAAGG	CTCCCGTGG	CTTTCTAAAG	CGAGTCTTCA	240
30	AGCGAAAGAA	GCCCTCAACT	CGTCTGGAGA	AAAGTGGTGA	CTTATTGGTC	CATCTGAACT	300
	GTTTACTGTT	TGTTCTATCGA	TTAGCAGAAG	AGTCCAGGAC	AAACGCTTGT	GCGAGTAAAT	360
	GTAGAGTCAT	TAACAAGGAG	CATGTACTGG	CCGCAGCAAA	GGTAATTCTA	AAGAAGAGCA	420
	GAGGTTAGAA	GTCAAAGAAC	ATATTCTTGA	AAGTTATGAT	GCATTCTTTT	GGGTGGTAAC	480
	AGATCATAAA	GACATTTTTT	ACACATCAGT	TAATATGGGA	TTATTAAATA	TTGG	

Seq ID NO: 61 Protein sequence:

Protein Accession #: Eos sequence

	1	11	21	31	41	51	
40	MALSTIVSQR	KQIKRKAPRG	FLKRVFKRKK	PQLRLEKSGD	LLVHLNCLLF	VHRLAESRT	60
	NACASKCRVI	NKERVLAALK	VILKKSRRG				

Seq ID NO: 62 DNA sequence

Nucleic Acid Accession #: NM_000094.2

Coding sequence: 99-8933

	1	11	21	31	41	51	
50	GGGCTGGAGG	GGCGCTGGGC	TCGGACCTGC	CAAGGCCACC	GCAGGGGGGA	GCAAGGGACA	60
	GAGGCGGGGG	TCCTAGCTGA	CGGCTTTTAC	TGCCTAGGAT	GACGCTGCGG	CTTCTGGTGG	120
	CCGCGCTCTG	CGCCGGGATC	CTGGCAGAGG	CGCCCCGAGT	GCGAGCCAG	CACAGGGAGA	180
	GAGTGACCTG	CACGCGGCTT	TACGCGCGTG	ACATTGTGTT	CTTACTGGAT	GGCTCCTCAT	240
	CCATTGGCCG	CAGCAATTTT	CGCGAGGTCC	GCAGCTTTCT	CGAAGGGCTG	GTGCTGCCTT	300
55	TCTCTGGAGC	AGCCAGTGCA	CAGGGTGTGC	GCTTTGCCAC	AGTGCAGTAC	AGCGATGACC	360
	CACGGACAGA	GTTCCGGCTG	GATGCACTTG	GCTCTGGGGG	TGATGTGATC	CGCGCCATCC	420
	GTGAGCTTAG	GTCACAGGGG	GGCAACACTC	GCACAGGGGC	TGCAATCTCT	CATGTGGCTG	480
	ACCATGTCTT	CCTGCCCCAG	CTGGCCCGAC	CTGGTGTCCC	CAAGGTCTGC	ATCCTGATCA	540
	CAGACGGGAA	GTCCCAAGAC	CTGGTGGACA	CAGCTGCCCA	AAGGCTGAAG	GGGACGGGGG	600
60	TCAAGCTATT	TGCTGTGGGG	ATCAAGAATG	CTGACCCCTG	GGAGCTGAAG	CGAGTTGCCT	660
	CACAGCCAA	CTCCGACTTC	TTCTTCTTCG	TCAATGACTT	CAGCATCTTG	AGGACACTAC	720
	TGCCCTCGT	TTCCCGGAGA	GTGTGCACGA	CTGCTGGTGG	CGTGCCCTGT	ACCCGACCTC	780
	CGGATGACTC	GACCTCTGCT	CCACGAGACC	TGGTGCTGTC	TGAGCCCAAG	AGCCATCCTC	840
	TGAGAGTACA	GTGGACAGCG	GCCAGTGGCC	CTGTGACTGG	CTACAAGGTC	CAGTACACTC	900
65	CTCTGACGGG	GCTGGGACAG	CCACTGCCGA	GTGAGCGGCA	GGAGGTGAAC	GTCCAGCTG	960
	GTGAGACCAG	TGTGCGGCTG	CGGGTCTCC	GGCCACTGAC	CGAGTACCAA	GTGACTGTGA	1020
	TTGCCCTCTA	CGCCAAACAG	ATCGGGGAGG	CTGTGAGCGG	GACAGCTCGG	ACCACTGCCC	1080
	TAGAAGGGCC	GGAATGACCT	ATCCAGAATA	CCACAGCCCA	CAGCCTCCTG	GTGGCTGGCC	1140
	GGAGTGTGCC	AGGTGCCACT	GGCTACCGTG	TGACATGGCG	GCTCCTCAGT	GGTGGGCCCA	1200
70	CACAGCAGCA	GGAGCTGGGC	CCTGGGCAGG	GTTTCACTGT	GCTGCGTGAC	TTGGAGCCTG	1260
	GCACGGACTA	TGAGGTGACC	GTGAGCACCC	TATTTGGCCG	CAGTGTGGGG	CCCGCACTT	1320
	CCCTGATGGC	TGCGACTGAC	GCTTCTGTGT	AGCAGACCCT	GCGCCCGGTC	ATCCTGGGCC	1380
	CCACATCCAT	CCTCTTTTCC	TGGAACCTGG	TGCCTGAGGC	CCGTGGCTAC	CGGTTGGAAT	1440
	GGCGGGCTGA	GACTGGCTTG	GAGCCACCGC	AGAAGGTGGT	ACTGCCCTCT	GATGTGACCC	1500
75	GCTACCAATT	GGATGGGCTG	CAGCCGGGCA	CTGAGTACCG	CCTCACACTC	TACACTCTGC	1560
	TGGAGGGCCA	CGAGGTGGCC	ACCCCTGCAA	CCGTGGTTCC	CAGTGGACCA	GAGCTGCCTG	1620
	TGAGCCCTGT	AACAGACCTG	CAAGCCACCG	AGCTGCCCGG	GCAGCGGCTG	CGAGTGTCTC	1680
	GGAGCCCACT	CCCTGGTGCC	ACCCAGTACC	GCATCAITGT	GCGCAGCAGC	CAGGGGGTTG	1740
	AGCGGACCC	GGTGCTTCTC	GGGAGTCAGA	CAGCATTCGA	CTTGAGTAC	GTTCAGGCTG	1800
80	GGCTTAGCTA	CAGTGTGCGG	GTGTCTGCTC	GAGTGGGTCC	CCGTGAGGGC	AGTGCCAGTG	1860
	TCTCACTGT	CCGCGGGGAG	CCGGAACACT	CAGTGTCTGT	TCCAGGGCTG	CGGGTGTGTG	1920
	TGTCAAGTGC	AACCGAGTGC	AGGGTGGCCT	GGGGACCCGT	CCCTGGAGAG	AGTGGATTTC	1980
	GGATTAGCTG	GAGCACAGGC	AGTGGTCCGG	AGTCCAGCCA	GACACTGCCC	CCAGACTCTA	2040
	CTGCCACAGA	CATCACAGGG	CTGCAGCCTG	GAACCACTTA	CCAGGTGGCT	GTGTGGGTAC	2100
85	TGCGAGGCAG	AGAGGAGGGC	CCTGCTGCAG	TCATCGTGGC	TGCAACGGAC	CCAATGGGGC	2160
	CAGTGAGGAC	GGTCCATGTG	ACTCAGGCCA	GCAGCTCATC	TGTCACCACT	ACCTGGACCA	2220
	GGGTCTCTGG	CGCCACAGGA	TACAGGGTTT	CCTGGCACTC	AGCCACGGCC	CCAGAGAAAT	2280

	CCCAGTTGGT	TTCTGGGGAG	GCCACGGTGG	CTGAGCTGGA	TGGACTGGAG	CCAGATACCTG	2340
	AGTATACGGT	GCATGTGAGG	GCCCATGTGG	CTGGCGTGGA	TGGGCCCCCT	GCCTCTGTGG	2400
	TTGTGAGGAC	TGCCCCCTGAG	CCTGTGGGTC	GTGTGTGAG	GCTGCAGATC	CTCAATGCTT	2460
5	CCAGCGAGCT	TCTACGATC	ACCTGGGTAG	GGGTCACTGG	AGCCACAGCT	TACAGACTGG	2520
	CCTGGGGCCG	GAGTGAAGGC	GGCCCCATGA	GGCACCAGAT	ACTCCCAGGA	AACACAGACT	2580
	CTGCAGAGAT	CCGGGGTCTC	GAAGGTGGAG	TCAGCTACTC	AGTCCGAGTG	ACTGCACTTG	2640
	TCGGGGACCG	CGAGGGCACA	CCTGTCTCCA	TTGTTGTAC	TACGCCGCT	GAGGCTCCGC	2700
	CAGCCCTGGG	GACGCTTCAC	GTGGTGCAGC	GCGGGGAGCA	CTCGCTGAGG	CTCGCTGGG	2760
10	AGCCGGTGCC	CAGAGCGCAG	GGCTTCCTTC	TGCATGGCA	ACCTGAGGGT	GGCCAGGAAC	2820
	AGTCCCGGGT	CCTGGGGCCC	GAGCTCAGCA	GCTATCACCT	GGACGGGCTG	GAGCCAGCGA	2880
	CACAGTACCG	CGTAGAGCTG	AGTGTCTTAG	GGCCGGCTGG	AGAAGGGCCC	TCTGCAGAGG	2940
	TGACTGCGCG	CACTGAGTCA	CCTCGTGTTC	CAAGCATTGA	ACTACGTGTG	GTGGACACCT	3000
	CGATCGACTC	GGTGACTTTG	GCCTGGACTC	CAGTGTCCAG	GGCATCCAGC	TACATCCTAT	3060
15	CCTGGCGGGC	ACTCAGAGGC	CCTGGCCAGG	AAGTGCCTGG	GTCCCCGAG	ACACTTCCAG	3120
	GGATCTCAAG	CTCCACGGCG	GTGACAGGGC	TAGAGCCTGG	CGTCTCTTAC	ATCTTCTCCC	3180
	TGACGCTGT	CTCGGGGTCT	GTGCGGGTCT	CTGAGGCATC	TGTACACAG	ACGCCAGTGT	3240
	GCCCCCTGG	CCTGGCGGAT	GTGGTGTTC	TACCACATGC	CACTCAAGAC	AATGCTCACC	3300
	GTGCGGAGGC	TACAGGAGG	GTCTGGAGC	GTCTGGTGT	GGCACTTGG	CCTCTTGGGC	3360
20	CACAGGCACT	TACAGTTGGC	CTGCTGTCTT	ACAGTCATCG	GCCCCCCTCA	CTGTTCCAC	3420
	TGAATGGCTC	CCATGACCTT	GGCATTATCT	TGCAAGGAT	CCGTGACATG	CCCTACATGG	3480
	AGCAAGTGG	GAACAACCTG	GGCAGAGCCG	TGGTCACAGC	TCACAGATAC	ATGTTGGCAC	3540
	CAGATGCTCC	TGGCGCGCGC	CAGCACGTAC	CAGGGGTGAT	GGTCTGCTA	GTGGATGAAC	3600
	CCTTGAGAGG	TGACATATTC	AGCCCCATCC	GTGAGGCCCA	GGCTTCTGGG	CTTAATGTGG	3660
25	TGATGTGGG	AATGGCTGGA	GCGGACCCAG	AGCAGCTGCG	TGCTTGGCG	CCGGGTATGG	3720
	ACTCTGTCCA	GACCTTCTTC	GCGTGGATG	ATGGGCCAAG	CCTGGACGAG	GCAGTCAGTG	3780
	GTCTGGCCA	AGCCCTGTGT	CAGGCATCTT	TCACACTCA	GCCCCGGCCA	GAGCCCTGCC	3840
	CAGTGTATTG	TCCAAAGGGC	CAGAAGGGGG	AACCTGGAGA	GATGGGCTG	AGAGGACAAG	3900
	TTGGGCTCC	TGGCGACCCCT	GGCCTCCCGG	GCAGGACCCG	TGCTCCCGGC	CCCCAGGGGC	3960
30	CCCTGGAAAG	TGCGCACTGCC	AAGGGCGAGA	GGGGCTTCCC	TGGAGCAGAT	GGGCGTCCAG	4020
	GCAGCCCTGG	CCGGCGCCGG	AATCCTGGGA	CCCTTGGAGC	CCCTGGCCTA	AAGGGCTCTC	4080
	CAGGGTTGCC	TGGCCCTCGT	GGGACCCCGG	GAGAGCGAGG	ACCTCGAGGC	CCAAAGGGGG	4140
	AGCCGGGGGC	TCCCGGACAA	GTGATCGGAG	GTGAAGGACC	TGGGCTTCTT	GGGCGGAAAG	4200
	GGGACCCCTG	ACCATCGGGC	CCCCCTGGAC	CTCGTGGACC	ACTGGGGGAC	CCAGGACCCC	4260
35	GTGGCCCCCC	AGGGCTTCTT	GGAAACAGCCA	TGAAGGTGTA	CAAAGGCGAT	CGTGGGGAGC	4320
	GGGGTCCCCC	TGGACCAAGT	GAAGGTGGCA	TTGCTCCTGG	GGAGCCTGGG	CTGCCGGGTC	4380
	TTCCCGGAAAG	CCCTGGAGCC	CAAGGCCCCG	TTGGCCCCCC	TGGAAGAAAG	GGAGAAAGAG	4440
	GTGACTCTGA	GGATGGAGCT	CCAGGCCCTC	CAGGACCAAC	TGGGTCTCCG	GGTGAGCAGG	4500
	GCCCCAGGGG	ACCTCCTGGA	GCTATTGGCC	CCAAAGGTGA	CCGGGGCTTT	CCAGGGCCCC	4560
40	TGGGTGAGGC	TGGAGAGAGG	GGCGAACGTG	GACCCCCAGG	CCCAGCGGGA	TCCCGGGGGC	4620
	TGCCAGGGGT	TGCTGGACGT	CCTGGAGCCA	AGGGTCTGTA	AGGGCCACCA	GGACCCACTG	4680
	GCGCCCAAGG	AGAGAAGGGG	GAGCCTGGTC	GCCCTGGGGA	CCCTGCACTG	GTGGGACCTG	4740
	CTGTGTCTGG	ACCCAAAGGA	GAAAGGGGAG	ATGTGGGGCC	CGCTGGGGCC	AGAGGAGCTA	4800
	CCGGAGTCCA	AGGGGAACCG	GGCCACCCCG	GCTTGGTTCT	TCCTGGAGAC	CCTGGCCCCA	4860
45	AGGGAGACCC	TGGAGACCGG	GGTCCCATTC	GCCTTACTGG	CAGAGCAGGA	CCCCCAGGTG	4920
	ACTCAGGGCC	TCCTGGAGAG	AAGGGAGACC	CTGGGCGGGC	TGGCCCCCTA	GGACCTGTTG	4980
	GCCCCCGAGG	ACGAGATGGT	GAAGTTGGAG	AGAAAGGTGA	CGAGGGCTCT	CCGGGTGACC	5040
	CGGGTTTGCC	TGGAAGAGCA	GCGAGCGGTG	GCCTTCGGGG	GGCACCTGGA	GTTCGGGGGC	5100
	CTGTGGGTGA	AAAGGGGAGC	CGGGAGATC	CTGGAGAGGA	TGGACGAAAT	GGCAGCCCTG	5160
50	GATCATCTGG	ACCCAAGGGT	GACCGTGGGG	AGCCGGGTCC	CCCAGGACCC	CCGGGACGCG	5220
	TGGTAGACAC	AGGACCTGGA	GCCAGAGAGA	AGGGAGAGCC	TGGGGACCCG	GGACAAGAGG	5280
	GTCTCGAGG	GCTCAAGGGT	GATCCTGGCC	TCCTTGGAGC	CCCTGGGGAA	AGGGGCATTG	5340
	AAGGGTTTCG	GGGACCCCCA	GGCCACAGG	GGGACCCAGG	TGTCGAGGCG	CCAGCAGGAG	5400
	AAAAGGGTGA	CCGGGTCTCC	CTGGGCTGG	ATGGCCGGAG	CGGACTGGAT	GGGAAACCCG	5460
55	GAGCCGCTGG	GCCCTCTGGG	CCGAATGGTG	CTGCAGGCAA	AGCTGGGGAC	CCAGGGAGAG	5520
	ACGGGCTTCC	AGGCCTCCGT	GGAGAACAAG	GCCTCCCTGG	CCCCCTCTGT	CCCCCTGGAT	5580
	TACCGGGAAA	CCCGGGGAGG	GATGGGAAAC	CTGGGCTGAA	TGGAAGAAAG	GGAGAACCTG	5640
	GGGACCTGG	AGAGAGCGGG	AGGAAGGGAG	AGAAAGGAGA	TTCAGGCGCC	TCTGGGAGAG	5700
	AAGGTCTGGA	TGGCCCCAAG	GATGAGCGTG	GAGCTCCTGG	TATCCTTGGA	CCCCAGGGGC	5760
60	CTCCAGGCCCT	CCCAGGGCCA	GTGGGCCCTC	CTGGCCAGGG	TTTTCTCTGT	GTCCAGGAG	5820
	GCACGGGGCC	CAAGGCTGAC	CGTGGGAGGA	CTGGATCCAA	AGGGGAGCAG	GGCCTCCCTG	5880
	GAGAGCGTGG	CCTGCGGAGG	GAGCCTGGAA	GTGTGCCGAA	TGTGGATCGG	TTGCTGGAAA	5940
	CTGCTGGCAT	CAAGGCATCT	GCCTTGGGGG	AGATCGTGGA	GACCTGGGAT	GAGAGCTCTG	6000
	GTAGCTTCTT	GCCTGTGCCC	GAACGGCGTC	GAGGCCCCAA	GGGGGACTCA	GGCGAACAGG	6060
65	GCCCCCAGG	CAAGGAGGGC	CCCATCGGCT	TTCTTGAGGA	ACGCGGGCTG	AAGGGCGACC	6120
	GTGGAGACCC	TGGCCCTCAG	GGGCCACCTG	GTCTGGCCCT	TGGGGAGAGG	GGCCCCCCCG	6180
	GGCCTTCCGG	CCTTGGCCGG	GAGCCTGGAA	AGCCTGGTAT	TCCCGGGCTC	CCAGGCAGGG	6240
	CTGGGGGTGT	GGGAGAGGCA	GGAAGGCCAG	GAGAGAGGGG	AGAACGGGGA	GAGAAAGGAG	6300
	AACGTGGAGA	ACAGGGCAGA	GATGGCCCTC	CTGGACTCCC	TGGAACCCCT	GGGCCCCCGG	6360
70	GACCCCTCTG	CCCCAAGGTG	TCTGTGGATG	AGCCAGGTCC	TGGACTCTCT	GGAGAACAGG	6420
	GACCCCTCTG	ACTCAAGGGT	GCTAAGGGGG	AGCCGGGCGG	CAATGGTGAC	CAAGGTCCCA	6480
	AAGGAGACAG	GGGTGTGCCA	GGCATCAAAG	GAGACCAGGG	AGAGCCTGGA	CCGAGGGGTC	6540
	AGGACGGCAA	CCCGGGTCTA	CCAGGAGAGC	GTGGTATGGC	TGGGCCTGAA	GGGAAGCCGG	6600
	GCTCTGAGGG	TCCAAGAGGG	CCCCCTGGCC	CAGTGGGTGG	TGATGGAGAG	CCTGGACCAAC	6660
75	CTGGTCCCCC	GGGTCTTGCT	GGCCTGCGAG	GACCCCAAGG	ACCTTCTGGC	CTGAAGGGGG	6720
	AGCCTGGAGA	GACAGGACCT	CCAGGAGCGG	GCCTGACTGG	ACCTACTGGA	GCTGTGGGAC	6780
	TTCTTGAGAC	CCCGGGCCCT	TCAGGGCCTG	TGGGTCCACA	GGGGTCTCCA	GGTTTGCCTG	6840
	GACAAGTGGG	GGAGACAGGG	AAGCCGGGAG	CCCCAGGTCT	AGATGGTGCC	AGTGGAAAAG	6900
	ATGGAGACAG	AGGAGTCCGG	GGTGTGCCAG	GGTCAACAGG	TCTGCTGGCG	CCTGTCCGAG	6960
80	CTAAAGGAGA	ACCTGGCCCC	ACGGGGGCCC	CTGGACAGGC	TGTGGTGGGG	CTCCCTGGAG	7020
	CAAAGGGAGA	GAAGGGAGCC	CCTGGAGGCC	TTGCTGGAGA	CCTGGTGGGT	GAGCCGGGAG	7080
	CCAAAGGTGA	CCGAGGACTG	CCAGGGCCCG	GAGGCGAGAA	GGGTGAAGCT	GGCCGTGCAG	7140
	GGGAGCCCGG	AQACCTTGGG	GAAGATGGTC	AGAAAGGGGC	TCCAGGACCC	AAAGGTTTCA	7200
	AGGGTGACCC	AGGAGTCCGG	TCCCGGGCT	CCCTTGGGCC	TCCTGGCCCT	CCAGGTGTGA	7260
	AGGGAGATCT	GGGCTTCCCT	GGCCTGCCCG	GTGCTCCTGG	TGTTGTTGGG	TTCCCGGGTC	7320
85	AGACAGGCCC	TCGAGGAGAG	ATGGGTGAGC	CAGGCCCTAG	TGGAGAGCGG	GGTCTGGCAG	7380
	GCCCCCAGG	GAGAGAAGGA	ATCCAGGAC	CCCTGGGGCC	ACCTGGACCA	CCGGGTCTAG	7440
	TGGGACACCC	TGGGGCTCTT	GGACTCAAAG	GAGACAAGGG	AGACCTGGA	GTAGGGCTGC	7500

	CTGGGCCCGG	AGGCGAGCGT	GGGGAGCCAG	GCATCCGGGG	TGAAGATGGC	CGCCCGGGCC	7560
	AGGAGGGACC	CCGAGSACTC	ACGGGGCCCC	CTGGCAGCAG	GGGAGAGCGT	GGGGAGAGGG	7620
	GTGATGTTGG	GAGTGCAGGA	CTAAAGGGTG	ACAAGGGAGA	CTCAGCTGTG	ATCCTGGGGG	7680
5	CTCCAGGGCC	ACGGGGTGCC	AAGGGGACAC	TGGGTGAACG	AGGGCCTCGG	GGCTTGGATG	7740
	GTGACAAAGG	ACCTCGGGGA	GACAAATGGG	ACCTCGGTGA	CAAGGGGAGC	AAGGGAGAGC	7800
	CTGGTGACAA	GGGCTCAGCC	GGGTGCGCAG	GACTGCGTGG	ACTCCTGGGA	CCCCAGGGTC	7860
	AACCTGGTGC	AGCAGGGATC	CCTGGTGACC	CGGGATCCCC	AGGAAAGGAT	GGAGTGCCTG	7920
	GTATCCGAGG	AGAAAAAGGA	GATGTTGGCT	TCATGGGTCC	CCGGGGCCTC	AAGGGTGAAC	7980
10	GGGGAGTGAA	GGGAGCCTGT	GGCCTTGATG	GAGAGAAGGG	AGACAAGGGA	GAAGCTGGTC	8040
	CCCCAGGGCC	CCCCGGGCTG	GCAGGACACA	AAGGAGAGAT	GGGGGAGCCT	GGTGTGCCGG	8100
	GCCAGTCGGG	GGCCCTTGCC	AAGGAGGGCC	TGATCGGTCC	CAAGGGTGAC	CGAGGCTTTG	8160
	ACGGGCAGCC	AGGCCCCAAG	GGTGACCAGG	GCAGAAAGGG	GGAGCGGGGA	ACCCAGGAA	8220
	TTGGGGGCTT	CCCAGGCCCC	AGTGGAAATG	ATGGCTCTGC	TGGTCCCCCA	GGGCCACCTG	8280
	GCAGTGTGGG	TCCAGAGGGC	CCCGAAGGAC	TTCAGGGCCA	GAAGGGTGAG	CGAGGTCCCC	8340
15	CCGGAGAGAG	AGTGGTGGGG	GCTCCTGGGG	TCCTCGGAGC	TCCTGGCGAG	AGAGGGGAGC	8400
	AGGGGCGGCC	AGGGCCTGCC	GGTCTCGAG	GCGAGAAGGG	AGAAGCTGCA	CTGACGGAGG	8460
	ATGACATCCG	GGGCTTTGTG	CGCCAAGAGA	TGAGTCAGCA	CTGTGCCTGC	CAGGGCCAGT	8520
	TCATCGCATC	TGGATCAGGA	CCCTCCCTA	GTTATGCTGC	AGACACTGCC	GGCTCCCAGC	8580
20	TCATGCTGTG	CGCTGTGCTC	CGCGTCTCTC	ATGCAGAGGA	GGAAGAGCGT	GTACCCCTCG	8640
	AGGATGATGA	TGACTCTGAA	TACTCCGAGT	ATTCTGTGGA	GGAGTACAGG	GACCCCTGAAG	8700
	CTCCTTGGGG	GTAGTCTGAC	CCCTGTTCCC	TGCCACTGGA	TGAGGGCTCC	TGCACTGCCT	8760
	ACACCTCTGG	CTGTGACCAT	CGGCTGTGTA	CAGGCAGCAC	AGAGGCCTGT	CACCCCTTTG	8820
	TCTATGGTGG	CTGTGGAGGG	AATGCCAACCC	GTTTTGGGAC	CCGTGAGGCC	TGCGAGCGCC	8880
25	GCTGCCACCC	CCGGGTGGTC	CCGAGCCAGG	GGACAGGTAC	TGCCCAGGAG	TGAGGCCCCAG	8940
	ATAATGAGCT	GAGATTGAGC	ATCCCCCTGA	GGAGTCCGGG	TCTCAGCAGA	ACCCCACTGT	9000
	CCCTCCCTCT	GGTCTGTAGG	GCTTGTGTGC	ACGTGAGCGT	GCGAGTGAC	GTCCGTATT	9060
	TCAGTGACTT	GGTCCCGTGG	GTCTAGCCTT	CCCCCTCTGT	GACAAACCCC	CATTGTGGCT	9120
	CTGCGCACCC	TGGCAGATGA	CTCACTGTGG	GGGGGTGGCT	GTGGGCACTG	AGCGGATGTG	9180
30	ACTGGCGTCT	GACCCGCCCC	TTGACCCAA	CCTGTGATGA	CATGGTGCTG	ATTCCTGGGG	9240
	GCATTAAAGC	TGCTGTTTAA	AAAGGCAAAA	AA			

Seq ID NO: 63 Protein sequence:
Protein Accession #: NP_000085.1

35	1	11	21	31	41	51	
	MTLRLVLAAL	CAGILAEAPR	VRAQHRERVT	CTRLVAADIV	FLLDGSSSIG	RSNFREVRSF	60
	LEGLVLPFSG	AASAQGVRF	TVQYSDDPRT	EFGLDALGSG	GDVIRAIREL	SYKGNTRTG	120
	AAILHVADHV	FLPLQARPGV	PKVCILITDG	KSQDLVDTA	QRLKGQGVKL	FAVGIKNADP	180
40	EELKRVASQP	TSDFFFVND	FSILRTLPL	VSRVCTTAG	GVPTRPDD	STSAPRDLVL	240
	SEFSSQSLRV	QSDATGTPV	GKVKYQYPLT	GLGQPLPSE	QEVNVPAGET	SVRLRGLRPL	300
	TEYQVTVIAL	VANSIGEA	GTARTALEG	PELTIQNTTA	HSLLVAMRSV	PGATGYRVTW	360
	RVLSSGGPTQ	QELPGQGSV	LLRDLEPGTD	YEVTVSTLFG	RSVGPATSLM	ARTDASVEQT	420
45	LRPVLIGPTS	ILLSNWLVPE	ARGYRLEWRR	ETGLEPPQKV	VLPSTDVTRY	LDGLQPGTEY	480
	RLTLTYLLEG	HEVATPATVV	PTGPELPVSP	VTDLQATELP	GQVRVWSWSP	VPATQYRII	540
	VRSTQGVERT	LVLGQSTAF	DLDVQAGLS	YTVRVSAVVG	PREGSASVLT	VREPEPTPLA	600
	VPGLRVVSD	ATRVRVANGP	VPASGFRIS	WSTGSGPSS	QTLPPDSTAT	DITGLQPGTT	660
	YQVAVSVLRG	REBGAAPVIV	ARTDPLGPVR	TVHVTQASS	SVTITWTRVP	GATGYRVSWH	720
	SAHGPEKSQL	VSGEATVAEL	DGLEPDTEYT	VHVRHVAVAG	DGPFASVVVR	TAPEPVGRVS	780
50	RLQILNASSD	VLRTTNGVGT	GATAYRLANG	RSEGGPMRQ	ILPGNTDSAE	IRGLEGGVSY	840
	SVRVTLVGD	REGTFVSIHV	TTPEAPPAL	GTLHVVRQGE	HSLRLRWEPV	PRAQGLLHV	900
	QPEGQEQEOR	VLGPELSSYH	LDGLEPATQY	VRVLSVLGPA	GEGPSAEVTA	RTESPRVPSI	960
	ELRVVDTSID	SVTLAWTFVS	RASSYILSNR	PLRGPGQEV	GSPQTLPGIS	SSQRTVGLPE	1020
55	GVSYIFSLTP	VLDGVRGPEA	SVTQTFVCP	GLADVVFLEH	ATQDNAHRAE	ATRRVLRLV	1080
	LALGPLGPA	VQGLLSYSH	RPSPLFPLNG	SHDLGILQR	IRDMFYMDPS	GNNLGTAVVT	1140
	AERYMLAPDA	PGRQHVPGV	MVLLVDEPLR	GDIFSPIREA	QASGLNVVML	GMAGADPEQL	1200
	RRLAPGMDG	QTFPAVDG	SLDQAVSGLA	TALCQASFTT	QPRPEPCFVY	CPKGGKGEPG	1260
	EMGLRGQVGP	PDGRLGPRG	GAPGPGQPPG	SATAKGERGF	PGADGRPGSP	GRAGNPGTGP	1320
60	APGLKGSPLG	PGPRGDPGER	GPRGPKGEPG	APGQVIGGEG	PGLPGRKGDP	GPSGPPGPRG	1380
	PLGDPGRGPR	PGLPGTAMKG	DKGDRGERGF	PGPGEGGIAP	GEPGLPGLPG	SPGPGQGVGP	1440
	PKKKGKGD	EDGAPGLPGQ	PGSPGEQGP	GPPGAIGPKG	DRGFPGLGE	AGEKGERGPP	1500
	GPAGSRGLPG	VAGRPAGKGP	EGPFGPTGRQ	GKGEPRGPRG	DPAVVGPAVA	GPKGEGKDVG	1560
	PAGPRGATGV	QGERGPPGLV	LPGDPGPKGD	PGDRGPIGLT	GRAGPPGDSG	FPGEKGDPR	1620
65	PGPPGVPGR	GRDGEVGEKG	DEGPPGDPGL	PGKAGERGLR	GAPGVRGPRG	EKGDQGDPE	1680
	DGRNGSPGSS	GPKGDRGEFG	PPGPPGRLVD	TGPGAREKGE	PGDRGQEGPR	GPKGDPGLPG	1740
	APGERGIEGF	RGPFGPGQDP	GVRGPAGEKG	DRGPPGLDGR	SGLDGKFGAA	GPSGPNAGAG	1800
	KAGDPGRDGL	PGLRGEQGLP	GPSGPPGLPG	KPGEDGKPLG	NGKNGEPGDP	GEDGRKGEKG	1860
	DSGASGRGPR	DGPKGERGAP	GILGPQGGPG	LPGPVGPPGQ	GFPVPGGGTG	PKGDRGETGS	1920
70	KGEQGLPGER	GLRGEPGSVP	NVDRLLETAG	IKASALREIV	ETWDESSGSF	LPVPERRRGP	1980
	KGDSGEQGGP	GKEGPIGFP	ERGLKGDGRD	PGPQGPGLA	LGERGPPGPS	GLAGEPGKPG	2040
	IPGLPGRAGG	VGEAGRPGER	GERGEKGERG	EQGRDGPPLG	PGTPGPPGPP	GPKVSVDEPG	2100
	PGLSGEQGPP	GLKGAKEPG	SNGDQGPXGD	RGVPGIKGDR	GEPGPRGQDG	NFGLPGERGM	2160
	AGPEGKPLGL	GPRFPFGPVG	GHGDPGPPGA	PGLAGPAGPQ	GPSGLKGEPE	ETGPPRGLT	2220
75	GPTGAVGLPG	PPGSPGLVGP	QSSPGLPCQV	GETGKPGAPG	RDGASGKGDG	RGSPPGVPSP	2280
	GLPFPVGPKG	EPGPTGAPGQ	AVVGLPGAAG	EXGAPGGLAG	DLVGEPAKAG	DRGLPGPRGE	2340
	KGEAGRAGEP	APGPKGPKGD	PGVGVPGSPG	PPGPPGVKGD	LGLPGLPGAP		2400
	GVVGPFGQTG	PRGEMQPGP	SGERGLAGPP	GREGIPGPLG	PPGPPGSPVG	PGASGLKGDK	2460
	GDPPGVGLPR	RGERGEPGIR	GRGLTGPPGS	RGERGEKGDV	GSAGLKGDGP		2520
80	DSAVILGPPG	PRGAKGDMGE	RGRGLDGDK	GPRGNDGDFG	DKGSKGEPGD	KGSAGLFLGR	2580
	GLLGPQGPQ	AAGIPGDPGS	PGKDGVPGR	GEKGDVGFMG	PRGLKGERGV	KGACGLDGEK	2640
	GDKEAGPPFG	RPGLAGHKGE	MGEPPGVPQS	GAPGKEGLIG	PKGDRGFDGQ	PGPKGDQGEK	2700
	GERGTPFGTG	PPGSPGNDGS	AGPPGPPGSP	GPRGPEGLQG	QKGERGPPGE	RVVGAAPGVP	2760
	APGERGEQGR	PPGAPGRGKE	GEAALTEDDI	RGFVRQEQMS	HCACQGQPTA	SGSRPLPSYA	2820
85	ADTAGSQLHA	VPVLRVSHAE	EEERVPPEDD	EYSEYSEYSV	EEYQDPEAPW	DSDDPCSLPL	2880
	DEGSCATYTL	RWYHRAVTGS	TEACHPFVYG	GCGGNANRFG	TREACERRCP	PRVVQSQGTG	2940
	TAQD						

WO 02/086443

PCT/US02/12476

Seq ID NO: 64 DNA sequence
Nucleic Acid Accession #: NM_006945
Coding sequence: 1-219

5
1 11 21 31 41 51
ATGTCCTTATC AACAGCAGCA GTGCAAGCAG CCCTGCCAGC CACCTCCTGT GTGCCCCACG 60
CCAAAGTGCC CAGAGCCATG TCCACCCCGG AAGTGCCCTG AGCCCTGCC ACCACCAAAG 120
TGTCACAGC CCGCCACC TCAGCAGTGC CAGCAGAAAT ATCCTCCTGT GACACCTTCC 180
10 CCACCTGCC AGCCAAAGTA TCCACCGAAG AGCAAGTAA

Seq ID NO: 65 Protein sequence:
Protein Accession #: NP_008876

15
1 11 21 31 41 51
MSYQQQQCKQ PCQPPPVCPPT PKCPBPCTPP KCPEPCPPPK CPQPCPPQCC QQKYPPVTPS 60
PPCQPKYPPK SK

Seq ID NO: 66 DNA sequence
Nucleic Acid Accession #: NM_005629.1
Coding sequence: 639-2546

25
1 11 21 31 41 51
TAGTCGGAGC GAGGTGGCGA GTCGCTGAGC CCGCCGCGGC CCGAGAGAGC GCTGCAGCCG 60
CCGCCGCGCG GAAGGAGAGG GCGAGGCGCG CCGAGCCGCG CCGCCGCGCG GCCACCGCCG 120
CCGCCGCGCAC CACCGCCACC GGAGTGCGCG GCCAGCCGCG CAGCCTCGCG GGGCCCCCGG 180
CGGGGCGGGG GGGCGCGGCC ACAGGCCCTT GCTCCGCGCG TCGTTTGCAG ACCCGGGGCG 240
30 CCGATGTGCG CCGCGCCCCG TTAGGATGAG TCTCGGTCG GCGAGGAGC CCGCGCAGCC 300
GCCGCCGCGG GAGCCGCGGG CAGGAGCCTC GGGAGCCGCG CCGCGCGCGG CCGCGCGCGG 360
GCCGGGCCCC GACGCCGCGG GCGCGCCCCG GGGCCCCCGA CACACATGAG ATTCTTACGG 420
CTCACTTTCA AGTGCTTCGT GGAAGTCTTC TGAAGTGCCT GCGCCGCGCG CCGACCCCGC 480
CGTCCGCGCG CCGCGCGCGT CCGCGCGCGG GCGCGCGCGG GCGCGCGCGG CCGCGCGCGG 540
35 CCTCGGGGCG CTCGCCGGTG CCGCGCGTGC CCGCGCGCTG ACCCGCGCG CCGGTGAGGC 600
GCCGCGAGCC CGCGCGCGG GTGCGCGCGG CCGGGGCGAT GCGAAGAAAG AGCGCGGAGA 660
ACGGCATCTA TAGGCTGTCC GCGAGCAGGA AGAAGGGCCC CCTCATCGCG CCGGGGCGCG 720
AOGGGGCCCC GGCAGAGGGC GACCGCCCCG TGGGCTTGGG GACACCCGCG GCGCGCTTGG 780
CGTGCGCGCG GCGCGAGACC TGGAGCGCGC AGATGGACTT CATCATGTCT TCGGTGGGCT 840
40 TGCGCGTGGG TTTGGGCAAC GTGTGGCGCT TCCCTACCTT GTGCTACAAG AACCGCGGAG 900
GTGTGTCTCT TATTCTCAAG CTCTGTATCG CCCTGGTTGG AGGAATCCCC ATTTTCTTCT 960
TAGAGATCTC GCTGGGCGAG TTCATGAAGG CCGGCAGCAT CAATGTCTGG AACATCTGTC 1020
CCCTGTTCAG AGGCCTGGGC TACGCTCTCA TGGTGTCTGT CTCTACTGCG AACACCTACT 1080
45 ACATCATGGT GCTGGCCTGG GGCTTCTATT ACCTGGTGAA GTCTTTTACC ACCACGCTGC 1140
CCTGGGCGAC ATGTGGCCAC ACCTGGAAAC CTCGCGACTG CGTGGAGATC TTCCGCCATG 1200
AAGACTGTGC CAATGCGAGC TGCGCCAAAC TCACCTGTGA CCAGCTTGCT GACCGCCGCT 1260
CCCTGTCTAT CAGGTTCTGG GAGAACAAAG TCTTGAGGCT GTCTGGGGA CTGGAGGTGC 1320
CAGGGGCCCT CACTGGGAG GTGACCTTTT GTCTGCTGGC CTGCTGGGTG CTGCTTACT 1380
50 TCTGTGCTG GAGGGGGGTC AAATCCACGG GAAAGATCGT GTACTTCACT GCTACATTCC 1440
CCTAGCTGTG CCGGTGCTG CTGCTGGTGC GTGGAGTGTG GTGCGCTGCG GCCCTGGATG 1500
GCATCATTTA CTATCTCAAG CCGTACTGGT CAAAGCTGGG GTCCCTCAG GTGTGGATAG 1560
ATGCGGGGAC CAGATTTTTC TTTTCTTACG CCAATGGCCT GGGGGCCCTC ACAGCCCTGG 1620
GCAGTCAACA CCGCTTCAAC AACAAGTGTG CCAAGGACGC CATCATCTCT GCTCTCATCA 1680
55 ACAGTGGGAC CAGCTTCTTT GCTGGCTTGC TGGTCTTCTC CATCTTGGGC TTCATGGCTG 1740
CAGAGCAGGG CGTGACATCT TCCAGGTGG CAGAGTCAGG GCGGGGCGCT GCCTTCATCG 1800
CCTACCGCGG GCTGTGTCAG CTGATGCCAG TGGCCCCACT GTGGGCTGCC CTGTTCTTCT 1860
TCATGCTGTG GCTGCTGGT CTGCGAGCGC AGTTTGTAGG TGTGGAGGGC TTCATCACCG 1920
GCCTCTGTA CCTCTCCCG GCTCTCTACT ACTTCCGTTT CCAAGGGGAG ATCTCTGTGG 1980
60 CCCTCTGTG TGCCCTCTGC TTTGTCTATG ATCTCTCCAT GGTGACTGAT GCGGGGATGT 2040
ACGTCTTCCA GCTGTTTGAC TACTACTCGG CCAGCGGCAC CACCTGCTC TGGCAGGCCT 2100
TTTGGGAGTG CGTGGTGGTG GCGTGGGTGT ACGGAGCTGA CCGCTTCATG GACGACATTG 2160
CCTGTATGAT CCGGTACCGA CCTTGGCCCT GGATGAAATG GTGCTGGTCC TTCTTCAACC 2220
CGCTGGTCTG CATGGGCGCC TTCATCTTCA ACGTTGTGTA CTACGAGCCG CTGGTCTACA 2280
65 ACAACACCTA CGTGTACCGG TGGTGGGGTG AGGCCATGGG CTGGGCTTTC GCCCTGTCTC 2340
CCATGCTGTG CGTGCCGCTG CACCTCCTGG GCTGCTCTCT CAGGGCCAAG GGCACCATGG 2400
CTGAGCGCTG GCAGCACCTG ACCAGGCCCA TCTGGGGCCT CCACCACTTG GAGTACCGAG 2460
CTCAGGACGC AGATGTGAGG GGCCTGACCA CCCTGACCCC AGTGTCCGAG AGCAGCAAGG 2520
TCGTGCTGGT GGAGAGTGTG ATGTGACAAC TCAGCTCACA TCACCACTG ACCTCTGGTA 2580
GCCATAGCAG CCGCTGTCTC AGCCCCACCG CACCCCTCCA GGGGGCCTGC CTTTCCCTGA 2640
70 CACTTTTGGG GTCTGCTCTG GGGAGGAGGG GAGAAAGCAC CATGAGTGTCT CACTAAAACA 2700
ACTTTTTCCT TTTTAAATAA AACGCCAAAA ATATCACAAAC CCACCAAAAA TAGATGCCTC 2760
TCCCTCTCCA GCGCTAGCCG AGCTGGTCTT AGGCCCGCGC TAGTGCCCA CCCCCACCCA 2820
CAGTGTGCTA CTCTCTCTGC CCGTGCCACG CCCACCCCTT GCCCACTCTT CCAGGCTCTG 2880
CTCTGCAGCA CACCGTGGG TGACCCCTCA CCCAGAAAGC AGCAGTGGCA GCTTGGGAAA 2940
75 TGTGAGGAAG GGAAGGAGGG AGAGACGGGA GGGAGGAGAG AGAGGAGAAG GGAGGAGGG 3000
GAGGGGCGAG GAAACCAAGG CAAATATTTT AGCTGGGCTA TACCCCTCTC CCCATCCCTG 3060
TTATAGAAGC TTAGAGAGCC AGCCAGCAAT GGAACCTTCT GGTTCCTGCG CCAATCGCCA 3120
CAGATATCAA TTGTGTGAGC TTGGGTGCGA GTGCACGCGT GCGTGAGTAC GGAGAGTATA 3180
TATAGATCTC TATCTCTTAG CAAAGGTGAA TGCCAGATGT AAATGGCGCC TCTGGGCAAA 3240
80 GAGGCTGTG ATTTTGCAAA TTTTATAAAA ACTTGAGAGA ATGAGATTTC TGCTTGTATA 3300
TTTCTAAAAA GAGGAAGGAG CCCAAACCAT CCTCTCTTCA CCACTCCCAT CCCTGTGAGC 3360
CCTACTTTAC CCCTCTGCCC CTAGCCAAAG AGTGTGAATT TATAGATCTA ACTTTCATAG 3420
GCAAAACAAA AGCTTCGAGC GTGTGCGTGT GTGAGTCTGT TGTGTGGATG TGCCTGTGTG 3480
GTCCCGAGCC CAGAGTGGTA TTGAAAAAGT GCATGGTGGG GGCCTCGGGG CTGTCCCGAC 3540
85 GCTGTCCCTT TGCCACAAGT CTGTGGGGCA AGAGGCTGCA ATATTCCGTC CTGGGTGTCT 3600
GGGCTGCTAA CCTGGCCTGC TCAGGCTTCC CACCTGTGTC GGGGCACACC CCCAGGAAGG 3660
GACCTTGGAC ACGCTCCCA CGTCCAGGCT TAAGTGGATG GCATTCCTCG CACCTCCAGT 3720

CTTCTGTGTA GCAGCTTTAA CCCACGTTTG TCTGTACGCT CCAGTCCCGA GACGGCTGAG 3780
 TGACCCCAAG AAAGGCTTCC CCGACACCCA GACAGAGGCT GCAGGGCTGG GGCTGGGTGA 3840
 GGGTGGCGGG CTTGCGGGGA CATTCTACTG TGCTAAAAAG CCACTGCAGA CATAGCAATA 3900
 AAAACATGTC ATTTTCC

5

Seq ID NO: 67 Protein sequence:
 Protein Accession #: NP_005620.1

10 1 11 21 31 41 51
 | | | | | |
 MAKKSAENGI YSVSGDEKKG PLIAPGPDGA PAKGDGPVGL GTPGGRLAVP PRETWTRQMD 60
 FIMSCVGFV GLGNVWRFPY LCYKNGGGVF LIPYVLIALV GGIPFFLEI SLGQPMKAGS 120
 INVWNICPLF KGLGYASMI VFYCNYYIM VLWNGFYLV KSFTTLPWA TCGHTWNTPD 180
 CVEIFRHEDC ANASLANLTC DQLADRRSPV IEFWENKVLRL LSGGLEVPGA LNWEVTLCLL 240
 15 ACWLVVYFCV WKGVKSTGKI VYFTATFPYV VLVLVLRGV LLLPGALDGI YYLKPDSWKL 300
 GSPQWIDAG TQIFPFAIG LGALTALGSY NFRNNCYKD AIIILALINSG TSFFAGFVVF 360
 SILGFMAAEQ GVHISKVAES GPGLAFIAYP RAVTLMPVAP LWAALPFFML LLLGLDSQFV 420
 GVEGFITGLL DLLPASYYFR FQREISVALC CALCFVIDLS MVTGDMYVF QLPDYYSASG 480
 20 TTLWQAFWE DVVPWWEAM DRFMDDIACM IGYRCPWMK WCNWSPFTPLV CMGIFINNV 540
 YYEPLVYNT YVVPWWEAM GWAFALSSML CVPLHLGLCL LRAKGTMAER WQHLTQPIWG 600
 LHHLEYRAQD ADVRGITLTLT PVSESSKVVV VESVM

25 Seq ID NO: 68 DNA sequence
 Nucleic Acid Accession #: NM_021953.1
 Coding sequence: 178-2469

30 1 11 21 31 41 51
 | | | | | |
 GGCACGAGGG GGCACCGGCC GGTCCGGCGC GAGCCCCCGT CCGGGGCCCT GGCTCGGCC 60
 CCAGGTGGGA GGAGCCCGGA GCCCGCTTC GGAGCTACGG CCTAACGGCG GCGGCGACTG 120
 CAGTCTGGAG GGTCCACACT TGTGATTCTC AATGGAGAGT GAAACCGCAG ATTCATAATG 180
 AAAGCTAGCC CCGCTCGGCC ACTGATTCTC AAAAGACGGA GGCTGCCCTC TCCTGTTCAA 240
 35 AATGCCCCAA GTGAAACATC AGAGGAGGAA CCTAAGAGAT CCGCTGCCCA ACAGGAGTCT 300
 AATCAAGCAG AGGCCCTCAA GGAAGTGGCG GAGTCCAACT CTGCAAGTT TCCAGCTGGG 360
 ATCAAGATTA TTAACCAACC CACCATGCCC AACACGCAAG TAGTGGCCAT CCCCAACAAT 420
 GCTAATATTC ACAGCATCAT CACAGCACTG ACTGCCAAGG GAAAGAGAG TGGCAGTAGT 480
 GGGCCCAACA AATTCATCCT CATCAGCTGT GGGGGAGCCC CAACTCAGCC TCCAGGACTC 540
 CGGCTCAAA CCAAAACCCAG CTATGATGCC AAAAGGACAG AAGTGACCC TCCAGGACTG 600
 40 GGACCAAAAC CTGCACTGTG GGAATGTAAT CTTCCTAGAC CACCTGGAGC CCTTGGCAG 660
 CAGAAACGGG AGACCTGTAG AGATGGTGAG GCAGCAGGCT GCACTATCAA CAATAGCCTA 720
 TCCAACATCC AGTGGCTTCG AAAGATGAGT TCTGATGGAC TGGGCTCCCG CAGCATCAAG 780
 CAAGAGATGG AGGAAAGGA GAATGTCTAC CTGGAGCAGC GACAGGTTAA GGTGAGGAG 840
 CCTTCGAGAC CTGGCAGAAC TCTGTGTCG AGCGGCCACC CTACTCTTAC 900
 45 ATGGCCATGA TACAAATCGC CATCAACAGC ACTGAGAGGA AGCGCATGAC TTTGAAAGAC 960
 ATCTATACGT GGAATGAGGA CCACTTTCCC TACTTTAAGC ACATTGCCAA GCCAGGCTGG 1020
 AAGAACTCCA TCCGCCACAA CCTTTCCCTG CACGACATGT TTGTCGGGA GACGTCTGCC 1080
 AATGGCAAGG TCTCCTTCTG GACCATTAC CCCAGTGCCA ACCGCTACTT GACATTGGAC 1140
 CAGGTGTTTA AGCCACTGGA CCCAGGCTCT CCACAATTGC CCGAGCACTT GGAATCAGAG 1200
 50 CAGAAACGAC CGAATCCAGA GCTCCGCGCG AACATGACCA TCAAAACCGA ACTCCCCCTC 1260
 GGCGCAGGGG GGAAGATGAA CCACGTGCTA CCACGGGTCA GCTCATACCT GGTACCTATC 1320
 CAGTTCCCGG TGAACCAATC ACTGTTGTTG CAGCCCTCGG TGAAGGTGCC ATTGCCCTCG 1380
 GCGGCTTCCC TCATGAGCTC AGAGCTTGCC GGCATAGCA AGCGAGTCCG CATTGCCCCC 1440
 AAGGTGCTGC TAGCTGAGGA GGGGATAGCT CCTCTTCTT CTGCAGGACC AGGAAAGAG 1500
 55 GAGAACTCC TGTGTGAGA AGGGTTTCT CCTTTGCTT CAGTTCAGAC TATCAAGGAG 1560
 GAAGAAATCC AGCCTGGGGA CACTTAGCGA GACCCATCAA AGTGGAGAGC 1620
 CCTCCCTTGG AAGAGTGGCC CTCCCGCGCC CCACTTTTCA AAGAGGAATC ATCTCACTCC 1680
 TGGGAGGATT CGTCCCAATC TCCCACCCCA AGACCCAAGA AGTCTACAG TGGGCTTAGG 1740
 TCCCAACCCC GGTGTGTCTC GGAATGTCT GTGATTCAAC ACAGGGAGAG GAGGGAGAGG 1800
 60 AGCCGCTCTC GGAAGAAACA GCATCTACTG CCTCCCTGTG TGGATGAGCC GGAGCTGCTC 1860
 TTCTCAGAGG GGGCCAGTAC TTCCCGCTGG GCCGCAGAGC TCCCGTTCCC AGCAGACTCC 1920
 TCTGACCTCG CCTCCAGCT CAGCTACTCC CAGGAAGTGG GAGGACCTTT TAAGACACCC 1980
 ATTAAGGAAA CGCTGCCCAT CTCTCCACC CCGAGCAAAT CTGTCTCCC CAGAACCCCT 2040
 65 GAATCCTGGA GGCTCAGGCC CCCAGCCAAA GTAGGGGGAC TGGATTTCAG CCCAGTACAA 2100
 ACCTCCAGG GTGCCCTGTA CCCCTTGCCT GACCCCTTGG GGCTGATGGA TCTCAGCACC 2160
 ACTCCCTTGC AAAAGTCTCC CCCCTTGAA TCACCGCAAA GGCTCCTCAG TTCAGAACCC 2220
 TTAGACCTCA TCTCCGTCCC CTTTGGCAAC TCTTCTCCCT CAGATATAGA CGTCCCCAAG 2280
 CCAGGCTCCC CGGAGCCACA GGTTCCTGGC CTTGCAGCCA ATGTTTCTCT GACAGAAGGC 2340
 70 CTGGTCTCG ACACAATGAA TGACAGCCTC AGCAAGATCC TGCTGGACAT CAGCTTTCCT 2400
 GGCCTGGAGC AGGACCCACT GGGCCCTGAC AACATCAACT GGTCCCAGTT TATTCTGAG 2460
 CTACAGTAGA GCCCTGCCCT TGCCCTGTG CTCAAGCTGT CCACCATCCC GGGCACTCCA 2520
 AGGCTCAGTG CACCCCAAGC CTCTGAGTGA GGACAGCAGG CAGGGACTGT TCTGCTCCTC 2580
 75 ATAGCTCCCT GCTGCCAGAT TATGCAAAAG TAGCAGTCAC ACCCTAGCCA CTGCTGGGAG 2640
 CTTGTGTTCC CCAAGAGTAT CTGATTCTCT TGCTGTCCCT GCCAGGAGCT GAAGGGTGGG 2700
 AACAAACAAAG GCAATGGTGA AAAGAGATTA GGAACCCCCC AGCCTGTTTC CATCTCTGCT 2760
 CCAGCAGTCT CTTACCTTCC CTGATCTTTG CAGGGGTGGTC CGTGTAATAA GTATAAATTC 2820
 TCCAAATAT CTCTAATTA TAAATGTAA CTTATTTCCCT TAGATCATTA TCCAGAGACT 2880
 GCCAGAGGGT GGGTCAAGAT ACCTGGGGTT TCAATTGACT TCTGTTCTTT GCTTTTAGTT 2940
 80 TTGATAGAA GGAAGACCTG CAGTGACCGG TTTCTTCCAG GCTGAGGTAC CTGGATCTTG 3000
 GGTCTTTCAC TGCAGGGACC CAGCAAGTG GATCTGCTTG CCAGAGTCTT TTTGCCCCCT 3060
 CCCTGCCACC CTGCCGTGTT TCCAAGTCAG CTTTCTTGCA AGAAGAAATC CTGTTTAAAA 3120
 AAGTCTTTTG TATTGGGTCA GGAGTTGAAT TTGGGGTGGG AGGATGGATG CAACTGAAGC 3180
 AGAGTGTGGT TGCCCTATTA GATGTTTCTC TGATAATGTC CCCAATCATA 3240
 85 CCAGGGAGAC TGGCATTGAC GAGAATCAG GTGGAGGCTT GAGAAGGCCG AAAGGGCCCC 3300
 TGACCTGCCT GGCTTCTTCA GCTTGCCCCC CAGCTTTGCA AAGAGCCACC CTAGGCCCCA 3360
 GCTGACCGCA TGGGTGTGAG CCAGCTTGAG AACACTAACT ACTCAATAAA AGCGAAGGTG 3420
 GACCNAAAAA AAAAAAATAA AAAA

Seq ID NO: 69 Protein sequence:
Protein Accession #: NP_068772.1

```

5      1      11      21      31      41      51
|      |      |      |      |      |
MKASPRRLPI LKRRRLPLPV QNAPSETSEE EPKRSPAQQE SNQABASKEV AESNSCKPFA 60
GIKINHPPTM PNTQVVAIPN NANIHSIITA LTKAGKESGS SGPNNKIFILIS CGGAPTQPPG 120
LRPQTQTSYD AKRTEVTLET LGPKPAARDV NLPRPPGALC EQKRETCADG EAAGCTINNS 180
10     LSNIQWLKRM SSDGLGSRSI KQEMEKEKENC HLEQRQVKVE EPSRPSASWQ NSVSERPPYS 240
YMAMIQFAIN STERKRMTLK DIYTWIEDHF PYFKHIAKPG WKNSIRHNL LDMFVRETS 300
ANGKVSFWTI HPSANRYLTL DQVFKPLDPG SPQLPEHLES QQKRPNPELR RNMTIKTELP 360
LGARRKMKPL LPRVSSYLVP IQFPVNQSLV LQPSVKVPLP LAASLMSSSEL ARHSKRVRIA 420
PKVLLAEEGI APLSSAGPGK EEKLLFGEGR SPLLPVQTIK EEEIQPGEEM PHLARPIKVE 480
15     SPPLLEEWSP APSKESSSH SWEDSSQSPT PRPKSYSGL RSPTRCVSEM LVIQHRERRE 540
RSRSRRKQHL LPPCVDEPEL LPSGSPSTSR WAAELFPFAD SSDPASQLSY SQEVGGPFKT 600
PIKETLPISS TPSKSVLPRT PESWRLTPPA KVGGLDFSPV QTSQGASDPL PDPLGLMDLS 660
TTPQLQAPPL ESQORLLSSE PLDLISVPFG NSSPSDIDVP KPGSPREPQVS GLAANRSLTE 720
20     GLVLDTMNDS LSKILLDISP PGLDEDPGPG DNINWSQFIP ELQ

```

Seq ID NO: 70 DNA sequence
Nucleic Acid Accession #: BC006529.1
Coding sequence: 178-2424

```

25     1      11      21      31      41      51
|      |      |      |      |      |
GGCAGGAGGG GGACCCGGCC GGTCCGGCGC GAGCCCCCGT CCGGGGCCCT GGCTCGGCC 60
30     CCAGGTGGGA GGAAGCCGGA GCCCGCCTTC GGAGCTACGG CCTAACGGCG CGGGCGACTG 120
CAGTCTGAGG GGTCCACACT TGTGATTCTC AATGAGAGT GAAACGCGAG ATTCATAATG 180
AAAACATAGC CCCCTCGGCG ACTGATTCTC AAAAGACGGA GGCTGCCCTT TCCTGTTCAA 240
AATGCCCCAA GTGAACATC AGAGGAGGAA CCTAAGAGAT CCCCTGCCCA ACAGGAGTCT 300
AATCAAGCAG AGGCTCCCAA GGAAGTGGA GAGTCCAACT CTGCAAGTTT TCCAGCTGGG 360
ATCAAGATTA TTAACCAACC CACCATGCCC AACACGCAAG TAGTGGCCAT CCCCACAACT 420
35     GCTAATATTC ACAGCATCAT CACAGCACTG ACTGCCAAGG GAAAGAGAG TGGCAGTAGT 480
GGGCCCAACA AATCTCTCTC CATCAGCTGT GGGGAGGCC CAACTCAGCC TCCAGGACTC 540
CGGCCTCAAA CCCAAACCAG CTATGATGCC AAAAGGACAG AAGTGACCTT GGAGACCTTG 600
GGACCAAAAC CTGACAGTAG GGATGTGAAT CTTCCTAGAC CACCTGGAGC CCTTTGCGAG 660
CAGAAACCGG AGACCTGTGC AGATGGTGAG GCAGCAGGCT GCACATCAA CAATAGCCTA 720
40     TCCAAACATCC AGTGGCTTCG AAAGATGAGT TCTGATGGAC TGGGCTCCCG CAGCATCAAG 780
CAAGAGATGG AGGAAAGAGA GAATGTGCAC CTGGAGCAGC GCAGAGTTAA GGTGAGGAG 840
CCTTCGAGAC CATCAGCGTC CTGGCAGAAC TCTGTGTCTG AGCGCCACC CTACTCTTAC 900
ATGGCCATGA TCAATTCGCG CATCAACAGC ACTGAGAGGA AGCGCATGAC TTTGAAGAGC 960
45     ATCTATAGCT GGATTGAGGA CCACTTTCCC TACTTTAAGC ACATTGCCAA GCCAGGCTGG 1020
AAGAACTCCA TCCGCCACAA CCTTTCCCTG CACGACATGT TTGTCGGGA GACGCTGCCC 1080
AATGGCAAGG TCTCTCTCTG GACCATTAC CCGAGTGCCA ACCGCTACTT GACATTGGAC 1140
CAGGTGTTTA AGCAGCAGAA ACCAGCGAAT CCAGAGCTCC GCGGAAACAT GACCATCAA 1200
ACCGAACTCC CCCTGGGGCG ACGGCGGAAG ATGAAGCCAC TGCTACCAGG GGTGAGCTCA 1260
50     TACCTGGTAG CTATCCAGTT CCGGTGAAC CAGTCACTGG TGTTCGAGCC CTCGGTGAAG 1320
GTGCCATTGC CCCTGGGGCG TCCCTCATG AGCTCAGAGC TTGCCCGCCA TAGCAAGCGA 1380
GTCCGCAATG CCCCAGAGGT GCTGCTAGCT GAGGAGGGGA TAGCTCCTCT TTTCTTGCA 1440
GGACCAAGGA AAGAGGAGAA ACTCCTGTTT GGAAGAGGTT TTTCTCTTTT GCTTCCAGTT 1500
CAGACTATCA AGGAGGAAGA AATCCAGCCT GGGGAGGAAA TGCCACACTT AGCGAGACCC 1560
55     ATCAAAGTGG AGAGCCCTCC TTGGAAGAG TGGCCCTCCC CGGCCCATC TTTCAAAGAG 1620
GAATCATCTC ACTCCTGGGA GGATTCGTCC CAATCTCCCA CCCCAGAGCC CAAGAAGTCC 1680
TACAGTGGGC TTAGGTCCCC AACCCGGTGT GTCTCGGAAA TGCTTGTGAT TCAACACAGG 1740
GAGAGGAGGG AGAGGAGCCG GTCTCGGAGG AAACAGCATC TACTGCCTCC CTGTGTGGAT 1800
GAGCCGAGGC TGCTCTTCTC AGAGGGGCCC GTTACTTCCC GCTGGGCCCG AGAGCTCCCG 1860
60     TTCCAGCAGC ACTCCTCTGA CCCTGCCTCC CAGCTCAGCT ACTCCCAGGA AGTGGGAGGA 1920
CCTTTTAAGA CACCAATTAAG GGAACAGCTG CCCATCTCCT CCACCCCGAG CAAATCTGTC 1980
CTCCCCAGAA CCCCTGATTC CTGGAGGCTC ACGCCCCCAG CCAAAGTAGG GGGACTGGAT 2040
TTCAGCCAGC TACAAACCCC CCAGGGTGCC TCTGACCCCT TGCTGACCC CCTGGGGCTG 2100
ATGGATCTCA GACCACCTCC CTTCGAAAGT GCTCCCCCCC TTGAATCACC GCAAAGGCTC 2160
65     CTCAGTTCAG AACCTTAGA CCTCATCTCC GTCCCTTTG GCAACTCTT TCCCTCAGAT 2220
ATAGACGTCC CCAAGCCAGG CTCCCGGAG CCACAGGTTT CTGGCCTTGC AGCCAAATCGT 2280
TCTCTGACAG AAGCCCTGGT CCTGGACACA ATGAATGACA GCCTCAGCAA GATCCTGCTG 2340
GACATCAGCT TTCTTGCCCT GGAAGAGGAC CCACTGGGCC CTGACACAT CAACTGGTCC 2400
CAGTTTATTC CTGAGCTACA GTAGAGCCCT GCCCTTGCCC CTGTGCTCAA GCTGTCCACC 2460
70     ATCCCGGCA CTCCAAGSCT CAGTGACCCC CAAGCCTCTG AGTGAGGACA GCAGGCAGGG 2520
ACTGTTCTGC TCCTCATAGC TCCTGCTGTC CTGATTATGC AAAAGTAGCA GTCACACCCT 2580
AGCCACTGCT GGGACCTGTG GTTCCCCAAG AGTATCTGAT TCCTCTGCTG TCCCTGCCAG 2640
GAGCTGAAGG GTGGGAACAA CAAAGGCAAT GGTGAAAAGA GATTAGGAAC CCCCAGCCT 2700
75     GTTTCATTC TCTGCCAGC AGTCTCTTAC CTTCCTGAT CTTTGCAAGG TGGTCCGCTG 2760
AAATAGTATA AATTCTCCAA ATTATCCTCT AATTATAAAT GTAAGCTTAT TTCTTAGAT 2820
CATTATCCAG AGACTGCCAG AAGGTGGGTA GGATGACCTG GGGTTTCAAT TGACTTCTGT 2880
TCCCTGCTTT TAGTTTGTAT AGAAGGGAAG ACCTGCAGTG CACGGTTTCT TCCAGGCTGA 2940
GGTACCTGGA TCTTGGGTTT TCACTGCAG GGAACCCAGC AAGTGGATCT GCTTGCCAGA 3000
80     GTCCTTTTTC CCCCTCCCTG CCACCTCCCC GTGTTTCCAA GTCAGCTTT CTGCAAGAAG 3060
AAATCCTGGT TAAAAAAGTC TTTTGTATTG GGTGAGGAGT TGAATTGGG GTGGGAGGAT 3120
GGATGCAACT GAAGCAGAGT GTGGGTGCCC AGATGTGCGC TATTAGATGT TTCTCTGATA 3180
ATGTCCCAAC TCATACCAGG GAGACTGGCA TTGACGAGAA CTCAGGTGGA GGCTTGAGAA 3240
GGCCGAAGG GCCCTGACC TGCCTGGCTT CCTTAGCTTG CCCCTCAGCT TTGCAAGAG 3300
85     CCACCTAGG CCCAGCTGA CCGCATGGGT GTGAGCCAGC TTGAGAACAC TAACTACTCA 3360
ATAAAAGCGA AGGTGAAAAA AAAAAA AAAAAA

```

Seq ID NO: 71 Protein sequence:
Protein Accession #: AAH06529.1

	1	11	21	31	41	51	
5	MKTSPPRLPI	LKRRRLPLPV	QNAPSETSEE	EPKRSPAQQE	SNQAEASKEV	AESNSCKFFA	60
	GIKIINHPTM	FNTOVVAIFN	NANIHSIITA	LTAKGKESGS	SGPNKFILIS	CGGAPTQPPG	120
	LRPQTQTSYD	AKRTEVTLET	LGPKEARDV	NLPRPPGALC	BQKRETCADG	EAAGCTINNS	180
	LSNIQWLKRM	SSDGLGSRSI	KQEMEKEKNC	HLEQRQVKVE	EPSPRSASWQ	NSVSRPPYS	240
	YMAMIQFAIN	STERKRMILK	DIYTWIEDHF	PYFKHIAKPG	WKNSIRHNLS	LHDMFVRETS	300
10	ANGKVSFWTI	HPSANRYLTL	DQVFKQKRP	NPELRRNMTI	KTELPLGARR	KMKPLLPVRS	360
	SYLVPIQFPV	NQSLVLQPSV	KVPLPLAASL	MSSELAHRSK	RVRIAPKVL	AEEGIAPLSS	420
	AGPGKEEKL	PGEGFSPLLP	VOTIKEEIQ	PGEEMPHLAR	PIKVESPPLE	EWSPAPSFK	480
	EESHSWEDS	SQSPTPRPKK	SYGLRLSPTR	CVSEMLVIQH	RERRERSRSR	RKQHLPPCV	540
	DEPELLFSEG	PSTRWAEL	FPADSSDPA	SQLSYSQEVG	GPFTPIKET	LPISSTPSKS	600
15	VLPTPESWR	LTPPAKVGGL	DFSPVQTFQG	ASDPLDPLG	LMDLSTPLQ	SAPPLESPQR	660
	LLSSEPLDI	SVFPGNSPSS	DIDVPKPGSP	EPQVSGLAAN	RSLEGLVLD	TMNDSLKIL	720
	LDISPPGLDE	DPLGPDNINW	SQFIPELQ				

Seq ID NO: 72 DNA sequence
Nucleic Acid Accession #: U74612.1
Coding sequence: 178-2583

	1	11	21	31	41	51	
25	GGCAGGAGGG	GGACCCGGCC	GGTCCGGCGC	GAGCCCCCGT	CCGGGGCCCT	GGCTCGGCCC	60
	CCAGGTGTGA	GGAGCCCGGA	GCCCGCCTTC	GGAGCTACGG	CCTAACGGCG	GCGGCGACTG	120
	CAGTCTGGAG	GGTCCACACT	TGTGATTCTC	AATGGAGAGT	GAAACGCGAG	ATTCTATAATG	180
	AAACTAGCC	CCCGTCGGCC	ACTGATTCTC	AAAAGACGGA	GGCTGCCCCT	TCCTGTTCAA	240
	AATGCCCCAA	GTGAACATC	AGAGGAGGAA	CCTAAGAGAT	CCCTGCCCCA	ACAGGAGTCT	300
30	AATCAAGCAG	AGGCGTCCAA	GGAAGTGGCA	GAGTCCAACT	CTTGCAAGTT	TCCAGCTGGG	360
	ATCAAGATTA	TTAACACACC	CACCATGCC	AACACGCAAG	TAGTGGCCAT	CCCCAACAT	420
	GCTAATATTC	ACAGCATCAT	CACAGCACTG	ACTGCCAAGG	GAAAGAGAG	TGGCAGTAGT	480
	GGGCCAACAA	AATTCATCCT	CATCAGCTGT	GGGGGAGCCC	CAACTCAGCC	TCCAGGACTC	540
	CGGCCTCAAA	CCCAACCCAG	CTATGATGCC	AAAAGGACAG	AAGTGACCCCT	GGAGACCTTG	600
35	GGACCAAAAC	CTGCAGCTAG	GGATGTGAAT	CTTCTAGAC	CACCTGGAGC	CCTTTGCGAG	660
	CAGAAACGGG	AGACTCTGTC	AGATGGTGAG	GCAGCAGGCT	GCATATCAA	CAATAGCCTA	720
	TCCAACATCC	AGTGGCTTCG	AAAGATGAGT	TCTGATGGAC	TGGGCTCCCG	CAGCATCAAG	780
	CAGAGATGG	AGGAAAAGGA	GAATTGTAC	CTGGAGCAGC	GACAGGTTAA	GGTTGAGGAG	840
	CCTTCGAGAC	CATCAGCTC	CTGGCAGAAC	TCTGTGCTG	AGCGGCCACC	CTACTCTTAC	900
40	ATGGCCATGA	TACATTTGCG	CATCAACAGC	ACTGAGAGGA	AGCGCATGAC	TTTGAAGAGC	960
	ATCTATACGT	GGATTGAGGA	CCACTTTCCT	TACTTTAAGC	ACATTGCCAA	GCCAGGCTGG	1020
	AAGAACTCCA	TCCGCCACAA	CCTTCCCTG	CACGACATGT	TTGTCCGGGA	GACGCTCTGC	1080
	AATGGCAAGG	TCTCCTTCTG	GACCATTAC	CCCAGTGCCA	ACCGTACTT	GACATTGGAC	1140
	CAGGTGTTTA	AGCCACTGGA	CCAGGGTCT	CCACAATTGC	CCGAGCACTT	GGAATCACAG	1200
45	CAGAAACGAC	CGAATCCAGA	GCTCCGCCGG	AAATGACCA	TCAAACCGA	ACTCCCCCTG	1260
	GGCGCACGGC	GGAAGATGAA	GCCACTGCTA	CCACGGGTCA	GCTCATACCT	GGTACCTATC	1320
	CAGTTCGCCG	TGAACCAATC	ACTGGTGTG	CAGCCCTCGG	TGAAGGTGCC	ATTGCCCTTG	1380
	GCGGCTTCCC	TCATGAGCTC	AGAGCTTGCC	CGCCATAGCA	AGCGAGTCCG	CATTGCCCCC	1440
	AAGGTTTTTG	GGGAACAGGT	GGTGTGTTG	TACATGAGTA	AGTTCCTTAG	TGGCGATCTG	1500
50	CGAGATTTTG	GTACACCCAT	CACCGACTTG	TTTAATTTTA	TCTTCTTTTG	TTTATCAGTG	1560
	CTGCTAGCTG	AGGAGGGGAT	AGCTCCTCTT	TCTTCTGCG	GACCAAGGAA	AGAGGAGAAA	1620
	CTCCTGTTTG	GAGAAGGGTT	TTCTCCTTTG	CTTCCAGTTC	AGACTATCAA	GGAGGAAGAA	1680
	ATCCAGCCTG	GGGAGGAAAT	GCCACACTTA	GCGAGACCCA	TCAAAGTGGA	GAGCCCTCCC	1740
	TTGGAAGAGT	GGCCCTCCCC	GGCCCCATCT	TTCAAAGAGG	AATCATCTCA	CTCCTGGGAG	1800
55	GATTGCTCCC	AATCTCCACC	CCCAAGACCC	AAGAAGTCTT	ACAGTGGGCT	TAGGTCCCCA	1860
	ACCCGGTGTG	TCTCGGAAT	GCTTGTGATT	CAACACAGGG	AGAGGAGGGA	GAGGAGCCGG	1920
	TCTCGGAGGA	AACAGCATCT	ACTGCCCTCC	TGTGTGGATG	AGCCGGAGCT	GCTCTTCTCA	1980
	GAGGGGCCCA	GACTTCTCCG	CTGGGCCGCA	GAGCTCCCGT	TCCAGCAGAG	CTCCTCTGAC	2040
	CCTGCCCTCC	AGCTCAGCTA	CTCCCAAGAA	GTGGGAGGAC	CTTTAAGAC	ACCCATTAA	2100
60	GAAACGCTGC	CCATCTCTCT	CACCCGAGC	AAATCTGTCC	TCCCAAGAAC	CCCTGAATCC	2160
	TGGAGGCTCA	CGACCCACAG	CAAAGTAGGG	GGAAGTGAAT	TCAGCCCACT	ACAAACCTCC	2220
	CAGGGTGCC	CTGACCCCTT	GCCTGACCCC	CTGGGGCTGA	TGGATCTCAG	CACCACTCCC	2280
	TTGCAAGATG	CTCCCTTCCC	TGAATCACCG	CAAAGGCTCC	TCAGTTTACA	ACCCCTAGAC	2340
	CTCATCTCCG	TCCCTTTTGG	CAACTCTTCT	CCCTCAGATA	TAGACGTCCC	CAAGCCAGGC	2400
65	TCCCGGAGC	CACAGGTTTC	TGGCCTTGCA	GCCATCGTT	CTCTGACAGA	AGGCCCTGGT	2460
	CTGGACACAA	TGAATGACAG	CCTCAGCAAG	ATCCTGCTGG	ACATCAGCTT	TCTTGGCCTG	2520
	GACGAGGACC	CAGTGGGCCC	TGACAAATC	AACTGGTCCC	AGTTTATTCC	TGAGCTACAG	2580
	TAGAGCCCTG	CGTTTCCCAAG	TGTGCTCAAG	CTGTCACCA	TCCGGGCGAC	TCCAAGGCTC	2640
	AGTGACCCCC	AAGCCTCTGA	GTGAGGACAG	CAGGCAGGGA	CTGTTCTGCT	CCTCATAGCT	2700
70	CCCTGCTGCC	TGATTATGCA	AAAGTAGCAG	TCACACCCTA	GCCACTGCTG	GGACCTTGTG	2760
	TTCCCCAAGA	GTATCTGATT	CCTCTGCTGT	CCCTGCCAGG	AGCTGAAGGG	TGGGAACAAC	2820
	AAAGGCAATG	GTGAAAAGAG	ATTAGGAACC	CCCCAGCCTG	TTTCCATTCT	CTGCCAGACA	2880
	GTCTCTTATC	TTCCCTGATC	TTTGACGGGT	GGTCCGTGTA	AATAGTATAA	ATTCTCCAAA	2940
	TTATCCTCTA	ATTATAAATG	TAAGCTTATT	TCCTTAGATC	ATTATCCAGA	GACTGCCAGA	3000
75	AGGTGGGTAG	GATGACCTGG	GGTTTCAATT	GACTTCTGTT	CCTTGCCTTT	AGTTTGTATA	3060
	GAAGGGAAGA	CCTGCAGTGC	ACGGTTTCTT	CCAGGCTGAG	GTACCTGGAT	CTTGGGTTCT	3120
	TCACTGACAG	GACCCAGACA	AGTGGATCTG	CTTGCCAGAG	TCCTTTTTCG	CCCTCCCTGC	3180
	CACCTTCCCG	TGTTTCCAA	TGACGCTTCC	TGCAAGAAGA	AATCCTGGTT	AAAAAGTCT	3240
	TTTGATTTGG	GTGAGGAGTT	GAATTTGGGG	TGGGAGGATG	GATGCAACTG	AAGCAGAGTG	3300
80	TGGGTGCCCA	GATGTGCGCT	ATTAGATGTT	TCTCTGATAA	TGTCCCAAT	CATACCAAGG	3360
	AGACTGGCAT	TGACGAGAAC	TCAGGTGGAG	GCTTGAGAAG	GCCGAAAGGG	CCCCTGACCT	3420
	GCCTGGCTTC	CTTAGCTTGC	CCCTCAGCTT	TGCAAGAGAC	CACCTTAGGC	CCCAGCTGAC	3480
	CGCATGGGTG	TGAGCCAGCT	TGAGAACACT	AACTACTCAA	TAAAGCGAA	GGTGACAAA	3540
85	AAAAAAAAAA	AAAAA					

Seq ID NO: 73 Protein sequence:
Protein Accession #: AAC51128.1

1 11 21 31 41 51
5 MKTSPRRPLI LKRRRLPLPV QNAPSETSEE EFKRSPAQQE SNQAEASKEV AESNSCKPPA 60
GIKIINHPTM PNTQVVAIPN NANIHSIITA LTAKGKESGS SGPKNKFILIS CGGAPTQPPG 120
LRPQTQTSYD AKRTEVTLET LGPKPAARDV NLPRPPGALC EOKRETCADG EAAGCTINNS 180
LSNIQWLRLM SSDGLGSRSI KQEMEEKENC HLEQRQVKVE EPSRPSASWQ NSVSERPPYS 240
YMAMIQFALN STERKRMTLK DIYTWIEDHF PYFKHIAKPG WKNSIRHNL LHMDFVRETS 300
10 ANGKVSFWTI HPSANRYLTL DQVFKPLDPG SFQLPEHLES QQKRPNPELR RNMTIKTELP 360
LGARRKMKPL LPRVSSYLVP IQFPVNOQLV LQPSVKVPLP LAASLMSEEL ARHSKRVRIA 420
PKVFGQVVFV GYMSKFFSGD LRDFGTPTS LFNFIPLCLV VLLAEEGIAP LSSAGPGKEE 480
KLLFGEQFSP LLFVQTIKEE EIQFGEEMPH LARPIKVESP PLEWPSAP SPKESSSHSW 540
EDSSQSPTFR FKSYSGLR S PTRCVSEMLV IQHRRERS RSRRKQHLPL PCVDEPELLF 600
15 SEGSPSTRWA AELFFPADSS DPASQLSYSQ EVGGPFKTP I KETLPISSSTP SKSVLPRTPPE 660
SWRLTPPAKV GGLDFSPVQT SQGASDPLPD PLGLMDLSTT PLQSAPPLES PQRLLSSEPL 720
DLISVFFGNS SPSPIDVPKP GSPEPVQVSL AANRSLTEGL VLDTMNDSLS KILLDISPPG 780
LDEDFLGPND INWSQFIPEL Q

20 Seq ID NO: 74 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 111-416

1 11 21 31 41 51
25 GGGAAGAGCC AGGCTGAGCC TTATAAAGGA CTGCTCTTTG TCCAAACACA CACATCTCAC 60
TCATCCTTCT ACTCGTGACG CTCCCAGCT CTGGCTTTT GAAAGCAAAG ATGAGCAACA 120
CTCAAGCTGA GAGGTCCATA ATAGGCATGA TCGACATGTT TCACAAATAC ACCAGACGTG 180
ATGACAAGAT TGAGAAGCCA AGCCTGCTGA CGATGATGAA GGAGAACTTC CCCAACTTCC 240
30 TTAGTGCCTG TGACAAAAG GGCACAAAT ACCTCGCCGA TGTCTTTGAG AAAAAGGACA 300
AGAATGAGGA TAAGAAGATT GATTTTCTG AGTTTCTGTC CTTGCTGGGA GACATAGCCA 360
CAGACTACCA CAAGCAGAGC CATGGAGCAG CGCCCTGTTC CGGGGGCAGC CAGTGACCCA 420
GCCCCACCAA TGGGCCTCCA GAGACCCAG GAACAATAAA ATGTCTTCTC CCACCAGA

35 Seq ID NO: 75 Protein sequence:
Protein Accession #: Eos sequence

1 11 21 31 41 51
40 MSNTQAERSI IGMIDMFHY TRRDDKIEKP SLLTMMKENF PNFLSACDKK GTNYLADVFE 60
KDKKNEDKKI DFSEFLSLLG DIATDYHKQS HGAAPCSGGS Q

45 Seq ID NO: 76 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 111-416

1 11 21 31 41 51
50 GGGAAGAGCC AGGCTGAGCC TTATAAAGGA CTGCTCTTTG TCCAAACACA CACATCTCAC 60
TCATCCTTCT ACTCGTGACA CTCCCAGTT CTGGCTTTT GAAAGCAAAG ATGAGCAACA 120
CTCAAGCTGA GAGTTCATA ATAGGCATGA TCGACATGTT TCACAAATAC ACCGACGTG 180
ATGGCAAGAT TGAGAAGCCA AGCCTGCTGA CGATGATGAA GGAGAACTTC CCCAACTTCC 240
TCAGTGCCTG TGACAAAAG GGCATACATT ACCTCGCCAC TGTCTTTGAG AAAAAGGACA 300
55 AGAATGAGGA TAAGAAGATT GATTTTCTG AGTTTCTGTC CTTGCTGGGA GACATAGCCG 360
CAGACTACCA CAAGCAGAGC CATGGAGCGG CGCCCTGTTC TGGGGGAAGC CAGTGATCCA 420
GCCCCACCAA GGGCCTCCA GAGACCCAG GAACAATAAG TGTCTCTCCT CACCAGA

60 Seq ID NO: 77 Protein sequence:
Protein Accession #: XP_048124.1

1 11 21 31 41 51
65 MSNTQAERSI IGMIDMFHY TGRDGKIEKP SLLTMMKENF PNFLSACDKK GIHYLATVFE 60
KDKKNEDKKI DFSEFLSLLG DIAADYHKQS HGAAPCSGGS Q

70 Seq ID NO: 78 DNA sequence
Nucleic Acid Accession #: Z73678.1
Coding sequence: 253-2433

1 11 21 31 41 51
75 GGGGTGGTGC AGGGCAGGGG TGGTATATCC TGTCTGACGG AGGGCGGGCC TCGCCAGTGC 60
CAGAGAGGGA CGAACCAGGG TGAAGCGCC AGGAGCAGCT GCAGGGAGCC CTCACGCGGA 120
CCTCGCAGTC TATGGCCGTA GGGAGCGGCT GAGAGCGAGA AGAGCAGCCT CCTGCCCGCC 180
CGCTGCACCG CACTCGCCT CGCTCTCTG CTCTCCTAGG CCGCGGCCG GCGCCACCG 240
CCTCCCGCCA CCATGAACCA CTGCGCGCTC AAGACCGCCT TGGCGTACGA ATGCTTCCAG 300
GACCAAGGGA ACTCCAGTT GCGTTTGGC TCGGACCAA AGATGAAAAC AGGCACGCT 360
80 GGCAGGCAGC GCGTGCAGGA GCAGGTGATG ATGACCGTCA AGCGGCAGAA GTCCAAGTCT 420
TCCCAGTCGT CCACCTGAG CCACTCCAAT CGAGGTTCCA TGTATGATGG CTTGGCTGAC 480
AATTACAAT ATGGGACCAC CAGCAGGAGC AGCTACTACT CCAAGTTCCA GGCAGGGAAT 540
GGCTCATGGG GATATCGAT CTACAATGGA ACCCTCAAGC GGGAGCCTGA CAACAGGCGC 600
TTCACTCTCT ACAGCCAGT GGAGAACTGG AGCCGCGACT ACCCCGCGG CAGCTGTAAC 660
ACCACCGCGC CAGGCAGCGA CATCTGCTTC ATGCAGAAA TCAAGCGCAG CCGCAGTGAG 720
85 CCGACCTCT ACTGTGACCC ACCGGGCACC CTGCGCAAGG GCACGCTGGG CAGCAAGGCG 780
CAGAAGACCA CCCAGAACG CTACAGCTT TACAGCACCT GCAGTGGTCA GAAGGCCATA 840
AAGAAGTGCC CTGTGCGCCC GGCCTCTTGT GCCTCCAAGC AGGACCTCTGT GTATATCCG 900

	CCCATCTCCT	GCAACAAGGA	CCTGTCTCTT	GGCCACTCTA	GGGCCAGCTC	CAAGATCTGC	960
	AGTGAGGACA	TCGAGTGCAG	TGGGCTGACC	ATCCCCAAGG	CTGTGCAGTA	CCTGAGCTCC	1020
	CAGGATGAGA	AGTACCAGGC	CATTGGGGCC	TATTACATCC	AGCATACCTG	CTTCCAGGAT	1080
5	GAATCTGCCA	AGCAACAGGT	CTATCAGCTG	GGAGGCATCT	GCAAGCTGGT	GGACCTCCTC	1140
	CGCAGCCCCA	ACCAGAACGT	CCAGCAGGCC	CGCGCAGGGG	CCCTGCGCAA	CCTGGTGTTC	1200
	AGGAGCACC	CCAACAAGCT	GGAGACCCGG	AGGCAGAAATG	GGATCCGCGA	GGCAGTCAAG	1260
	CTCCTGAGGA	GAACCCGGAA	CGCCGAGATC	CAGAAGCAGC	TGACTGGGCT	GCTCTGGAAC	1320
	CTGTCTTCCA	CTGACGAGCT	GAAGGAGGAA	CTCATTGGCCG	ACGCCCTGCC	TGTTCTGGCC	1380
10	GACCCGCTCA	TCATTCCCTT	CTCTGGCTGG	TGCGATGGCA	ATAGCAACAT	GTCCCGGGAA	1440
	GTGCTGGACC	CTGAGGTCTT	CTTCAATGCC	ACAGGCTGCT	TGAGGAACCT	GAGCTCGGCC	1500
	GATGCAGGCC	GCCAGACCAT	GCGTAACTAC	TCAGGGCTCA	TTGATTCCCT	CATGGCCTAT	1560
	GTCCAGAACT	GTGTAGCGGC	CAGCCGCTGT	GACGACAAGT	CTGTGGAAAA	CTGCATGTGT	1620
	GTTCCTGCAC	ACCTCTCCTA	CCGCCCTGGAC	GCCGAGGTGC	CCACCCGCTA	CCGCCAGCTG	1680
15	GAGTATAACG	CCGCAACGCG	CTACACCGAG	AAGTCCCTCA	CTGGCTGCTT	CAGCAACAAG	1740
	AGCGACAAGA	TGATGAACAA	CAACTATGAC	TGCCCCCTGC	CTGAGGAAGA	GACCAACCCC	1800
	AAGGGCAGCG	GCTGGTGTGA	CCATTCAAGT	GCCATCCGCA	CCTACCTGAA	CCTCATGGGC	1860
	AAGAGCAAGA	AAGATGCTAC	CCTGGAGGCC	TGTGCTGGTG	CCCTGCAGAA	CCTGACAGCC	1920
	AGCAAGGGCG	TGATGTCCAG	TGGCATGAGC	CAGTTGATTTG	GGCTGAAGGA	AAAGGGCCTG	1980
20	CCACAAATTC	CCGACTCTCT	GCAATCTGGC	AACTCTGATG	TGGTGGGCTC	CGGAGCCTCG	2040
	CTCCTGAGCA	ACATGTCCCG	CCACCCCTCG	CTGCACAGAG	TGATGGGGAA	CCAGGTGTTC	2100
	CCGGAGGTGA	CCAGGCTCCT	CACCAGCCAC	ACTGGCAATA	CCAGCAACTC	CGAAGACATC	2160
	TTGTCTCGGG	CCTGCTACAC	TGTGAGGAAC	CTGATGGCCT	CGCAGCCACA	ACTGGCCAAAG	2220
	CAGTACTTCT	CCAGCAGCAT	GCTCAACAAC	ATCATCAACC	TGTGCCGAAG	CAGTGCCTCA	2280
25	CCCAAGGGCG	CCGAGCTTGC	CCGGCTTCTC	CTGTCTGACA	TGTGGTCCAG	CAAGGAACCTG	2340
	CAGGGTGTCC	TCAGACAGCA	AGGTTTCGAT	AGGAACATGC	TGGGAACCTT	AGCTGGGGCC	2400
	AACAGCCTCA	GGAACCTCAC	CTCCGATTTC	TAAGAAGAGA	CTGTCCAAGC	AAGTTAGGCT	2460
	TGCAGGAAGA	TATGACCCAG	CTGAGAAGCC	CTCAGGCCTC	GCTGGATGGG	GTTCCTGTTC	2520
	CATCCTGTGC	AGTATTTGGG	AAAGTTTACA	AGAAACTGAG	AAGAAACCTA	AAAACCTGTG	2580
30	ATAGTGGAAA	GATTTTATGA	TTTTTTTTTT	CCTTGGGGAA	ACTGGCAGGC	AATGGGGGTT	2640
	AGGGAGGTTG	GGGCGGGGGG	GGCTTTCTTG	AGTTAAAGGG	GCTTATATGT	GATGTCAATA	2700
	TTTCTTCTTC	TGAGAAATGG	TATATATATG	TGTCTAATGT	AAGTGTGTGC	ATGCATGTGC	2760
	GCGTGCATGT	GTGTGTGTGT	GAGTGTCTTA	AAGCATAACC	ACAAACTGCA	AAAAGCTAGG	2820
	TAAGCTATTT	TGTTGCAAGT	CATAAGGTGG	TGAAAGAGAC	TCTCCTGTGT	TTCTTACTCA	2880
35	TAGGCAAGGA	CAACATGTGC	TTTTTGGTGA	GCTGCTCATA	ATTCCTGAAA	TGTGTGGTGC	2940
	CAGGGCAAGG	GGGCCATCAC	TGCAGTCAGG	CCCTCAGAGG	AGTCTCTGAG	GCTTCTCTACC	3000
	AGTGTCTTCC	AAGGGTGCAG	GAGTAACTGG	GGCTGGGCCA	GCCTCCCCCC	TTACAAGGCT	3060
	GCCTTCCACG	AAGGGAGGTC	TGGTGTATCT	CATGGGAGAA	TCTGGGGTGT	CTGTAGTGTG	3120
	ACCCCTCCAG	CAGGCCACCA	AGGACTGAGG	TTGGGTAGGT	GTGAGGTTC	AGAGGACAGC	3180
40	AGGACACTCT	CGCTACTTTT	GCCAAATGAG	GCCTGCTCAG	AGGAGTAGGA	GCTGAAAGAT	3240
	GGTGCTCTCA	ACCTCTCTTG	GCTGTGTGCC	CATCAGAGCA	GGCTCAGCCT	GCAAGGCCCC	3300
	TGCATTCCAG	GGTCTTGATA	TCTACTTGTT	GCAGGAGAAA	GAAGGTAAAA	AATGATTTTT	3360
	TTAAGAAAAG	CTATTTTATT	GCAGCTCTTT	CCCAAGAGCT	GTTCTGGGAA	TGGCTGGTCT	3420
	TCATATTTCC	AGTGGAGAGG	AGAACAAAGT	GGGCTGGGCA	TATACCTATT	CCGGCTTCTA	3480
45	GTGGGATGGA	GTGGGGTAT	AGAAATTAAC	CAGGAAGATG	TTTCCACCAA	GCCTGCTGTG	3540
	AGTCAATTTA	GGGAGTGTTC	GGGTCCCAAG	AGACTTGGAC	GGGGGGAGTT	TGGGTAGACT	3600
	AGGAAGGAA	AGTCCCATAT	CAGGGTACCG	GTACCGGCAA	GCTCACATCT	CAGCCAGGGG	3660
	CCATGCCCCA	CTTCCCTGTA	CCCCAGCTGT	CTTGTCTCCA	CTCTGTGAAA	CCACAGGGG	3720
50	ATGTGATAAA	CAGGGCTATT	AGGGGTATCA	GCCAGTTCGA	GCCCCCAGAC	TCTGTGCACT	3780
	TCAGACCAAG	GTGAGCAGGA	GGGCTCCCGA	GGGCTTATG	AGAAAACTTG	TGTGGACATC	3840
	CCCTGGTGTA	CACATAAGACA	GAGCAGAGCC	CAGCGCTCCC	AAGCCTTCTT	CCTTCCAGCT	3900
	TCTACTTCCA	TGCTAGCATT	GCTGGTGTTA	GAGAGGAATT	AACCTTCTGG	TCTGTGCCCT	3960
	TCTCTAGAAG	AATATAAGAT	GCTCCTCCTC	CTCACCCCTT	CTCAGCCTCC	TCCCAAGTCT	4020
	TCTCTTCTG	CACCACCCCC	GAGTCCAAAC	CCACCTCTTG	CCCCCAGATT	CAGGCTGGAA	4080
55	AACACTGATG	TGGACTCAGT	ATGACCAACT	AGATGGGGGA	AGCCAGACAT	GTGAGGACGC	4140
	TGTCCTCCGA	GAGGTGTCCC	CGGCTGTTAG	CCAGCTGTGC	TGTGGTGTCT	TGGGTCTGTG	4200
	ATACCTCTCC	TGCTTCTCTG	TCACACTGGG	AGGCCCACTC	CTGGCTCACC	TCTCCCTCTC	4260
	AGGGACCCAC	GTGGGAGCCT	GGATCCCTGG	ACTGTCTCTG	GCATAGGTTT	CAGGGGCTCT	4320
	CTTTGTGTGC	ATCAGAACCC	AGAGGAATTC	TTCTCTTAAA	AAATAAGTAT	GGCATACCAA	4380
60	TCTGTGCGGG	GCAGTGTCTT	AAGCACTTAG	ACTACATCAG	GGAAGAACAC	AGACCACATC	4440
	CCCGTCTCTA	TGCGGCTTAT	GTTCCTCTGA	GGAAGTGGGA	GACACAAGTC	CTTGGCTTTA	4500
	GGGCTCCCCC	GGCTGGGGGC	TGTGAGTCC	GGTCAGGGCG	GGAGGGGAAA	TGCACCGCTG	4560
	CATGTGAACC	TTACCAGCCC	AGGCGGATGC	CCCTTCCCCT	TAGCACTACC	CTGGCCTCCT	4620
	GCATCCCCCT	GCCTCATGTT	CCTCCACCTT	TCAAAGAAATG	AAGAGCCCCA	TGGGCCCAGC	4680
65	CCCTGCCCTG	GGAAACAGGC	AGCCTTCCAG	ACCTCAGGGG	CTGAGGCAGA	CTATTAGGGC	4740
	AGGGCTGACT	TGCTGTACAT	TGCCCATTCC	CTCTCAGGCC	AGCTCAGGTC	ACCCGGGCCCT	4800
	CTGACCCAGG	CCTGTCACTT	TGAGAGGGGC	AAAACTGAGA	GGGGCTTTTC	CTAGAGAAAAG	4860
	AGAACAAGGA	GCTTGCCAGG	CTTCATGTAG	CCGACACACG	TCTCAGGATT	TTAAGTCCAC	4920
	ATTGGCCTCA	CACATAGCTA	GGCCATATGCC	CAAAATAAGG	AGTTCCAATT	TGGGGCCAAA	4980
70	TGAGGAAGGA	CACAGACTCT	GCCTGGGAT	CTCCTGTGCT	AGCGGCCAAT	GACAAATCCA	5040
	GTCAATGGCC	ACCAGCCACC	TCTGCACTGG	GGACCACTCT	AGCAGCCCTG	ACTCCACACT	5100
	CTCCTGGGGG	ACCCAAGAGT	CAGTGTGTCT	GTCTGCGTGT	CCACCTTGGA	ATCTGGCTGA	5160
	ACTGGCTGGG	AGGACCAAGA	CTGCGGCTGG	GGTGGGCAGG	GAAGGGGAAG	CGGGGGCTGC	5220
	TGTGAGGGAT	CTTGGAGCTT	CCCTGTAGCC	CACCTTCCCC	TGCTTCTATG	TTTGTAGAGG	5280
75	AACCTTGTGC	CGGCCAGGCC	CAGTTTCTCT	GTGTGATACA	CTAATGTATT	TGCTTTTTTT	5340
	GGAAATAGAG	AAAATCAATA	AATTGCTAGT	GTTTCTTTGA	AAAAAATA		

Seq ID NO: 79 Protein sequence:
Protein Accession #: CAA98022.1

80	1	11	21	31	41	51	
	MNHSPLKTLA	AYECFQDQDN	STLALPSDQK	MKTGTSGRQR	VQEQVMVTVK	RQKSKSSQSS	60
	TLSHSNRGM	YDGLADNINY	GTTSRSSYYG	KFQAGNGSWG	YPIYNGTLKR	EPDNRRFSSY	120
	SQMNWSRHY	PRGSCNTTGA	GSDICFMQKI	KASRSEPDLY	CDPRGTLRKG	TLGSKGQKTT	180
85	QKNRYSFYST	SGQKAIKKCP	VRPPSCASKQ	DPVYIPIPI	NKDLSPFGHR	ASSKICSEDI	240
	ECSGLTIPKA	VQYVSSQDEK	YQAIGAYYIQ	HTCFQDESAK	QVYQLGGGIC	KLVDLLRSPN	300
	QNVQQAAGA	LRNLVFRSTT	NKLETRRQNG	IREAVSLRR	TGNAEIQKQL	TGLLWNLSST	360

WO 02/086443

PCT/US02/12476

DELKEELIAD ALPVLADRV I PPSGWCODN SNMSREVDP EVFFNATGCL RNLSSADAGR 420
QTMRYNSGLI DSLMAYVQNC VAASRCDDKS VENCVCVLHN LSYRLDAEVP TRYRQLEYNA 480
RNAYTEKSSST GCFPSNKSDDK MNMNYDCPLP EBETNPCKSG WLYHSDAIRT YLNLMGKSKK 540
DATLEACAGA LQNLTAASKGL MSSGMSQLIG LKEKGLPQIA RLQSGNSDV VRSGASLLSN 600
MSRHPLLRV MGNGVFFEVF RLLTSHTGNT SNSEDISSA CYTVRNLMAS QPQLAKQYFS 660
SSMLNNIINL CRSSASPKAA EAARLLSDM WSSKELQGV L RQQGFDRNML GTLAGANSLR 720
NFTSRP

Seq ID NO: 80 DNA sequence
Nucleic Acid Accession #: NM_006516.1
Coding sequence: 180-1658

1 11 21 31 41 51
TAGTCGCGGG TCCCCGAGTG AGCAGCGCCAG GGAGCAGGAG ACCAAACGAC GGGGGTCGGA 60
GTCAGAGTCG CAGTGGGAGT CCCCAGGACC GAGCAGCAGC CTGAGCGGGA GAGCGCGCT 120
CGCAGCGCCG TCGCCACCCG CGTACCGGGC GCAGCCAGAG CCACAGCGC AGCGCTGCCA 180
TGGAGCCGAG CAGCAAGAAG CTGACGGGTC GCCTCATGCT GGCTGTGGGA GGAGCAGTGC 240
TTGGCTCCCT GCAGTTTGGC TACAACACTG GAGTCATCAA TGCCCCCAG AAGGTGATCG 300
AGGAGTTCTA CAACGACACA TGGGTCCACC GCTATGGGGA GAGCATCCTG CCCACCACGC 360
TCACCACGCT CTGGTCCCTC TCAGTGGCCA TCTTTTCTGT TGGGGGCATG ATTGGCTCCT 420
TCTCTGTGGG CCTTTTCGTT AACCGCTTGG GCCGGCGGAA TTCAATGCTG ATGATGAACC 480
TGCTGGCCTT CGTGTCCGCC GTGCTCATGG GCTTCTCGAA ACTGGGCAAG TCCTTTGAGA 540
TGCTGATCCT GGGCGGCTTC ATCATCGGTG TGTACTGCGG CCTGACCACA GGCTTCGTGC 600
CCATGTATGT GGTGTAAGTG TCACCACAG CCTTTCTGGG GGCCCTGGGC ACCCTGCACC 660
AGCTGGGCGT CGTGTCCGCC ATCCTCATCG CCCAGGTGTT CGGCCTGGAC TCCATCATGG 720
GCAACAAGGA CCTGTGGCCC CTGCTGCTGA GCATCATCTT CATCCCGGCC CTGCTGCAGT 780
GCATCGTCTC GCGCTCTGTC CCGAGAGTCT CCGCTTCTCT GCTCATCAAC CGCAACGAGG 840
AGAACCGGGC CAAGAGTGTG CTAAGAAGC TGGCGGGGAC AGCTGACGTG ACCCATGACC 900
TGCAGGAGAT GAAGGAAGAG ATCGGSCAGA TGATGCGGGA GAAGAAGGTC ACCATCCTGG 960
AGCTGTTCCG CTCGCCCGCC TACCGCCAGC CCATCCTCAT CGCTGTGGTG CTGCAGCTGT 1020
CCCAGCAGCT GTCTGGCATC AACGCTGTCT TCTATTACTC CAGGAGCATC TTCGAGAAGG 1080
CGGGGGTGCA GCGCCTGTGT TATGCCACCA TTGGCTCCGG TATCGTCAAC ACGGCTTCA 1140
CTGTCTGTCT GCTGTTTGTG GTGAGGCGAG CAGGCGCGCG GACCCCTGCAC CTCATAGGCC 1200
TCGCTGGCAT GGGCGGTGTG GCCATACTCA TGACCATCGC GCTAGCACTG CTGGAGCAGC 1260
TACCTTGGAT GTCTATCTG AGCATCGTGG CCATCTTTGG CTTTGTGGCC TTCCTTGAAG 1320
TGGGTCTCGG CCCCATCCCA TGGTTCATCG TGGCTGAAC CTTCAGCCAG GGTCCACGTC 1380
CAGCTGCCAT TGCCGTTCGA GCGCTTCTCA ACTGAGCTC AAATTTTCAT GTGGGCATGT 1440
GCTTCCAGTA TGTGGAGCAA CTGTGTGGTC CCTACGCTT CATCATCTTC ACTGTGCTCC 1500
TGGTCTGTGT TGTGCTCTTC ACCTACTTCA AAGTTCCTGA GACTAAAGGC CGGACCTTCG 1560
ATGAGATCGC TTCGCGTTC CCGCAGGGGG GAGCCAGCCA AAGTGATAAG ACACCCGAGG 1620
AGCTGTTCCA TCCCCTGGGG GCTGATTCCC AAGTGTGAGT CGCCCCAGAT CACCAGCCCG 1680
GCTGTCTCCC AGCAGCCCTA AGGATCTCTC AGGAGCACAG GCAGCTGGAT GAGACTTCCA 1740
AACCTGACAG ATGTACGCGG AGCGGGGCTT GGGGCTCCTT TCTCCAGCCA GCAATGATGT 1800
CCAGAAGAA ATTCAGAGT TACCGGCTCC AGGATTTTAA CAAAAGCAAG ACTGTTGCTC 1860
AAATCATATC AGACAAGCAA CAGGTTTTAT AATTTTTTAA TTAAGTATTT TGTATTTT 1920
ATATCAGCCT GAGTCTCCTG TGCCACATC CCAGGCTTCA CCTGAATGG TTCATGCCT 1980
GAGGGTGGAG ACTAAGCCCT GTGAGACAC TTGCTTCTT CACCCAGCTA ATCTGTAGGG 2040
CTGGAACCTAT GTCTTAAGGA CACACTAATC GAACTATGAA CTACAAGCT TCTATCCAG 2100
GAGGTGGCTA GTGCCACCCG TTCTGCTGGC CTGGATCTCC CCACTTAGG GGTGAGGCTC 2160
CATTAGGAT TTGCCCTTCC CATCTCTTCC TACCAACCA CTCAAATTA TCTTTCTTTA 2220
CCTGAGACCA GTTGGGAGCA CTGGAGTGCA GGGAGGAGAG GGGAAAGGCC AGCTGGGCT 2280
GCCGGGTTCT AGTCTCCTTT GCACTGAGGG CCACACTATT ACCATGAGAA GAGGGCCTGT 2340
GGGAGCCTGC AAATCACTG CTCAAGAAGA CATGGAGACT CCGCCCTGT TGTGTATAGA 2400
TGCAAGATAT TTATATATAT TTTTGGTTGT CAATATTAAA TACAGACACT AAGTTATAGT 2460
ATATCTGGAC AAGCAACTT GTAAATACAC CACCTCACTC CTGTTACTTA CCTAAACAGA 2520
TATAAATGGC TGGTTTTTAG AAACATGGTT TTGAAATGCT TGTGGATTGA GGTAGGAGG 2580
TTTGGATGGG AGTGAGACAG AAGTAAGTGG GGTGCAACC ACTGCAACCG CTTAGACTTC 2640
GACTCAGGAT CAGTCCCTT ACACGTACCT CTCATCAGTG TCCTCTTGCT CAAAATCTG 2700
TTGATCCCT GTTACCACGA GAATATATAC ATTCTTTATC TTGACATTCA AGGCATTCT 2760
ATCACATATT TGATAGTTGG TGTCAAAAA AACACTAGTT TTGTGCCAGC CGTGATGCTC 2820
AGGCTTGAAT TCGCATTATT TTGAATGTGA AGGGAA

Seq ID NO: 81 Protein sequence:
Protein Accession #: NP_006507.1

1 11 21 31 41 51
MEPSSKKLTG RLMLAVGGAV LGSLLQGYNT GVINAPQKVI EEFYNQTVWH RYGESILPTT 60
LTTLWSLSVA IFSVGMIGS FSVGLFVNRF GRRNSMLMMN LLAFFVSAVLM GFSKLGKSPF 120
MLILGRFIIG VYCGLTTFGV PMYVGEVSPT AFRGALGTLH QLGIIVVGILI AQVPGLDSIM 180
GNKDLWPIIL SIIFIPALLQ CIVLPFCPEP PRFLLINRNE ENRAKSVLKK LRGTADVTHD 240
LQEMKEBSRQ MMREKVTIL ELFRSPAYRQ PILIAVVLQL SQQLSGINAV PYYSTSIKFE 300
AGVQQPVYAT IGSIVNTAF TVVSLFVVER AGRRTLHLIG LAGMAGCAIL MTIALALLEQ 360
LPWMSYLSIV AIFGPVAPFE VGGPIPWFI VAEFLSQGPR PAALIAVAGFS NWTNFIIVGM 420
CFQVVEQLCG PYVFIIFTVL LVLFFIFTYF KVPETKGRTF DEIASGFRQG GASQSDKTPE 480
ELFHLGADS QV

Seq ID NO: 82 DNA sequence
Nucleic Acid Accession #: BC001291
Coding sequence: 44-541

1 11 21 31 41 51
GGGGGCGCCG CGCGCTGACC CTCCTTGGGC ACCGCTGGGG ACGATGGCGC TGCTCGCCTT 60
GCTGCTGGTC GTGCCCTTAC CCGCGGTGTG GACAGACGCC AACCTGACTG CGAGACAAAC 120

	1	11	21	31	41	51	
40	TTTTTTTTTT	TTTTTGTCTT	AAAAAAAAAGC	CATGACGGCT	CTCCCACAAT	TCATCTTCCC	60
	TGCGCCATCT	TTGTATTATT	TCTAATTTAT	TTTGGATGTC	AAAAGGCGACT	GATGGAAGTA	120
	TTTTCTCTGG	AGTCTCTTAT	TTCTTAACCC	GGCTCTCCCG	ATGTGAACAG	AGCGCTCGTC	180
	CGCCCGCCGC	CGCCGCGGCC	GC0CGCCGCC	CCGCGCCCGC	AGCCCCACAT	TCTCTGCGCG	240
45	AAGCAAGGCA	AACCCGACGA	CTTAAAGCAA	CGCGAATTCG	CGCCCGAGTC	TCTTGAAGCC	300
	ATTTCTTAGC	ATGATGAACC	AGACCAACGC	CCGTTGGGAG	CTCCAGAAAG	GGATCATGAC	360
	CTCTCTCACT	TGTGGGCAGT	CCAGATGAAC	TTTCCCATAT	GGGACATTTT	TATTTTATTC	420
	GAGCAACAAC	GGAAACAATG	CATTGGCGAG	CTCTGCTTAG	AAAAGAGTGT	GATGAAGCCA	480
50	CCTTCCCCCT	CACCAATCGA	GATGAAAAAA	GCATCCAATC	CCGTGGAGGT	TGCCATCCAG	540
	GTCAACGCGC	AAGATGAAGT	TTGTTTATCA	ACGTCATCTA	GAGAAGATTG	CCCCAAACAG	600
	GAAACATACG	CAGATAAACT	TCTGCATCGG	AGGGGGCTCT	CTCTCCCTCG	TTCCTGCACAT	660
	GGAGCTCTAA	TCCCCACGCC	TGGGATGAGT	GCAGAAATAT	CCCCCGAGG	TATTTGTAAA	720
55	GATGAGCCCA	CAGCTACAC	ATGTACAAT	TGCAAAACAG	CATTCAACG	TGCATGTGTT	780
	CTCTTGCAAC	ACGCACAGAA	CATCTATGGA	TTAAGAACT	ACTTAGAGCT	CGAACACGGA	840
	AGTCCCTCTG	CCCCCGGGT	TGGTATCCCT	TACGAGACTG	GTGCAGAATG	TCCTTCCCAAG	900
	CCACCTCTCC	ATGGGATTCA	TATTGACAG	AATAACCCCT	TTAACTTGCT	AAGAATACCA	960
60	GGATCAGTAT	CGAGAGAGGC	TTCCGGCCTG	GCAGAAAGGC	GCCTTCCACC	CACCTCCCCC	1020
	CTGTTTATGC	CACCAACGAG	ACATCACTTG	ACACCCCAAC	CGCTAGAGAG	CTGTGGGGCG	1080
	GAGAAGATGG	CCCTGGCCAC	CCATCACC0G	AGTGCCTTTG	AGGGGTGCT	CGGGTGTGAAT	1140
	CCAAATGAAT	TGGAGCCTCC	CGCCATGGAT	TTCTCTAGGA	GACTTAGAGA	CTGTGGCAGG	1200
65	AACACGTCTA	GCCACCGCCT	TCTCCCAGGC	CGGCGACGCC	CTATGCAAAG	GTTACTGCAA	1260
	CCATTCTCAG	CAGGTAGCAA	GC0CGCCCTC	TGTGGCAGCG	CCCCCTCTCC	TCCTCTGCAA	1320
	TCCGCCCCCT	CTCCTTCCCA	CGCCCCCGTC	ATAGTCCAAG	CTAGCGAGTT	CTGCGCGAAG	1380
	ACGTTCAAAT	TTCAGAGCAA	CTCGGTGGTG	ACCCGCGCGA	GCCAACGAG	CGAGAGAGCC	1440
70	TACAAGTGCA	ACCTGTGCGA	CCACGCTGTC	ACCCAGGCCA	GCAAGCTGGA	CGCCACATGT	1500
	AAGACGCACA	TGCACAAATC	GTCCCCCATG	ACGGTCAAGT	CCGACGACGG	TCTCTCCACC	1560
	GCGAGCTCCC	CGAAGCCCGG	CACCAAGCGC	TTGGTGGGCA	CGCGCAGCAG	CGCGCTCAAG	1620
	TGCTGTGTGT	CCAAGTTCAA	GAGCGAGAAC	GACCCCAAC	TGATCCCGGA	GAACTGGGAG	1680
75	GAGGAGGAGA	AGGAGGACGA	CAGGGAAGAG	GAAAGAGAGG	AGGAAGAGGC	GAGGAGGAGG	1740
	CTACGCGAGA	CGCAGAGGCT	GGACTCATGC	TCTGGCTGTA	GCCTGAGAGG	GGCGCGCCAC	1800
	CACGAGAACA	GCTCGCGGGG	CGCGGTGCTG	GGCGTGGGCG	ACGAGAGCCG	CGCCTGSCCC	1860
	GACGTCTATG	AGGGGATGAT	GCTCAGCTCC	ATGACGCTCT	TCAGCGAGGC	CTTCCACCAG	1920
80	GTCTCTGGGC	AGAAAGCATGT	GGCGGGCCAC	CTTGCCGAGG	CCGAGGGGCA	CAGGGACACT	1980
	TGCGACAGAG	ACTCGGTGCA	CGGCGAGTCG	ACCGCATACG	ACGATGGCAC	TGTTAATGGC	2040
	CGCGCTCGAT	CCCCGGGCGC	TGCGGCTGAT	GGAGGCGCTG	CCAAAAAGCT	CGCTGTGGGC	2100
	AGCCCCAGCT	CGCTGAGCCC	CTTCTCTAAG	CGCATCAAGC	TCGAGAAGGA	GTTTCGACTG	2160
85	CCCCCGGCCA	CGATGCCCAA	CAGGGAGAAC	GTGTACTCGC	AGTGGCTCGC	CGGCTAGCCG	2220
	CGCTTCAGAG	AGCTCAAAGA	TCCTCTCCTT	AGCTTCCGAG	ACTCCAGACA	ATCGCTCTTT	2280
	GCCTCTCGT	CGGAGCACTC	CTCGGAGAAC	GGGAGCTTGC	GCTTCTCCAC	ACCGCCCGGG	2340
	GAGCTGCGAG	GGGGATCTCT	GGGCGCGAGC	GGCAGCGGAA	TGTGAGAGGC	CACGCCCCAT	2400
90	ATTAGTGGTC	CGGGCACGGG	CAGGCCACGC	TCAAAAAGGG	GCAGACGCGA	CGACACTTGT	2460
	GAGTACTGTG	GGAAAGCTTT	CAAGGAATGT	AGCAATCTCA	CTGTCCACAG	GAGAAGCCAG	2520
	ACCGGGCGAA	GGGCTTATAA	CGAGGAGCTG	TGCAACTATG	CCGTGTGCCA	GAGTAGCAAC	2580
	CTCAACAGGC	ACATGAAAC	GCATGGCCAG	GTGGGGGAAG	ACGTTTACAA	TGTGAAATTT	2640
95	TGTAAGATGT	CTTTTAGCGT	GTACAGTACC	CTGTAGAAAC	ACATGAAAAA	ATGGCACAGT	2700
	GATCGAGTGT	TGAATAATGA	TATAAAAACT	GAATAGAGGT	ATATTATATC	CCCTCCCTCA	2760
	CTCCACCTGT	ACACCCCTTT	TTTCCACACT	CCCTTTCCCT	ATCGCCCTCC	AGCCCACTC	2820

	ATCTGTATGG	GGCAATACTA	TTCATTTTAA	CGCAAACTTT	GAGCCTTTCT	CTTGTGCAAT	3060
	AATTTACATG	TTGTGTATGT	TTTTTTTAA	ACTTAGACAG	CAITGATGGT	ATGTTATGGC	3120
	TATTTTAAAT	TGTCCTTAAT	TCGTTGCTGA	GCAAAACATG	TGCTGTTTCC	AGTTCCTGTC	3180
5	TGAGAGAAAA	AGAGAGAGAG	AGAGAAAAAG	ACCATGCTGC	ATACATTCTG	TAATACATAT	3240
	CATGTACAGT	TTTATTTTAT	AACGTGAGGA	GGAAAAACAG	TCTTTGGATT	AACCCCTCTAT	3300
	AGACAGAATA	GATAGCACTG	AAAAAAAATC	TCTATGAGCT	AAATGCTCTG	CTCTAAAGGG	3360
	TTAAATGTAT	CAATTGGAAG	GGAAGAAAAA	AGGCCTTGAA	TTGACAAATT	AACAGAAAAA	3420
	CAGAACAAAT	TTATTCATAT	ATTTGGTTTT	AAAAATATGAG	TGCCTTGGAT	CTATTAAAAA	3480
10	CACATCGATG	GTTCTTTCTA	CTTGTATATA	ACTTGTAGCT	TAATTCAGCA	TGCGGTGAGG	3540
	TAATAAACCT	TAGGAACATG	CATATAATTC	TATATTGTAT	TTCTCACAAC	AATGGCTACC	3600
	TAAAAAGATG	ACCATTTATG	TCTAGTTTAA	TCATCATTTT	TCCTTTAGTT	TAATTTTATA	3660
	AACAAAACCT	ATTATACCAG	TATAAAGCT	ACTTTGCTCC	TGGTGAGAGC	TTAAAGAAAA	3720
	TGGGCTGTTT	TGCCCAAAGT	TTTATTTTTT	TAAACAAATG	ATTAATTTGA	ATGTGTAATG	3780
15	TGCAAAAGCC	CTGGAACGCA	ATTAATAACA	CTAGTAAGGA	GTTCAATTTA	TGAAGATATT	3840
	TGCTTTAATA	ATGTCTTTTT	AAAAAATCTG	GCACCAAAAG	AAATAGATCC	AGATCTACTT	3900
	GGTGTGCAAG	TGACATAATC	TTAAGACCT	TGTATACCAT	ATTGAAAGGA		3960
	AGAGGCTGAC	AATAAGGTTT	GACAGAGGGG	AACAGAGAA	AATAATATGA	TTTATTAGCA	4020
	CAACGTGGTA	CTATTTGCCA	TTTAAACTTA	GAACAGGTAT	ATAAGCTAAT	ATTGATACAA	4080
20	TGATGATTAA	CTATGAATTC	TTAAGACTTG	CATTTAATAG	TGACATTCTT	AAAAAAGAA	4140
	GAGAAAGAA	TTTAAGAGTA	GCAGTATATA	TGCTGTGCT	CCCTAAAGT	TGTACTTCAT	4200
	TTCTTTTCCA	TACACTGTGT	CTATTTTGTG	TAAACATGGA	AGAGGATTCA	TTGTTTTTAT	4260
	TTTTATTTTT	TTAATTTTTT	CTTTTTTATT	AAGCTAGCAT	CTGCCCCAGT	TGGTGTTCAT	4320
	ATAGCACTTG	ACTCTGCCGT	TGATATCTGT	ATCTTTTCTC	TAATCAGAGA	TACAGAGGTT	4380
25	GAGTATAAAA	TAAACTGTCT	CAGATAGGAC	AATTAAGTGC	ACTGTACAAT	TTTCCCAGTT	4440
	TACAGGTCTA	TACTTAAGGG	AAAAGTTGCA	AGAAATGCTG	AAAAAAATG	AACACAATCT	4500
	CATTGAGGAG	CATTTTAA	AACTAAAAA	AAAAAAACT	TTGCCAGCCA	TTTACTTGAC	4560
	TATTGAGCTT	ACTTACTTGG	ACGCAACATT	GCAAGCGCTG	TGAATGGA	CAGATACAC	4620
	TTAACATAGA	AATGAATGAT	TGCTTTCGCT	TCTACAGTGC	AAGGATTTTT	TTGTACAAAA	4680
30	CTTTTTTAAA	TAAATAGTGT	AAGAAAAATT	TTTTTTTAAA	AACACTTCAT	TATGTTTAGG	4740
	GGGGAACATG	ATTTAGGCT	TCCATTGTCT	TGGTGGTGT	ACAAGACTTG	TTATCCATTT	4800
	AAAAATGGTA	GTGGAAATTC	TATGCTTGG	ATACACACCG	CTCTTCAGGT	TGTAAAAAAA	4860
	AAAAACATAC	ATTGGGGA	GGTTTAAGAT	TATATAGTAC	TTAAATATAG	GAATATGCAC	4920
	ACTCATGTTG	ATTCCATATG	TAAATACAT	TTATGGTCTT	TTTTCTGTAT	TTCTAGAAATG	4980
35	GTATTTGAAT	TAAATGTCTA	TCTAGTGTTA	GGCACTATAG	TATTTATATT	GAAGCTTGTA	5040
	TTTTTAACCTG	TGCTTGTCT	TCTTAAAGG	TATCAATGTA	CCTTTTTGG	TAGTGGAAAA	5100
	AAAAAAGACA	GGCTGCCACA	GATATTTTT	TAAATTTGGC	AGGATAATAT	AGTGCAAAAT	5160
	ATTTGTATGC	TTCAAAAAA	AAAAAAGAG	AGAAACAAAA	AAGTGTGACA	TTACAGATGA	5220
	GAAGCCATAT	AATGGCGGTT	TGGGGGAGCC	TGCTAGAAATG	TCACATGGAT	GGCTGTGCATA	5280
40	GGGGTTGTAC	ATATCTTTTT	TTGTTCTTTT	TTCTGTCTGC	CATATGTAT	GCAGTACTGC	5340
	AAGCTAATAA	OGTTGGTTTG	TTATGTAGTG	TGCTTTTGT	CCCTTTCTCT	CTATCACCTT	5400
	ACATTCACAG	CTCTTACCTT	CATATGCAGT	AAAAGAAAGA	AAGAAAAAAA	AAGGAAAAAA	5460
	AAAAAAAAC	CAATGTTTTG	CAGTTTTTTT	CATTGCCAAA	AACTAAATGG	TGCTTTATAT	5520
	TTAGATTGGA	AAGAATTTCA	TATGCAAAAG	ATATTAAAGA	GAAAGCCCGC	TTTACTCAAT	5580
45	ACTTTTTTGT	AATGTGCAAT	GCAGAAATAT	TTGTTATTGG	CCTTTTCTAT	TCCTGTAAATG	5640
	AAAGCTGTTT	GTGTAACAT	GAAATTTTAT	CTTTTACTAT	GGGAGTCACT	ATTTATTATT	5700
	GCTTATGTGC	CCTGTTTCAA	ACAGAGGCAC	TTAATTTGAT	CTTTTATTTT	TCTTTGTTTT	5760
	TATTTTTTTT	TTTATTTAGA	TGACCAAAAG	TCATTACAAC	CTGGCTTTTT	ATTGTATTTG	5820
	TTTCTGGTCT	TTGTTAAGTT	CTATTGGA	AACCACTGTC	TGTGTTTTTT	TGGCAGTTGT	5880
50	CTGCATTAA	CTGTTACATC	ACCCATTTTG	TCCCTTTATT	GAAAAAATAA	AAAAAATTAA	5940

Seq ID NO: 85 Protein sequence:
Protein Accession #: NP_075044.1

55	1	11	21	31	41	51	
	MSRRKQGRKP	HLKREFSPE	PLEAILTDEE	PDHGFPLGAP	GDHDLTTCGQ	QMNFFPLGDI	60
	LIFIEHKRQK	CNGSLCLEKA	VDKPPSPSP	EMKKASNPVE	VGIQVTPEDD	DCLSTSSRR	120
60	CPKQEHIAAD	LLHWRGLSSP	RSAGHALIPT	PGMSAEYAPQ	GICKDEPSSY	TCTTCKQFFT	180
	SAWFLQHAQ	NTHGLRIYLE	SEHGSPLTFR	VGIPSGLGAE	CPSPPLHGI	HIADNNPFL	240
	LRIPGSVSR	ASGLAEGRFP	PTPPLFSPPP	RHLLDPHRIE	RLGAEMALA	THPSAFDRV	300
	LRLNEMAMEP	PAMDFSRRLR	ELAGNTSSFP	LSFGRPSFMQ	RLLPFPQPS	KPPFLATPPL	360
	PPLQSAPPPS	QPPVKSKECE	FCGKTFKFS	NLVVHRRSHT	GEKPYKCNLC	DHACTQASKL	420
65	KRHKMTHMHK	SSPMTVKSDD	GLSTASSPEP	GTSDLVGSAS	SALKSVVAKF	KSENDPNLIP	480
	ENGDEEEED	DEEBEEEEEE	EEBELTESER	VDYGFGLSLE	AARHHENSSR	GAVVGVDGDS	540
	RALPDVMQGM	VLSSMQHFSE	APHQVLGEKH	KRGHLABAE	HRDTCDEDSV	AGESDRIDDD	600
	TVNGRGCSFG	ESASGGLSKK	LLGLSPSSLS	PFSKRIKLEK	EPDLPPATMP	NTENVYSQWL	660
	AGYAAARQLK	DPPLSFQDSR	QSPFSSSEH	SENGSLRFS	TPPGELDGGI	SGRSVTGSGG	720
70	STPHISGPCT	GRPSSKEGRR	SDTCEYCGKV	PKNCSNLTVH	RRSHTGERPY	KCELCNYACA	780
	QSSKLTRHMK	THQVGKDVY	KCEICKMPFS	VYSTLEKHKM	KWHSRVLN	DIKTE	

Seq ID NO: 86 DNA sequence
Nucleic Acid Accession #: XM_035292.2
Coding sequence: 53-1576

75	1	11	21	31	41	51	
80	GCTCGCTGGG	CCGCGGCTCC	CGGGTGTCCC	AGGCCCGGCC	GGTGCGCAGA	GCATGGCGGG	60
	TGCGGGCCCG	AAGCGGCGCG	CGCTAGCGGC	GCCGGCGGCC	GAGGAGAAGG	AAGAGGCGCG	120
	GGAGAAGATG	CTGGCGCGCA	AGAGCGCGGA	CGGCTCGGCG	CGGCGAGGCG	AGGGCGAGGG	180
	CGTGACCTCTG	CAGCGGAACA	TCACGCTGCT	CAACGGCGTG	GCCATCATCG	TGGGGACCAT	240
	TATCGGCTCG	GGCATCTTGG	TGACGCCAC	GGCGGTGCTC	AAGGAGGCAG	GCTCGCGGG	300
85	GCTGGCGCTG	GTGGTGTGGG	CGCGTGGCG	CGTCTTCTCC	ATCGTGGGCG	CGCTCTGCTA	360
	GGCGGAGCTC	GGCACCACCA	TCTCCAAATC	GGCGGCGGAC	TACGCTACAC	TGCTGGAGGT	420
	CTACGCGCTG	CTGCGCGCTC	TCTCAAGCT	CTGGATCGAG	CTGCTCATCA	TCCGCGCTTC	480
	ATCGCAGTAC	ATCGTGGCCC	TGGTCTTCGC	CACCTACCTG	CTCAAGCCGC	TCTTCCCCAC	540

CTGCCCGGTG CCCGAGGAGG CAGCCAAGCT CGTGGCCTGC CTCTGCGTGC TGCTGCTCAC 600
 GGCCTGGAAC TGCTACAGCG TGAAGGCCGC CACCCGGGTC CAGGATGCCT TTGCCGCGCG 660
 CAAGCTCCTG GGCCTGGCCC TGATCATCCT GCTGGGCTTC GTCCAGATCG GGAAGGGTGA 720
 TGTGTCCAAT CTAGATCCCA ACTTCTCATT TGAAGGCACC AAAGTGGATG TGGGGAACAT 780
 TGTGCTGGCA TTATACAGCG GCCTCTTTGC CTATGGAGGA TGAATTACT TGAATTTCTG 840
 CACAGAGGAA ATGATCAACC CCTACAGAAA CTTGCCCTCG GCCATCATCA TCTCCCTGCC 900
 CATCGTGACG CTGGGTGTACG TGCTGACCAA CCTGGCCTAC TTCACCACCC TGTCCACCGA 960
 GCAGATGCTG TCGTCCGAGG CCGTGGCCGT GGACTTCGGG AACTATCACC TGGGCGTCAT 1020
 GTCCCTGGATC ATCCCCGTCT TCGTGGGCCT GTCTGCTTC GGCTCCGTCA ATGGGTCCCT 1080
 GTTCACATCC TCCAGGCTCT TCTTCGTGGG GTCCCGGAA GGCCACCTGC CCTCCATCCT 1140
 CTCATGATC CACCCACAGC TCCTACCCC CGTGGCGTCC CTCGTGTTCA CGTGTGTGAT 1200
 GACGCTGCTC TACGCTTCT CCAAGGACAT CTTCTCCGTC ATCAACTTCT TCAGCTTCTT 1260
 CAACTGGCTC TGGTGGCCCC TGGCCATCAT CGGCATGATC TGGCTGCGCC ACAGAAAGCC 1320
 TGAGCTTAGG CGGCCCATCA AGGTGAACCT GGCCCTGCCT GTGTCTTCA TCCTGGCCTG 1380
 CCTCTTCTG ATCGCGCTCT CCTTCTGGAA GACACCCGTG GAGTGTGGCA TCGGCTTCAC 1440
 CATCATCTC AGCGGCTGC CGCTCACTT CTTGGGGTCT TGGTGGAAAA ACAAGCCCAA 1500
 GTGGCTCCTC CAGGGCATCT TCTCCACGAC CGTCTGTGT CAGAAGCTCA TGCAGGTGGT 1560
 CCCCCAGGAG ACATAGCCAG GAGGCCGAGT GGCTGCCGGA GGAGCATGC

Seq ID NO: 87 Protein sequence:
 Protein Accession #: XP_035292.2

1 11 21 31 41 51
 MAGAGPKRRA LAAPAAEBKE EAREKMLAAK SADGSAPAGE GEGVTILQRNI TLLNGVAIIV 60
 GTIIGSGIFV TPTGVLEKAG SGLALVWMA ACGVFSIVGA LCYAEIGTTI SKSGGDYAYM 120
 LEVYGSLLPAF LKLWIELLII RPSSQYIVAL VFATYLLKPL PPTCPVPEEA AKLVACLVL 180
 LLTAVNCYSV KAATRVQDAF AAKLLALAL IILGPFVQIG KGDVSNLDPN FPFEGTKLVD 240
 GNIVLALYSG LFAYGGWNYL NFVTEEMINP YRNPLALIII SLPIVTLVYV LTNLAYPTTL 300
 STEQMLSSSEA LAVDFGNHYL GVMSWIIIPV VGLSCFGSVN GSLFTSSRLF FVSGREGLHP 360
 SILSMIHPQL LVTPVPSLVFT VMTLLLYAFS KDIFSVINFP SPFNWLCVAL AIGMIWLRH 420
 RKPELERPIK VNIALPVFFI LACLFILAVS FWKTFVECGI GPTIILSLPL VYFFGVWVWN 480
 KPKNLLQGIF STTVLCQKLM QVVPQET

Seq ID NO: 88 DNA sequence
 Nucleic Acid Accession #: NM_005268.1
 Coding sequence: 168-989

1 11 21 31 41 51
 TAAAAAGCAA AAGAAATTCGC GGCCTGGCTG ACACGGGCTT CCCCAGAAAC CTTCCTCCGT 60
 TCTGGATATG AAATTCAGAG TGCTTGCTGA GTCTATTGCG CGGCTGCTGG GAGCCAGGAG 120
 AGCCCTGAGG AGTAGTCACT CAGTAGCAGC TGACGCGTGG GTCCACCATG AACTGGAGTA 180
 TCTTTGAGGG ACTCCTGAGT GGGGTCAACA AGTACTCCAC AGCCTTTGGG CGCATCTGGC 240
 TGTCTCTGGT CTTCATCTTC CGCGTGTGG TGTACCTGGT GACGCGCCAG CGTGTGTGGA 300
 GTGATGACCA CAAGGACTTC GACTGCAATA CTCGCCAGCC CGGCTGCTCC AACGTCTGCT 360
 TTGATGAGTT CTTCCTCTGT TCCCATGTGC GCCTCTGGGC CTTGCACTT ATCTGTGTGA 420
 CATGCCCTC ACTGCTCGTG GTCATGCACG TGGCCTACCG GGAGGTTTCA GAGAAGAGGC 480
 ACCGAGAAGC CCAATGGGAG AACAGTGGGC GCCTCTACCT GAACCCCGCG AAGAAGCGGG 540
 GTGGGCTCTG GTGACATAT GTCTGCAGCC TAGTGTTCAA GGCGAGCGTG GACATCGCCT 600
 TTCTCTATGT GTTCCACTCA TTCTACCCCA AATATATCCT CCTCTCTGTG GTCAGTGCC 660
 ACGCAGATCC ATGTCCCAAT ATAGTGGACT GCTTCATCTC CAAGCCCTCA GAGAAGAACA 720
 TTTTCAACCT CTTCATGGTG GCCACAGCTG CCACTGTGAT CTGTCTCAAC CTCGTGGAGC 780
 TCATCTACCT GGTGAGCAAG AGATGCCACG AGTGCCTGGC AGCAAGGAAA GCTCAAGCCA 840
 TGTGCACAGG TCATACCTTC CACGGTACCA CCTCTCTCTG CAAACAAGAC GACCTCCTTT 900
 CGGGTGACCT CATCTTCTG GGTCTCAGCA GTCATCTTCC TCTCTTACCA GACCGCCCC 960
 GAGACCATGT GAAGAAAACC ATCTTGTGAG GGGCTGCTCG GACTGGTCTG GCAGGTGGG 1020
 CCTGGATGGG GAGGCTCTAG CATCTCTCAT AGGTGCAACC TGAGAGTGGG GGAGCTAAGC 1080
 CATAGGTAG GGGCAGGCAA GAGAGAGGAT TCAGACGCTC TGGGAGCCAG TTCCTAGTCC 1140
 TCAACTCCAG CCACCTGCC CAGCTCGACG GCACTGGGCC AGTTCGCCCT CTGCTCTGCA 1200
 GCTCGGTTTC CTTTCTAGA ATGGAATAG TGAGGGCCAA TGC

Seq ID NO: 89 Protein sequence:
 Protein Accession #: NP_005259.1

1 11 21 31 41 51
 MNWSIFEGLL SGVNYSTAF GRWLVLVFI FRVLVYLVT A ERVWSDHDKD FDCNTRQPGC 60
 SNVCFDEFFP VSHVRLWALQ LILVTCPSLL VMHVAYREV QEKRRHREAHG ENSGRLYLNP 120
 GKRRGGLWWT VVCSLVFKAS VDIAPLYVPH SFYPKYILPP VVKCHADPCP NIVDCFISKP 180
 SEKNIFTLFM VATAAICILL NLVELIYLV KRCHECLAAR KAQAMCTGHH PHGTTSSCKQ 240
 DDLLSGDLIF LGSDSHPPLL PDRPRDHVKK TIL

Seq ID NO: 90 DNA sequence
 Nucleic Acid Accession #: NM_002391.1
 Coding sequence: 26-457

1 11 21 31 41 51
 CGGGCGAAGC AGCGCGGGCA GCGAGATGCA GCACCGAGGC TTCTCTCTCC TCACCTCCT 60
 CGCCTCTGCT GCGCTCACCT CCGCGGTGCG CAAAAAGAAA GATAAGGTGA AGAAGGGCGG 120
 CCGGGGGAGC GAGTGCCTG AGTGGGCTG GGGGCCCTGC ACCCCAGCA GCAAGGATTG 180
 CGGCTGGGT TTCCGCGAGG GCACCTGCGG GGCCAGACC CAGCGCATCC GGTGCAGGCT 240
 GCCCTGCAAC TGAAGAAGG AGTTGGAGC CGACTGCAAG TACAAGTTT AGAAGCTGGG 300
 TCGTGTGAT GGGGGCAGC GCACCAAGT CCGCAAGGC ACCCTGAAGA AGCGCGCTA 360

CAATGCTCAG TGCCAGGAGA CCATCCGCGT CACCAAGCCC TGACCCCCCA AGACCAAAGC 420
 AAAGGCCAAA GCCAAGAAAG GGAAGGGAAA GGACTAGACG CCAAGCCTGG ATGCCAAGGA 480
 GCCCCTGGTG TCACATGGGG CCTGGGCCAG CCCTCCCTCT CCCAGGCCCG AGATGTGACC 540
 CACCAGTGCC TTCTGTCTGC TCGTAGCTT TAATCAATCA TGCCTGGCCT TGTCCCTCTC 600
 ACTCCCCAGC CCCACCCTTA AGTGCCCAAA GTGGGGAGGG ACAAGGGATT CTGGGAAGCT 660
 TGAGCCTCCC CCAAGCAAT GTGAGTCCCA GAGCCCGCTT TTGTTCTTCC CCACAATTCC 720
 ATTACTAAGA AACACATCAA ATAAACTGAC TTTTCCCTCC CAATAAAAGC TCTTCTTTT 780
 TAATAT

Seq ID NO: 91 Protein sequence:
 Protein Accession #: NP_002382.1

1 11 21 31 41 51
 | | | | |
 MQHRGFLLLT LLALLALTSA VAKKKDKVKK GPGSECAEW AWGPCTPSSK DGVGFREGT 60
 CGAQTRIRRC RVPCNWKKEF GADCKYKFEN WGACDGGTGT KVRQGTLRKA RYNAQCQRTI 120
 RVTKPCTPKT KAKAKARKGK GKD

Seq ID NO: 92 DNA sequence
 Nucleic Acid Accession #: NM_005130.1
 Coding sequence: 98-802

1 11 21 31 41 51
 | | | | |
 CTCTACCTGA CACAGCTGCA GCCTGCAATT CACTCCCACT GCCTGGGATT GCACTGGATC 60
 CGTGTGCTCA GAACAAGGTG AACGCCCAGC TGCAGCCATG AAGATCTGTA GCCTCACCCT 120
 GCTCTCCTTC CTCTACTGCG CTGCTCAGGT GCTCCTGGTG GAGGGGAAAA AAAAAGTGAA 180
 GAAATGACTT CACAGCAAAAG TGGTCTCAGA ACAAAGGAC ACTCTGGGCA ACACCCAGAT 240
 TAAGCAGAAA AGCAGGCCCG GGAACAAAGG CAAGTTTGTC ACCAAAGACC AAGCCAACTG 300
 CAGATGGGCT GCTACTGAGC AGGAGGAGGG CATCTCTCTC AAGGTTGAGT GCACTCAATT 360
 GGACCATGAA TTTTCTGTGT TCTTTGCTGG CAATCCAACC TCATGCCTAA AGCTCAAGGA 420
 TGAGAGAGTC TATTGGAAAC AAGTTGCCCG GAATCTGCGC TCACAGAAAG ACATCTGTAG 480
 ATATTCCAAG ACAGCTGTGA AAACCAAGAG GTGCAGAAAG GATTTTCCAG AATCCAAGTCT 540
 TAAGCTAGTC AGCTCCACTC TATTGGGAA CACAAAGCCC AGGAAGGAGA AAACAGAGAT 600
 GTCCCCCAGG GAGCACATCA AGGCAAAAGA GACCACCCCT TCTAGCCTAG CAGTGACCCA 660
 GACCATGGCC ACCAAAGCTC CCGAGTGTGT GGAGGACCCA GATATGGCAA ACCAGAGGAA 720
 GACTGCCCTG GAGTTCTGTG GAGAGACTTG GAGCTCTCTC TGCACATTCT TCCTCAGCAT 780
 AGTGCAGGAC ACCTCATGCT AATGAGGTCA AAAGAGAACG GGTTCCTTTA AGAGATGTCA 840
 TGTGTAAGT CCCTCTGTAT ACTTTAAAGC TCTCTACAGT CCCCCCAAAA TATGAACCTT 900
 TGTGCTTAGT GAGTGCAACG AATATTTTAA ACAAGTTTGT TATTTTGTGC TTTTGTGTTT 960
 TGGAAATTTG CTTATTTTTC TTGGATGCGA TGTTCAGAGG CTGTTTCCTG CAGCATGTAT 1020
 TTCCATGGCC CACACAGCTA TGTGTTTGTG CAGCGAAGAG TCTTTGAGCT GAATGAGCCA 1080
 GAGTGATAAT TTCAGTGCAA CGAACTTTCT GCTGAATTAA TGGTAATAAA ACTCTGGGTG 1140
 TTTTTCAAAA AAAAAAAAAA AAA

Seq ID NO: 93 Protein sequence:
 Protein Accession #: NP_005121.1

1 11 21 31 41 51
 | | | | |
 MKICSLTLLS FLLLAQVLL VEGKKKVKNG LHSKVVSQK DTLGNTQIKQ KSRPKNKGKP 60
 VTKDQANCRW AATEQEEGIS LKVECTQLDH EFSCVFAGNP TSCLKLKDER VYWKQVARNL 120
 RSQKDICRYS KTAVKTRVCR KDFPESSLKL VSSTLFGNTK PRKEKTEMSF REHIKKEKTT 180
 PSSLAVTQTM ATKAPECED PDMAQRKTA LEFCGETWSS LCTFFLSIVQ DTSC

Seq ID NO: 94 DNA sequence
 Nucleic Acid Accession #: NM_012101
 Coding sequence: 125-1891

1 11 21 31 41 51
 | | | | |
 CTCCTCACAG GTGTGTCTCT AGTCCTCGTG GTTGCTGCCC CCACTCCCTG CCGAGACGCC 60
 TGCCAGAAAG GTCACCTATC CTGAACCCCA GCAAGCCTGA AACAGCTCAG CCAAGCACCC 120
 TCGATGGAA GCTGCAGATG CCTCCAGGAG CAACGGGTGG AGCCAGAGAG CCAGGGATGC 180
 CCGGAGCCCG TCGGGCCCCA GTGGCAGCCT GGAGAAATGC ACCAAGGCTG ACGGCAAGGA 240
 TGCCAGAGCC ACCAACGGGC ACGCGCGGGA GGCAGCTGAG GGCAAGAGCC TGGGCAGCGC 300
 CCTGAAGCCA GCGGAAGGTA AGAGCGCCTT GTTCGCGGGC AATGAGTGGC GGCAGCCCAT 360
 CATCCAGTTT GTCGAGTCCG GGGACGACAA GAACTCCAAC TACTTCAGCA TGGACTCTAT 420
 GGAAGGCAAG AGGTGCGCGT ACGCAGGGCT CCAGCTGGGG GCTGCCAAGA AGCCACCCGT 480
 TACCTTTGCC GAAAAGGGCG ACGTGCACAA GTCCATTTTC TCGGAGTCCC GGAAGCCAC 540
 GGTGTCCATC ATGGAGCCCG GGGAGACCCG GCGGAACAGC TACCCCCGGG CCGACACGGG 600
 CCTTTTTCCT CCGTCCAAGT CCGGCTCCGA GGAGGTGCTG TGGAGTCTCT GCATCGGCAA 660
 CAAGCAGAA GCGGTCAAGT CCGCTCTGGT GTGCCAGGCC TCCTTCTGCG AGCTGCATCT 720
 CAAGCCCCAC CTGGAGGGCG CCGCTTCCG AGACCCACAG CTGCTCGAGC CCATCCGGGA 780
 CTTTGAGGCC CGCAAGGTGTC CCGTGATGG CAAGACGATG GAGCTCTTCT GCCAGACGGA 840
 CCAGACCTGC ATCTGCTACC TTTGATGTT CCAGAGCAC AAGAAATCATA GCACCGTGAC 900
 AGTGGAGGAG GCGGAAGGCG AGAAGGAGAC GGAGCTGTCA CTGCAAAAGG AGCAGCTGCA 960
 GCTCAAGATC ATTGAGATTG AGGATGAAGC TGAGAAGTGG CAGAAGGAGA AGGACCGCAT 1020
 CAAGAGCTTC ACCACCAATG AGAAGGCCAT CCTGGAGCAG AACTTCCGGG ACCTGGTGGC 1080
 GGACCTGGAG AAGCAAAAGG AGGAAGTGAG GGCTGCGCTG GAGCAGCGGG AGCAGGATGC 1140
 TGTGGACCAA GTGAAGGTGA TCATGGATGC TCTGGATGAG AGAGCCAAGG TGCTGCATGA 1200
 GGACAGCAG ACCCGGAGC AGCTGCATAG CATCAGCGAC TCTGTGTTGT TTCTGCAGGA 1260
 ATTTGGTGCA TTGATGAGCA ATTACTCTCT CCCCCACCC CTGCCCACT ATCATGTCTT 1320
 GCTGGAGGGG GAGGGCCTGG GACAGTCACT AGGCAACTTC AAGGACGACC TGCTCAATGT 1380
 ATGCATGGCG CACGTTGAGA AGATGTGCAA GGCGGACCTG AGCCGTAAC TCACTGAGAG 1440
 GAACCATAG GAGAACGGTG GTGACCATCG CTATGTGAAC AACTACACGA ACAGCTTCGG 1500

GGGTGAGTGG AGTGACCCGG ACACCATGAA GAGATACTCC ATGTACCTGA CACCCAAAGG 1560
 TGGGTGCCGG ACATCATACC AGCCCTCGTC TCCTGCGCGC TTCACCAAGG AGACCAACCA 1620
 GAAGAAATTC AACATCTCT ATGGCACCAG AGGTAACCTAC ACCTCCCGGG TCTGGGAGTA 1680
 CTCCTCCAGC ATTCAGAACT CTGACAAATGA CCTGCCCGTC GTCCAAGGCA GCTCCTCTTT 1740
 CTCCTCGAAA GGCTATCCCT CCCTCATGCG GAGCCAAAGC CCCAAGGCCC AGCCCCAGAC 1800
 TTGGAATCT GGCAAGCAGA CTATGCTGTC TCACTACCGG CCATTCTACG TCAACAAAGG 1860
 CAACGGGATT GGGTCCAAAG AAGCCCCATG AGCTCCTGGC GGAAGGAACG AGGCGCCACA 1920
 CCCCTGCTCT TCCTCCTGAC CCTGCTGCTC TTGCTTCTTA AGTACTGTG CTGTCTGGG 1980
 TGGGAGGGAG CTTGGTCTGT CACCTGCCCT CTGCAGCCCT CTGCCAGCCT CTTGGGGGCA 2040
 GTTCCGGCCT CTCGCACTTC CCCACTGGCC AACTCCATT CAGACTCCTT TCCTGCTTG 2100
 TGACCTCAGA TGGTCACCAT CATTCCTGTG CTCAGAGGCC AACCCATCAC AGGGGTGAGA 2160
 TAGGTTGGGG CCTGCCCTAA CCCGCCAGCC TCCTCCTCTC GGGCTGGATC TGGGGGCTAG 2220
 CAGTGAGTAC CGCAGCTTAA TCAGCCCTGCC TCCTCCGCCC ACGCCCTGCT GTCTCCAGGC 2280
 CTATAGACGT TTCTCTCCAA GGCCTATACC CCCAATGTTG TCAGCAGATG CCTGGACAGC 2340
 ACAGCCACCC ATCTCCCATT CACATGGCCC ACCTCCTGCT TCCAGAGGA CTGGCCCTAC 2400
 GTGCTCTCTC TCGTCTTACC TATCAATGCC CAGCATGGCA GAACCTGCAG TGGCCAAAGG 2460
 CTGCAGATGG AAACCTCTCA GTGTCTTGAC ATCACCCTAC CCAGGCGGTG GGTCTCCACC 2520
 ACAGCCACTT TGAGTCTGTG GTCCCTGGAG GGTGGCTTCT CCTGACTGGC AGGATGACCT 2580
 TAGCCAAGAT ATTCTCTGTG TCCTCTGCT GAGATAAAGA ATTCCTTAA CATGATATA 2640
 TCCACCCATG CAAATAGCTA CTGGCCAGC TACCATTAC CATTGCTTA CAGAAATTTCA 2700
 TTCAGTCTAC ACTTTGGCAT TCTCTCTGCG GATGGAGTGT GGTGGGCTG ACCGCAAAAG 2760
 GTGCCCTTACA CACTGCCCCC ACCCTCAGCC GTTGCCCAT CAGAGGCTGC CTCTCTCTC 2820
 TGATTACCCC CCATGTTGCA TATCAGGGTG CTCAGGATT GGAGAGGAGA CAAACCAGG 2880
 AGCAGCACAG TGGGACATC TCCGCTCTCA ACAGCCCAAG GCCTATGGGG GCTCTGGAAG 2940
 GATGGGCCAG CTTGACGGGG TTGGGGAGGG AGACATCCAG CTTGGGCTTT CCCCTTGA 3000
 ATAAACCATT GGTCTGTC

Seq ID NO: 95 Protein sequence:
 Protein Accession #: NP_036233.1

1 11 21 31 41 51
 MEAADASRSN GSSPEARDAR SPSGSPSGSLE NGTKADGKDA KTTNGHGGEA AEGKSLGSAL 60
 KPGEGRSALP AGNEWRRPII QFVESGDDKN SNYFSMDSME GKRSYPAGLQ LGRAAKPPVT 120
 FAEKGDVRKS IPFSESRKPTV SIMEPGETRR NSYPRADTGL FSRKSGSSEE VLCDSCIGNK 180
 QKAVKSCLVK QASFCLEHLK PHLEGAAPRD HQLEPIRDF EARKCPVHGK TMELFCQTDQ 240
 TCICYLCMFQ EHKHNSHTVTV EBAKAEKETE LSLQKEQLQL KIIEIEDEAE KWQREKDRIK 300
 SFTTNEKAIL EONFRDLVRD LEKQKEEVRA ALEQRBDQAV DQVKVIMDAL DERAKVLHED 360
 KQTRQLHSI SDLVFLQEF GALMSNYSLP PPLETYHVLL EGEGLGQSLG NFKDDLNLVC 420
 MRHVEKMCKA DLGRNFIERN HMENGGDHRY VNNYTNFSGG ENSAPDTMKR YSMYLTPEKGG 480
 VRTSYQSSP GRPTKETTKO NFNNLYGTKG NYTSRVWEYS SSIQNSDNDL FVVQSSSFS 540
 LKGYPSLMRS QSPKAQPQTW KSGKQTMLSH YRPFYVKNKG GIGSNEAP

Seq ID NO: 96 DNA sequence
 Nucleic Acid Accession #: NM_080668.1
 Coding sequence: 83-841

1 11 21 31 41 51
 GGCACGAGGG CAGCGAGTGG CCTTCCCGGT TGGCGCGCGC CCGGGGCGGC GGCCTGGAG 60
 GAGCTCGAGA CGGAGCCTAG TTATGTCTGG GAGGCGAACG CGGTCCGGAG GAGCCGCTCA 120
 GCGCTCCGGG CCAAGGGCCC CATCTCCTAC TAAGCCTCTG CCGAGGTCCC AGCGGAAATC 180
 AGGCTCTGAA CTCCCGAGCA TCCTCCCTGA AATCTGGCCG AAGACACCCA GTGCGGCTGC 240
 AGTCAGAAAG CCCATCGTCT TAAAGAGGAT CGTGGCCCAT GCTGTAGAGG TCCAGCTGT 300
 CCAATCACTC CGCAGGAGCC CTAGGATTTC CTTTTCTTG GAGAAAGAAA ACGAGCCCCC 360
 TGGCAGGGAG CTTACTAAGG AGGACCTTTT CAAGACACAC AGCGTCCCTG CCACCCCCAC 420
 CAGCACTCCT GTGCCGAACC CTGAGGCCGA GTCCAGCTCC AAGGAAGGAG AGCTGGAAGC 480
 CAGAGACTTG GAAATGTCTA AGAAAGTCAG GCGTTCCTAC AGCCGCTGAG AGACCTGGG 540
 CTCTGCTCTT ACCTCCACCC CAGGCCCGCG GTCTCTGCTT GGCTTCGAGG GGCTGCTGGG 600
 GGCAGAAAGC TTGTCCGGAG TCTCGCCAGT GGTGTGCTCC AAATCACCAG AGGTCCCCAG 660
 GGTGTGTGCA AAGCCCTGGG CCCAGACAT GACTCTCCCT GGAATCTCCC CACCACCCGA 720
 GAAACAGAAA CGTAAGAAGA AGAAAATGCC AGAGATCTTG AAAACGGAGC TGGATGAGTG 780
 GGCTGCGGCC ATGAATGCCG AGTTTGAAGC TGCTGAGCAG TTTGATCTCC TGGTTGAATG 840
 AGATGCAATG GGGGGTGAC CTGGCCAGAC TCTCCCTCCT GTCTGTACA TAGCCACCTC 900
 CCTGTGAGGA GGAACCTTAG GGTCCCTTCC CTTGCTCTTG TTACCTGTGT GTGTGCTGGT 960
 GCTGCGCATG AGGACTGTCT GCCTTTGAGG GCTTGGGCGC CAGCGGCAGC CATCTTGTT 1020
 TTAGGAAATG GGGCCGCTG GCCAGCCAC TCACTGGTGT CCTGTCTCTT GTCGTCTGT 1080
 CCTTCTATC TCCCAAAGT ACCATAGCCA GTTCCAGAT GGGCCACAGA CTGGGGAGGA 1140
 GAATCAGTGG CCCAGCCAGA AGTTAAAGGG CTGAGGGTTG AGGTGAGAGG CACCTCTGCT 1200
 CTTGTTGGGA GGGGTGCTG CTGGGAAATA GCGCCAGGGG CTCTGCCAGC CTCGGCTCT 1260
 CCCTCCTGAG TTGCTTCTG TTGGTGGCTT TCTTCTTCAA CCCACCTGTG TAAAGAGGTT 1320
 TTCAGTTCCT TGGGTTTCCC CTTTGATTCT GTAAATAGTC CCAGAGAGAA TTCGTGGGCT 1380
 GAGGGCAATT CTGTCTTGGG GGAAGAAGCT GGACATTGAG CCTGTGGAGT CTGAGTTTGT 1440
 AAGGATGTAG GAGGCTTAG TTGGGTCTCA GACCATAAGT GTGTACTACA CAGAAGCTGT 1500
 GTTTCTAGT TGTGGTCTGC TTTTGAATG TTTGTAATG GCCAGGTGTA TAGGGCGCTG 1560
 GCTGCTTGA GCAAGGGGTG CATTTAGGGG TGTGGCCACC AGGTGCTGTG AGTTTCTGTG 1620
 GCTCATGGCC LCTRNGICTG TCCCTTGCAC AGGGCCCAAG CTGGAGTCTT ACCACTCTGC 1680
 TGCAGGGGTG GAAGGTGGCC CCTCTTGTCA CCCATACCCA TTTCTTACAA AATAAGTTAC 1740
 ACCGAGTCTA CTGGGCCCTA GAAGAGAAAG TTGAAGAGTC CCAGACCTAC TAGCATTTTG 1800
 CAACTATGCT TGTAAGTCTC TCGGAAAGTT TCTCGCGTGA CCAGACAGCG GCGGGGGCTG 1860
 ATAGCAATTT TAGTTTGTGG CCTCCCTATC CTCTCACATG AGAACACTGC CTGGATGCAT 1920
 CTCATGATCT CTGAGAAATT TCCCATCTT TCTCTCTTT CCACTCGTGT GATTCAATAG 1980
 TTTGATTTG AAGGCTGCCC TGCCCCGAC TCTCTGCGG CACCCCTGGC CATTGTACCT 2040
 TTTGATGTTT AGAAGTTCGT GGAAGTAGAC GCTGAGGTGT GCAGAGGAGC TGGTGGATAA 2100
 CAGAGAATGC CAGGGAAGAT GAGTGCTGGG TCAGGGTACT TGGATGAAAC GGTGCAGGCC 2160
 AGCGGGGCC TAATAAAACC CTCTGCCAGG TCTGGGAGTC CCAGGCCATC TGCTCAACGC 2220

TCTGTGGTTT GTGAGACCTG CAAGCAAGCC CCCTGCTGGG GAAGCCTAGG TGTCTTGAG 2280
 CTGAACCGCA CTGAAGAACT CTTGTCTCTA CTGGCTGATG CAGCAGAACT CTTGGGAAAT 2340
 GTCTTAGTCT TCACAGATCA GGAGTCACCA GATGATGCAG AGTTGAGATC ATCATTGCAA 2400
 AGTTCTCTGT TCCTGAGGAA CTAAATTTAA GGAAAAATG GGATTTTGT TTAGAGTTGG 2460
 AAAAAAGCC TGATTAAGA GTTCTGCTT GTTAAAAAA AAAAAAAA AAAAAA

Seq ID NO: 97 Protein sequence:
 Protein Accession #: NP_542399.1

1 11 21 31 41 51
 MSGRRTRSGG AAQRSGPRAP SPTKPLRRSQ RKSGSELPSI LPEIWPKTPS AAARVKPIVL 60
 KRIVAHAVEV PAVQSPRRSP RISFFLEKEN EPPGRELTKE DLFKTHSVPA TPTSTPVFNP 120
 EAESSSEKEG LDARDLEMSK KVRRSYSRLT TLGSASTSTP GRRSCFGFEG LLGAEDLSGV 180
 SPVVCCKLTE VPRVCAKPWA PDMTLPGISP PFEKQKRRKK KMPEILKTEL DEWAAAMNAE 240
 FEAAEQPDLL VE

Seq ID NO: 98 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 58-12444

1 11 21 31 41 51
 GGGGCATTTC CGGGTCCGGG CCGAGCGGGC GCACGCGGGG GAGCGGGACT CGGCGGCATG 60
 GCGGGCTCCG GAGCCGGTGT GCGTTGCTCC CTGCTGCGGC TGCAGGAGAC CTTGTCCGCT 120
 GCGGACCGCT GCGGTGCTGC CCGGCGCGGT CATCAACTGA TCCGCGCGCT GGGGCAGGAA 180
 TCGTCTCTGA GCAGCAGCCC CCGGTGCTG GCATTACAGA CATCTTAGT TTTTCCAGA 240
 GATTTCCGTT TGCTTGATTT TGTCCGGAAG TCACCAACA GTATTGAAT TCGTGAATGT 300
 AGAGAAGAAA TGCTAAAGTT TTTATGATTT TCTTAGAAAA AAATGGGCCA GAAGATCGCA 360
 CCTTACTCTG TTGAAATTA GAACACTTGT ACCAGTGT TTACAAAAGA TAGAGCTGCT 420
 AAATGTAAAA TTCCAGCCCT GGACCTTCTT ATTAAGTTAC TTCAGACTTT TAGAAGTTCT 480
 AGACTCATGG ATGAATTTAA AATTGGAGAA TTATTTAGTA AATTCATAGG AGAAGTTGCA 540
 TTGAAAAAAA AAATACCAGA TACAGTTTAA GAAAAAGTAT ATGAGCTCCT AGGATTATTG 600
 GGTGAAGTTT ATCTTAGTGA GATGATAAAT AATGCAGAAA ACCTGTTCCG CGCTTTCTG 660
 GGTGAACCTA AGACCCAGAT GACATCAGCA GTAAGAGAGC CCAAACTACC TGTCTGCGCA 720
 GGATGCTGTA AGGGGTTGTC CTCACCTCTG TGCAACTTCA CTAAGTCCAT GGAAGAGAT 780
 CCCCAGACTT CAAGGGAGAT TTTTAATTTT GTACTAAAGG CAATTCGTCC TCAGATTGAT 840
 CTGAAGAGAT ATGCTGTGCC CTCAGCTGGC TTGCGCCTAT TTGCCCTGCA TGCATCTCAG 900
 TTAGCACCTT GCCTTCTGGA CAACTACGTT TCTCTATTG AAGTCTTGT AAAGTGGTGT 960
 GCCCACACAA ATGTAGAAAT GAAAAAGCT GCACCTTCAG CCTTGAATC CTTTCTGAAA 1020
 CAGGTTCTTA ATATGGTGGC GAAAAATGCA GAAATGCATA AAAATAAACT GCAGTACTTT 1080
 ATGGAGCAGT TTTATGGAAT CATCAGAAAT GTGGATTGCA ACAACAAGGA GTTATCTATT 1140
 GCTATCCGTG GATATGAGCT TTTTGCAAGA CGTGCAAGG TTATAAACGC AAAAGATGTT 1200
 GACTTCATGT ACCGTAGAGT CATTCAGCGC TGCAAGCAGA TGTTCCTCAC CCAGACAGAC 1260
 ACTGGTGACG ACCGTGTTTA TCAGATGCCA AGCTTCCTCC AGTCTGTTGC AAGCGTCTTG 1320
 CTGTACCTTG ACACAGTCTC TGAGGTGTAT ACTCCAGTTC TGGAGCACTT CGTGGTGATG 1380
 CAGATAGACA GTTTCACACA GTACAGTCCA AAAATGCAGC TGGTGTGTTG CAGAGCCATA 1440
 GTGAAGGTGT TCTTAGCTTT GGCAGCAAAA GGGCCAGTTC TCAGGAATTG CATTAGTACT 1500
 GTGGTGCACT AGGCTTTAAT CAGAATATGT TCTAAACCAG TGGTCTCTCC AAAGGGCCCT 1560
 GAGTCTGAAT CTGAAGACCA CCGTGCTTCA GGGGAAGTCA GAACTGGCAA ATGGAAGGTG 1620
 CCCACATACA AAGACTACGT GATCTCTTC AGACATCTCC TGAGCTCTGA CCAGATGATG 1680
 GATTCTATTT TAGCAGATGA AGCATTTTTC TCTGTGAATT CCTCCAGTGA AAGTCTGAAT 1740
 CATTTACTTT ATGATGAATT TGTAATATCC GTTTTGAAGA TTGTTGAGAA ATTTGGATCTT 1800
 ACATCTGAAA TACAGACTGT TGGGGAACAA GAGAATGGAG ATGAGGCGCC TGGTGTTTGG 1860
 ATGATCCCAA CTTAGATCTC AGCGGCTAAC TTGCATCCAG CTAAACCTAA AGATTTTTCG 1920
 GCTTTCAATA ACCCTGGTGA ATTTGACAGA GAGATTCTCC CTGAGAAACA AGCAGAAATT 1980
 TTTGAACCAT GGGTGTACTC ATTTTCATAT GAATTAATTT TGCAATCTAC AAGGTTGCC 2040
 CTCATCAGTG GTTCTACAAA ATTGCTTTCT ATTACAGTAA GAAATGCCAA GAAAAATAA 2100
 TATTTGAGG GAGTTAGTCC AAAGAGTCTG AAACACTCTC CTGAAGACCC AGAAAAGTAT 2160
 TCTTGCTTTG CTTTATTGTT GAAATTTGGC AAAGAGGTGG CAGTAAAAAT GAAGCAGTAC 2220
 AAAGATGAAC TTTTGGCTCC TTTCTTCTGT CCTTGCCACA CAACATCATT 2280
 GAACCTGATG TTAGAGCCTA CGTTCCTGCA CTGCAGATGG CTTTCAAAC GGGCCTGAGC 2340
 TATACCCCTT TGCAGAAAGT AGCCCTGAAT GCTCTAGAAG AATGGTCAAT TTATATTGAG 2400
 AGACATGTAA TGCAGCCTTA TTACAAAGAC ATTTCTCCCT GCCTGGATGG ATACCTGAAG 2460
 ACTTCAGCCT TGTCAGATGA GACCAAGAA AACTGGGAAG TGTCAGCTCT TTCTCGGGCT 2520
 GCCCAGAAAG GATTTAATAA AGTGGTGTTA AAGCATCTGA AGAAGACAAA GAACTTTTCA 2580
 TCAACGAAAG CAATATCCTT AGAAGAAATA AGAATTAGAG TAGTACAAAT GCTTGGATCT 2640
 CTAGGAGGAC AAATAAACAA AAATCTCTG ACAGTCACGT CCTCAGATGA GATGATGAAG 2700
 AGCTATGTGG CCTGGGACAG AGAGAAGCGG CTGAGCTTTG CAGTGCCCTT TAGAGAGATG 2760
 AAACCTGTCA TTTTCTCTGA TGTGTTCTCT CCTCGAGTCA CAGAATTAGC GCTCACAGCC 2820
 AGTGACAGAC AAACATAAGT TGCAGCCTGT GAACTTTTAC ATAGCATGGT TATGTTTATG 2880
 TTGGGCAAG CCACGAGATG GCCAGAAAGG GGACAGGGAG CCCCACCCAT GTACCAAGCTC 2940
 TATAAGCGGA CGTTTCTCTG GCTGCTTCGA CTTGCGTGTG ATGTTGATCA GGTGACAAGG 3000
 CAACGTATG AGCCACTAGT TATGCAGCTG ATTCAGTGGT TCACTAACAA CAAGAAATTT 3060
 GAAAGTCAGG ATACTGTGTC CTTACTAGAA GCTATATTGG ATGGAATTGT GGACCTGTT 3120
 GACAGTACTT TAGAGATATT TTGTTGCTCG TGTATTGAG AATTCCTTAA ATGGTCCATT 3180
 AAGCAATAA CACCAAGCA GCAGGAGAA AGTCCAGTAA ACACCAAAAT GCTTTTCAAG 3240
 CGACTTTATA GCCTTGCGCT TCACCCCAAT GCTTTCAAGA GGCTGGGAGC ATCACTTGCC 3300
 TTTAATAATA TCTACAGGGA ATTCAGGGAA GAAGAGTCTC TGGTGGAAAC GTTGTGTTT 3360
 GAAGCCTTGG TGATATACAT GGAGAGTCTG GCCTTAGCAC ATGCAGATGA GAAGTCTCTA 3420
 GGTACAAATC AACAGTGTG TATGCTCATT GATCACTTAT GCGCATCAT TGAAAAAGAG 3480
 CATGTTTCTT TAAATAAAGC AAAGAAACGA CGTTTGGCGG GAGGATTTC ACCTTCCGCA 3540
 TCAATGTGTT TATTGATCT GTTCAAGTGG CTTTATGCTC ATTGTGGGAG GCCCAGACA 3600
 GAATGTGAC ACAAATCCAT TGAATCTTT TATAAATTCG TTCCTTTATT GCCAGGCAAC 3660
 AGATCCCCTA ATTTGTGGCT GAAAGATGTT CTCAAGGAAG AAGGTGTCTC TTTTCTCATC 3720
 AACACCTTTG AGGGGGTGG CTGTGGCGCA CCTGCGGCA TCTGCGCCA GCCACCTC 3780
 TTGTACCTTC GGGGGCCATT CAGCCTGCAG GCCACGCTAT GCTGGCTGGA CTGCTCTCTG 3840

	GCCGCGTTGG	AGTGCTACAA	CACGTTTCATT	GGCGAGAGAA	CTGTAGGAGC	GCTCCAGGTC	3900
	CTAGGTACTG	AAGCCAGTGC	TTCACCTTTTG	AAAGCAGTGG	CTTCTCTCTT	AGAAAGCATT	3960
	GCCATGTCAT	ACATTTATAGC	AGCAGAAAAG	TGCTTTTGCCA	CTGGGGCAGC	AGGTAAACAGA	4020
5	ACAAGCCAC	AAGAGGGAGA	AAGGTACAA	TACAGCAAAT	GCACCGTTGT	GGTCCGGATT	4080
	ATGGAGTTTA	CCACGACTCT	GCTAAACACC	TCCCGGGAAG	GATGGAAGCT	CCTGAAGAAG	4140
	GACTTGTGTA	ATACACACCT	GATGAGAGTC	CTGGTGCAGA	CGCTGTGTGA	GCCCGCAAGC	4200
	ATAGGTTTCA	ACATCGGAGA	CGTCCAGGTT	ATGGCTCATC	TTCTGTATGT	TTGTGTGAAT	4260
	CTGATGAAAG	CTCTAAAGAT	GTCCCCATAC	AAAGATATCC	TAGAGACCCA	TCTGAGAGAG	4320
10	AAAAATAACAG	CACAGAGCAT	TGAGGAGCTT	TGTGCCGTCA	ACTTGTATGG	CCCTGACGGC	4380
	CAAGTGGACA	GGAGCAGGCT	GGCTGCTGTT	GTGTCTGCCT	GTAAACAGCT	TCACAGAGCT	4440
	GGGCTTCTGC	ATAATATATT	ACCGTCTCAG	TCCACAGATT	TGCATCATTC	TGTTGGCACA	4500
	GAACTTCTTT	CCCTGGTTTA	TAAAGGCATT	GCCCTGGAG	ATGAGAGACA	GTGTCTGCCT	4560
	TCTCTAGACC	TGAGTTGTAA	GCAGCTGGCC	AGCGGACTTC	TGGAGTTAGC	CTTTGCTTTT	4620
15	GGAGGACTGT	TGAGAGCGCT	TGTGAGTCTT	CTCCTGAACC	CAGCGGTGCT	GTCCACGGCG	4680
	TCCTTGGGCA	GCTCAGAGGG	CAGCGTCATC	CACCTCTCCC	ATGGGGAGTA	TTTCTATAGC	4740
	TTGTTCTCAG	AAACGATCAA	CACGGAATTA	TTGAAAAATC	TGGATCTTGC	TGTATTGGAG	4800
	CTCATGCACT	CTTCAGTGA	TAATACCAA	ATGGTGAGTG	CCGTTTTGAA	CGGCATGTTA	4860
	GACCAGAGCT	TCAGGAGCG	AGCAAAACAG	AAACACCAAG	GACTGAAACT	TGCGACTACA	4920
20	ATTCTGCAAC	ACTGGAAGAA	TGTGATTCA	TGGTGGGCCA	AAGATTCCCC	TCTCGAAACT	4980
	AAAATGGCAG	TGCTGGCCTT	ACTGGCAAAA	ATTTTACAGA	TTGATTCACT	TGTATCTTTT	5040
	AATACAAGTC	ATGGTTTCATT	CCCTGAAGTC	TTTACAACAT	ATATTAGTCT	ACTTGTCTGAC	5100
	ACAAAGCTGG	ATCTACATTT	AAAGGGCCAA	GCTGTCACTC	TTCTTCCATT	CTTCACCAGC	5160
	CTCACTGGAG	GCAGTCTGGA	GGAACTTAGA	CGTGTCTGG	AGCAGCTCAT	CGTTGCTCAC	5220
25	TTCCCATGCG	AGTCCAGGGA	ATTTCTCCA	GGAACTCCGC	GGTTCAATAA	TTATGTGGAG	5280
	TGCATGAAAA	AGTTTCTAGA	TGCATTGGAA	TTATCTCAAA	GCCCTATGTT	GTGGGAATTG	5340
	ATGACAGAA	TTCTTTCTCG	GGAAACAGCAG	CATGTCTGGA	AAGAATTATT	TCAATCCAGT	5400
	TTCAGGAGGA	TGCGCAGAA	GGGTTTCATG	GTACACACAG	TAGGCCCTCT	GGAAAGCGTG	5460
	TATGAAATGT	TCAGGAAGGA	TGACCCCGCG	CTAAGTTTCA	CACGCCAGTC	CTTTGTGGAC	5520
30	CGCTCCCTCC	TCACTCTGCT	TGCGCACTGT	AGCCTGGATG	CTTTGAGAGA	ATTCTTCAGC	5580
	ACAATTGTGG	TGGATGCCAT	TGATGTGTGT	AAGTCCAGGT	TTACAAAGCT	AAATGAATCT	5640
	ACCTTTGATA	CTCAATATCAC	CAAGAAGATG	GGCTACTATA	AGATTCTAGA	CGTGATGTAT	5700
	TCTCGCCTTC	CCAAAGATGA	TGTTTCATGCT	AAGGAATCAA	AAATTAATCA	AGTTTTCCAT	5760
	GGCTCGTGTA	TTACAGAAGG	AAATGAACTT	ACAAAGACAT	TGATTAAAT	GTGCTACGAT	5820
35	GCATTTACAG	AGAACATGGC	AGGAGAGAA	CAGCTGCTGG	AGAGGAGAAG	ACTTTACCAT	5880
	TGTGCAGCAT	ACAATCTGCG	CATATCTGTC	ATCTGCTGTG	TCTTCAATGA	GTAAAAATTT	5940
	TACCAAGGTT	TTCTGTTTAG	TGAAAAACCA	GAAAGAACT	TGCTTATTTT	TGAAAACTCG	6000
	ATCGACCTGA	AGCGCCGCTA	TAAATTTTCT	GTAGAAGTTG	AGGTTCTTAT	GGAAAGAAAG	6060
	AAAAAGTACA	TGAAATTTAG	GAAAGAAAGC	AGAGAAGCAG	CAAATGGGGA	TTGAGATGGT	6120
40	CCTTCTTATA	TGCTTCTCCT	GTCAATTTTG	GCAGACAGTA	CCCTGAGTGA	GGAAATGAGT	6180
	CAATTTGATT	TTCTCAACCG	AGTTCAGAGC	TATTCATACA	GCTCCCAAGA	CCCTAGACCT	6240
	GCCACTGGTC	TTGTTTGGAG	ACGGAGCAG	CGGACCCCA	CGGTGCATGA	TGATGTGCTG	6300
	GAGCTGGAGA	TGGACGAGCT	CAATCGGCAT	GAGTGCAATG	CGCCCTGAC	GGCCCTGGTC	6360
	AAGCAGATGC	ACAGAGGCT	GGGCCCGCCT	CAAGGAGAAG	AGGATTTCAGT	GCCAAAGAT	6420
45	TCTCCTTCTT	GGATGAAAT	CCTCATGGC	AAACTGGGAA	ATCCAATAGT	ACCATTAAT	6480
	ATCCGTCTCT	TCTTAGCCAA	GCTTGTATT	AATACAGAA	AGGTCTTTCG	CCCTTACGCG	6540
	AAGCACTATC	TGAGCCCTT	GCTGCAGCTG	GCTGCTTCTG	AAAACAATGG	AGGAGAAGGA	6600
	ATTCACTACA	TGGTGGTTGA	GATAGTGGCC	ACTATTCTTT	CATGGACAGG	CTTGGCCACT	6660
	CCACACGGGG	TCCTTAAAGA	TGAAGTGTTA	GCAAAATCGAT	TGCTTAATTT	CCTAATGAAA	6720
50	CATGCTCTTC	ATCCAAAAG	AGCTGTGTTT	AGACACAACC	TTGAAATTAT	AAAGACCTT	6780
	GTGAGTGCT	GGAGAGATTG	TTTATCCATC	CCTTATAGGT	TAATATTGTA	AAAGTTTTCG	6840
	GGTAAAGATC	CTAATCTTAA	AGACAACTCA	GTAGGGATTG	AATTGCTAGG	CATCGTATG	6900
	GCCAAATGACC	TGCTTCCCTA	TGACCCACAG	TGTGGCATCC	AGAGTAGCGA	ATACTTCCAG	6960
	GCTTTGGTGA	ATAATATGTC	CTTTGTAAGA	TATAAAGAAG	TGTATGCCCG	TGCAGCAGAA	7020
55	GTTCAGGAC	TTATACTTGC	ATATGTTATG	GAGAGAAAAA	ACATACTGGA	GGAGTCTCTG	7080
	TGTGAACCTG	TGCGAAACCA	ATTGAAGCAA	CATCAGAAAT	CTATGGAGGA	CAAGTTTATT	7140
	GTGTGCTTGA	ACAAAGTGAC	CAAGAGCTTC	CCTCCTCTTG	CAGACAGGTT	CATGAATGCT	7200
	GTGTTCTTTC	TGCTGCCAAA	ATTTCAATGA	GTGTGAAAA	CACCTGTCTC	GGAGGTGGTA	7260
	CTTTGTCGTG	TGGAGGGAAT	GACAGAGCTG	TACTTCCAGT	TAAAGAGCAA	GGACTTCTGT	7320
60	CAAGTCATGA	GACATAGAGA	TGATGAAAGA	CAAAAAGTAT	GTTTGGACAT	AATTTATAAG	7380
	ATGATGCCAA	AGTTAAAAACC	AGTAGAACTC	CGAGAACTTC	TGAACCCCGT	TGTGGAATTC	7440
	GTTTCCCATC	CTTCTACAAC	ATGTAGGGAA	CAAAATGTATA	ATATTCTCAT	GTGGATTCTAT	7500
	GATAATTACA	GAGATCCAGA	AAGTGAGACA	GATAATGACT	CCCAGGAAAT	ATTTAAGTTG	7560
	GCAAAAGATG	TGCTGATTCA	AGGATTGATC	GATGAGAACC	CTGGACTTCA	ATTAATTATT	7620
65	CGAAATTTCT	GGAGCCATGA	AACTAGGTTA	CCTTCAARTA	CCTTGGACCG	GTGCTGGCA	7680
	CTAAATTCCT	TATATTCTCC	TAAAGTAGAA	GTGCACTTTT	TAGTTTAGC	AACRAATTTT	7740
	CTGCTCGAAA	TGACCCAGAT	GAGCCAGAT	TATCCAAACC	CCATGTTCTGA	GCACTCTCTG	7800
	TCAGAATGCG	AAATTTCAGGA	ATATACCAT	GATTCTGATT	GGCGTTTTCG	AAGTACTGTT	7860
	CTCACTCCGA	TGTTTGTGGA	GACCCAGGCC	TCCAGGGCCA	CTCTCCAGAC	CCGTACCCAG	7920
70	GAAGGGTCCC	TCTCAGCTCG	CTGGCCAGTG	GCAGGGCAGA	TAAGGGCCAC	CCAGCAGCAG	7980
	CATGACTTCA	CATGACACA	GACTGCAGAT	GGAGAAGCT	CATTTGATTG	GCTGACCGGG	8040
	AGCAGCACTG	ACCGCTGGT	CGACCAACCC	AGTCCCTCAT	CTGACTCCTT	GCTGTTTGGC	8100
	CACAGAGGA	GTGAAAGGTT	ACAGAGAGCA	CCCTTGAAGT	CAGTGGGGCC	TGATTTTGGG	8160
	AAAAAAAGGC	TGGCCCTTCC	AGGGGACGAG	GTGGATAACA	AAGTGAAGG	TGCGGCCGGC	8220
75	CGSACGGACC	TACTACGACT	GCGCAGACGG	TTTATGAGGG	ACCAGGAGAA	GCTCAGTTTG	8280
	ATGTATGCCA	GAAAAGGCGT	TGCTGAGCAA	AAACGAGAGA	AGGAAATCAA	GAGTGAGTTA	8340
	AAAAATGAAG	AGGATGCCCA	GGTCTTCTG	TACAGAACTC	ACCGGACCGG	AGACCTTCTT	8400
	GACATTGAGA	TCAGACACAG	CAGCCTCATC	ACCCCGTTAC	AGGCCGTGGC	CCAGAGGGAC	8460
	CCAAATATTG	CAAAACAGCT	CTTTAGCAGC	TTGTTTCTG	GAATTTTGAA	AGAGATGGAT	8520
80	AAATTTAAGA	CACGTCTGTA	AAAAAACAA	ATCACTCAA	AGTTGCTTCA	AGACTTCAAT	8580
	CGTTTCTTCA	ATACCACCTT	CTCTTCTTTT	CCACCTTTTG	TCCTTGTAT	TCAGGACATT	8640
	AGCTGTGAGC	ACCGACGCTT	GCTGAGCCTC	GACCCAGCGG	CTGTTAGCGC	TGTTTGCCTG	8700
	GCCAGCCTAC	AGCAGCCCGT	GGGCATCCGC	CTGCTAGAGG	AGGCTCTGCT	CCGCTGCTG	8760
	CCTGCTGAGC	TGGCTGCCAA	GGGAGTCCGT	GGGAAGGCC	GCCTCCCTCC	TGATGTCTCT	8820
	AGATGGGTGG	AGCTTGCTAA	GCTGTATAGA	TCAATTGGAG	AATACGAGCT	CCTCCGTGGG	8880
85	ATTTTACCA	TGAGATAGG	AACAAAGCAA	ATCACTCAGA	GTGCATTATT	AGCAGAGCC	8940
	AGAAGTGATT	ATTCTGAAGC	TGCTAAGCAG	TATGATGAGG	CTCTCAATAA	ACAAGACTGG	9000
	GTAGATGGTG	AGCCCAAGAA	ATCCGAGAGG	GATTTTGGG	AACTTGCACT	CCTTGACTGT	9060

	TACAACCCACC	TTGCTGAGTG	GAAATCACTT	GAATACTGTT	CTACAGCCAG	TATAGACAGT	9120
	GAGAACCCCC	CAGACCTAAA	TAAATCTGG	AGTGAACCAT	TTTATCAGGA	AACATATCTA	9180
	CCTTACATGA	TCCGACAGCA	GCTGAAGCTG	CTGCTCCAGG	GAGAGGCTGA	CCAGTCCCTG	9240
5	CTGACATTAA	TTGACAAAGC	TATGCACGGG	GAGCTCCAGA	AGGCGATTCT	AGAGCTTCAT	9300
	TACAGTCAAG	AGCTGAGTCT	GCTTTACCTC	CTGCAAGATG	ATGTTGACAG	AGCCAAATAT	9360
	TACATTCAAA	ATGGCATTCA	GAGTTTTATG	CAGAATTATT	CTAGTATTGA	TGTCCTCTTA	9420
	CACCAAAAGTA	GACTCACCAA	ATTGCAGTCT	GTACAGGCTT	TAACAGAAAT	TCAGGAGTTC	9480
	ATCAGCTTTA	TAAGCAAAAC	AGGCAATTTA	TCATCTCAAG	TTCCCTTAA	GAGACTTCTG	9540
10	AACACCTGGA	CAACACGATA	TCCAGATGCT	AAAATGGACC	CAATGAACAT	CTGGGATGAC	9600
	ATCATCACAA	ATCGATGTTT	CTTCTCAGC	AAAATAGAGG	AGAAGCTTAC	CCCTCTTCCA	9660
	GAAGATAATA	GTATGAATGT	GGATCAAGAT	GGAGACCCCA	GTGACAGGAT	GGAAAGTCAA	9720
	GAGCAGGAAG	AAGATATCAG	CTCCCTGATC	AGGAGTTGCA	AGTTTTCCAT	GAAATGAAG	9780
	ATGATAGACA	GTCCCCGGAA	GCAGAACAT	TTCTCATTG	CTATGAAACT	ACTGAAGGAG	9840
	CTGCATAAAG	AGTCAAAAC	CAGAGACGAT	TGGCTGGTGA	GCTGGGTGCA	GAGCTACTGC	9900
15	CGCCTGAGCC	ACTGCCGGAG	CGGCTCCAG	GGCTGCTCTG	AGCAGGTGCT	CACTGTGCTG	9960
	AAAACAGTCT	CTTTGTGGGA	TGAGAACAAC	GTGTCAAGCT	ACTTAAGCAA	AAATATTCTG	10020
	GCTTTCCGTG	ACCAGAACAT	TCCTTGGGT	ACAACTTACA	GGATCATAGC	GAATGCTCTC	10080
	AGCAGTGAGC	CAGCCTGCCT	TGCTGAAATC	GAGGAGGACA	AGGCTAGAAG	AATCTTAGAG	10140
20	CTTTCTGGAT	CCAGTTTCTG	GCAGTTCAG	AAGGTGATCG	CGGGTCTGTA	CCAGAGAGCA	10200
	TTCCAGCACC	TCTCTGAGGC	TGTGACGGCG	GCTGAGGAGG	AGGCCAGGCC	TCCCTCTGG	10260
	AGCTGTGGGC	CTGCAGCTGG	GGTGATTGAT	GCTTACATGA	CGCTGGCAGA	TTCTGTGAC	10320
	CAACAGCTGC	GCAGAGGAGGA	AGAGAAATGA	TCAGTTATTG	ATTCTGCAGA	ACTGCAGGCG	10380
	TATCCAGCAC	TTGTGGTGGG	GAAATGTGTG	AAAGCTTTAA	AAATTAATTC	CAATGAAGCC	10440
25	AGATTGAAGT	TTCTCAGATT	ACTTCAGATT	ATAGAACGGT	ATCCAGAGGA	GACTTTGAGC	10500
	CTCATGACAA	AAGAGATCTC	TTCCGTTCCT	TGCTGGCAGT	TCATCAGCTG	GATCAGCCAC	10560
	ATGGTGGCCT	TACTGGACAA	AGACCAAGCC	GTTGCTGTTT	AGCACTCTGT	GGAAAGAAATC	10620
	ACTGATAACT	ACCCGACAGC	TATTTGTTAT	CCCTTCATCA	TAAGCAGCGA	AAGCTATTCC	10680
	TTCAAGGATA	GCTTCTACTGG	TCATAAGAAT	AAGGAGTTTG	TGGCAAGGAT	TAAAGTAAG	10740
30	TTGGATCAAG	CAGGAGTGAT	TCAGGATTTT	ATTAATGCTT	TAGATCAGCT	CTCTAATCCT	10800
	GAACTGTCTC	TTAAGGATTG	GAGCAATGAT	GTAAGAGCTG	AACTAGCAAA	AACCCCTGTA	10860
	AATAAAAAAA	ACATTGAAAA	AATGTATGAA	AGAATGTATG	CAGCCTTGGG	TGACCCAAAG	10920
	GCTCCAGGCC	TGGGGGCCCT	TAGAAGGAAG	TTTATTGAGA	CTTTTGGAAA	AGAATTTGAT	10980
	AAACATTTTG	GGAAAGGAGG	TTCTAAACTA	CTGAGAATGA	AGCTCAGTGA	CTTCAACGAC	11040
35	ATTACCAACA	TGCTACTTTT	AAAAATGAAC	AAAGACTCAA	AGCCCCCTGG	GAATCTGAAA	11100
	GAATGTTTAC	CCTGGATGAG	CGACTTCAAA	GTGGAGTTCC	TGAGAAATGA	GCTGGAGATT	11160
	CCCGTCACT	ATGACGGTAG	GGGAAAGCCA	TTGCCAGAGT	ACCACGTGCG	AATCGCCGGG	11220
	TTTGATGAGC	GGGTGACAGT	CATGGCGTCT	CTGCCAAGGC	CCAAGCGCAT	CATCATCCGT	11280
	GGCCATAGCT	AGAGGGAAAC	CCCTTTCTCT	GTGAAGGGTG	GCGAGGACCT	GCGGCAGGAC	11340
40	CAGCGCGTGG	GCAGCTCTTT	CCAGGTCATG	AATGGGATCC	TGGCCCAAGA	CTCCGCTGCT	11400
	AGCCAGAGGG	CCCTGCAGCT	GAGGACCTAT	AGCGTTGTGC	CCATGACCTC	CAGGTTAGGA	11460
	TTAATTGAGT	GGCTTGAAAA	TACTGTTACC	TTGAAGGACC	TTCTTTTGAA	CACCATGTCC	11520
	CAAGAGGAGA	AGGCGGCTTA	CCTGAGTGAT	CCCAGGGCAC	CGCCGTGTGA	ATATAAAGAT	11580
	TGGCTGACAA	AAATGTCAGG	AAAACATGAT	GTTGGAGCTT	ACATGCTAAT	GTATAAGGGC	11640
45	GCTAATCTAC	CTGAACAGT	CACGTCTTTT	AGAAAAACGAG	AAAGTAAAGT	GCCTGCTGAT	11700
	CTCTTAAAGC	GGGCTTTCGT	GAGGATGAGT	ACAAGCCCTG	AGGCTTTCCT	GGCGCTCCGC	11760
	TCCCACTTCG	CGCTCTGATA	TGCATCAGCC	ACTGGATCCT	CGGGATGGA	CGGGATGGA	11820
	GACAGACATC	TGAACAACTT	TATGGTGGCC	ATGGAGACTG	GCGGCGTGAT	CGGGATGGA	11880
	TTTGGGCATG	CGTTTGGATC	CGCTACACAG	TTTCTGCCAG	TCCCTGAGTT	GATGCCTTTT	11940
50	CGGCTAACTC	GCAGCTTTAT	CAATCTGATG	TTACCAATGA	AAGAAACGGG	CCTTATGTAC	12000
	AGCATCATGG	TACACGCACT	CCGGGCTTTC	CGCTCAGACC	CTGGCCTGCT	CACCAACACC	12060
	ATGGATGTGT	TTGTCAAGGA	CGCCTCCTTT	GATTGGAAAA	ATTTTGAACA	GAAAAATGCTG	12120
	AAAAAAGGAG	GGTCATGGAT	TCAAGAAATA	AATGTTGCTG	AAAAAATTG	GTACCCCGGA	12180
	CAGAAATAT	GTTACGCTAA	GAGAAAGTTA	GCAGGTGCCA	ATCCAGCAGT	CATTACTTGT	12240
55	GATGAGCTAC	TCCTGGGTCA	TGAGAAGGCC	CCTGCCTTCA	GAGACTATGT	GGCTGTGGCA	12300
	CGAGGAAGCA	AAGATCACAA	GATCTGTGCC	CAAGAACCCG	AGAGTGGGCT	TTCAGAAAGG	12360
	ACTCAAGTGA	AGTGCCTGAT	GCACAGGCCA	ACATCCTTGG	CAGAACCTGG	GAGAACCTGG	12420
	GAAGGATGGG	AGCCCTGGAT	GTGAGGTCTG	TGGGAGTCTG	CAGATAGAAA	GCATTACATT	12480
	GTTTAAAGAA	TCTACTATAC	TTTGGTTGGC	AGCATTCCAT	GAGCTGATT	TCCTGAAACA	12540
60	CTAAAGAGAA	ATGTCITTTG	TGCTACAGTT	TCGTAGCATG	AGTTTAAATC	AAGATTATGA	12600
	TGAGTAAATG	TGATGTGGTT	AAATCAAGAA	TAAGGTTATA	GTAACATCAA	AGATTAGGTG	12660
	AGGTTTATAG	AAAGATAGAT	ATCCAGGCTT	ACCAAGATAT	TAAGTCAAGA	ATATAATATG	12720
	TGATCAGCTT	TCAAGACATT	TACAAGTGCT	GCAAGTTAGT	GAAACAGCTG	TCTCCGTAAA	12780
	TGGAGGAAAT	GTGGGGAAGC	CTTGGAAATG	CCTTCTGGTT	CTGGCACATT	GGAAAGCACA	12840
65	CTCAGAAGGC	TTCATCACCA	AGATTTTGGG	AGAGTAAAGC	TAAGTATAGT	TGATGTAACA	12900
	TTGTAGAAGC	AGCATAGGAA	CAATAAGAAC	AATAGGTAAA	GCTATAATTA	TGGCTTATAT	12960
	TTAGAAATGA	CTGCATTGTA	TATTTTAGGA	TATTTTCTTA	GGTTTTTTCC	TTTCATTTTA	13020
	TTCTCTTCTA	GTTTTCATAT	TTTATGATAG	ATTTGCTCTC	TAGAAGGAAA	CGTCTTTATT	13080
	TAGGAGGGCA	AAAATTTTGG	TCATAGCATT	CACTTTGTCT	ATTTCCAATCT	ACAACTGGAA	13140
70	GATACATAAA	AGTGCTTTGC	ATTGAATTTG	GGATAACTTC	AAAAATCCCA	TGGTTGTTGT	13200
	TAGGGATAGT	ACTAAGCATT	TCAGTTCCAG	GAGAATAAAA	GAAATTCCTA	TTTGAAATGA	13260
	ATTCCTCATT	TGGAGGAAAA	AAAGCATGCA	TTCTAGCACA	ACAAGATGAA	ATTATGGAAT	13320
	ACAAAGTGG	CTCCTTCCCA	TGTGCAGTCC	CTGTCCCTCC	CCGCCAGTCC	TCCACACCCA	13380
	AACTGTTTCT	GATGGCTTTT	TAGCTTTTGT	TTGTTTTTTT	TTTTCTTTCT	AACACTTGTA	13440
75	TTTGGAGGCT	CTTCTGTGAT	TTTGAGAAAT	ATACTCTTGA	GTGTTTAATA	AAGTTTTTTT	13500
	CCAAAGTA						

Seq ID NO: 99 Protein sequence:
Protein Accession #: NP_008835.5

80	1	11	21	31	41	51	
	MAGSGAGVRC	SLRLQETLS	AADRCGAALA	GHQLIRGLGQ	ECVLSSSPAV	LALQTSLVFS	60
	RDFGLLVFR	KSLSNIEFRE	CREEILKFLC	IFLEKMGQKI	APYSVEIKNT	CTSVYTKDRA	120
	AKCKIPALDL	LILKLQTFRS	SRLMDEFKIG	ELFSKFYGL	ALKKIPDVT	LEKVYELLGL	180
85	LGEVHPSEMI	NNAENLPRAF	LKELKTQMTS	AVREPKLFLV	AGCLKGLSSL	LCNFTKSMEE	240
	DPQTSREIFN	FVLKAIRPQI	DLKRYAVPSA	GLRLFALHAS	QFSTCLLDNY	VSLFEVLLKW	300
	CAHTNVELKK	AALSALESFL	KQVSNMVAKN	AEHMKNLQY	FMEQFYGIIR	NVDSNNKELS	360

	IAIRGYGLFA	GPCKVINAKD	VDFMYVELIQ	RCKQMPLTQT	DTGDDRVYQM	PSFLQSVASV	420
	LLYLDTVPEV	YTPVLEHLVV	MQIDSFPQYS	PKMQLVCCRA	IVKVFLALAA	KGPVLRNCIS	480
	TVVHQLGRLI	CSKPVVLPKG	PESESEDHRA	SGEVRTGKWK	VPTYKDYVDL	FRHLLSSSDQM	540
5	MDSILADEAF	FSVNSSSES	NHLLYDEFVK	SVLKIVEKLD	LTLLEIQTVE	QENGDEAPGV	600
	WMIPTSDFAA	NLHPAKPKDF	SAPINLVEFC	REILPEKQAE	FFEPWVYSFS	YELILQSTRL	660
	PLISGFYKLL	SITVRNAKKI	KYFEGVSPKS	LKHSPEDEPK	YSCFALFVKF	GKEVAVKMKQ	720
	YKDELLASCL	TFLLSLPHNI	IELDVRAVVP	ALQMAFKLGL	SYTPLAEVGL	NALEEWSIYI	780
	DRHVMQPYK	DILPCLDGYL	KTSALSDETK	NNWEVSALSR	AAQKGFNKVV	LKHLKKTKNL	840
10	SSNEAISLEE	IRIRVQMLG	SLGGQINKNL	LTVTSSDEMM	KSYVANDREK	RLSPAVPFRE	900
	MKPVIFLDVF	LPRVTELALT	ASDRQTKVAA	CELLHSMVMF	MLGKATQMP	GGQGAAPPYQ	960
	LYKRTFPVLL	RLACDVQVDT	RQLYEPLVMQ	LIHWFTNNKK	PESQDTVALL	EAILDGIIVDP	1020
	VDSTLRDFCG	RCIREFLKWS	IKQITPQQQE	KSPVNTKSLF	KRLYSALALP	NAFKRLGASL	1080
	AFNNIYREFR	EEESLVEQFV	FEALVIYMES	LALAHADEKS	LGTIQCCDA	IDHLCRIIEK	1140
15	KHVSINKAKK	RLPRGFFPFS	ASLCLDLVK	WLLAHCGRPO	TECRHKSIEL	FYKFVPLLPQ	1200
	NRSPNLWLKD	VLEEGVSFPL	INTFEGGGCG	QPSGILAQPT	LLYLGRPFSL	QATLCWLDLL	1260
	LAALECYNTF	IGERTVGALQ	VLGTEAQSSL	LKAVAPFLES	IAMHDIIAE	KCPGTGAAGN	1320
	RTSPQEGERY	NYSKCTVVVR	IMEFTTLLN	TSPGKWLLK	KDLCNTHLMR	VLVQTLCEPA	1380
	SIGFNIQDVQ	VMAHLPDVCV	NLMKALKMSP	YKDILETHLR	EKITAQSIEE	LCAVNLVYGP	1440
20	AQVDRSLAA	VVSACKQMLR	AGLLHNILPS	QSTDHHSVVG	TELLSLVYKG	IAPGDERQCL	1500
	PSLDLSCQQL	ASGLLELAPA	FGGLCERLVS	LLLNPAVLST	ASLGSSQSGV	IHFSGHEYFY	1560
	SLFSETINTE	LLKNLDLAVL	ELMQSSVDNT	KMVSAVLNGM	LQSPFRERAN	QKHQGLKLAT	1620
	TILQHWKKCD	SWWAKDSPLE	TKMAVLALLA	KILQIDSSVS	FNTSHGSPFE	VFTTYISLLA	1680
	DTKLDLHLKG	QAVTLLPFPT	SLTGGSLLEL	RRVLEQLIVA	HFPMQSREFF	PQTTPRFNNYV	1740
25	DCMKKFLDAL	ELSGSSPMLL	LMTVELCREQ	QHVMEELFQS	SFRRIARRGS	CVTQVGLLES	1800
	VYEMFRKDDP	RLSFTQSFV	DRSLTLTLWH	CSLDALREFF	STIVVDADIV	LKSRTFKLNE	1860
	STFDTOITKK	MGYYKILDVM	YSRLPKDDVH	AKESKINQVF	HGSCITEGNE	LTKTLIKLCY	1920
	DAFTENMAGE	NQLLERRRLY	HCAAYNCATS	VICCVFNLK	FYQGLFSEK	PEKNLLIFEN	1980
30	LIDLKRRYNF	PVEVEVEMER	KKKYIEIRKE	AREAANGSDS	GPSYMSLSY	LADSTLSEAM	2040
	SQDFDSTGVQ	SYSYSSQDPR	PATGRFRRRR	QRDPTVHDDV	LELEMDLNR	HECMAPLTAL	2100
	VKHMRRSLGP	PQGEEDSVPR	DLPSPMKPLH	GKLGNIPIVL	NIRLFLAKLV	INTEEVFRPY	2160
	AKHWLSPLLQ	LAASENNGGE	GIHYMVVEIV	ATILSWTGLA	TPTGVPKDEV	LANRLLNPLM	2220
	KHVFPKRAV	FRHNLEIKIT	LVCEWDCLES	IPYRLIFEKF	SGKDPNSKDN	SVGIQLLGIV	2280
35	MANDLPPYDP	QCGIQSSEYF	QALVNNMSFV	RYKEVYAAAA	EVGLGLILRV	MERNILLES	2340
	LCELVAQKQL	QITQSALLDK	IVCLNKVTKS	FPLADRFPMN	AVFFLLPKFH	GVLTCLCLEV	2400
	VLCRVEGMTE	LYPQLKSKDF	VQVMRHRDDE	RQKVCLDIY	KMPKLPKVE	LRELLNPVVE	2460
	FVSHPSITCR	BQMYNILMIL	HDNYRDPSE	TNDNSQIFK	LAKDVLIOGL	IDENPGLQLI	2520
	IRNFWSHETR	LPSNTLDRLL	ALNSLYSPKI	SVHFLSLATN	FLLEMTSMSP	DYPNPMFEHP	2580
	LSECFEQEYT	IDSDWRFRST	VLTMPFVETQ	ASQGTQLQRT	QEGSLSARWP	VAGQIRATQQ	2640
40	QHDFTLTQTA	DGSSSPDWLT	GSSDPLVDH	TSPSSDLSLF	AHKRSERLQR	APLKSVPDPF	2700
	GKKRLGLPGD	EVDNKVGKAA	GRDILLRLRR	RFMRDQEKLS	LMYARKGVAE	QKREKEIKSE	2760
	LKMKQDAQV	LYRSYRHGDL	PDQIKHSSL	ITPLQAVAR	DPIIAKQLFS	SLPSGILKEM	2820
	DKPKTLSEKN	NITQKLLQDF	NRFLNTTFSF	PPPFVSCIQD	ISCQHAALLS	LDPAAVSAGC	2880
	LASLQQPVGI	RLLEEALLRL	LPAELPAKRV	RGKARLPDVP	LRWVELAKLY	RSIGEDVLR	2940
45	GIFTSEIGTK	QITQSALLAS	ARSDYSEAAK	QYDEALNKQD	WVDGEPTAE	KDPWELASLD	3000
	CYNHLAEWKS	LEYCSTASID	SENPPDLNKI	WSEPFYQETY	LPYMRSLKL	LLLQGEADQS	3060
	LLTFIDKAMH	GELQKAILLE	HYSQELSLLY	LLQDDVDRAK	YYIQNGIQSF	MQNYSSIDVL	3120
	LHQSRLLTKLQ	SVQALTEIQE	FISFISKQGN	LSSQVPLKRL	LNTWNTNRYD	AKMDPMNIWD	3180
	DIITNRCCFL	SKIEEKLTPL	PEDNSMNVQD	DGDPDSRMEV	QEQUEEDISS	IRSCFKFSMK	3240
50	KMIDSARKQN	NFSLAMKLLK	ELHKESKTRD	DWLVSWSQSY	CRLSHCRSRS	QCSQEVQLTV	3300
	LKTVSLLEDN	NVSSYLSKNI	LAFRDQNIL	GTTYRIIANA	LSSEPAACLB	IEEDKARRIL	3360
	ELSGSSSEDS	NEISYAGLYR	APQHLSEAVQ	AAEEEAQPPS	WSCGPAAGVI	DAYMTLADFC	3420
	DQQLRKEEN	ASVIDSAELQ	AYPALVVEKM	LKALKLNSNE	ARKLPRLRLQ	IERYPBEETL	3480
	SLMTKEISSV	PCNQFISWIS	HMVALLDKQD	AVAVQHSVEE	ITDNYPQAI	YPFIISSSEY	3540
55	SFKDTSTGKH	NKEEFVARIKS	KLDQGGVQD	FINALDQLSN	PELLPKDWSN	DVRAELAKTP	3600
	VNKNKIEKMY	ERNYAALGDP	KAPGLGAFRR	KFIQTFGKEF	DKHFGKGGSK	LLRMKLSDFN	3660
	DITNMLLLKM	NKDSKPPGCL	KCCSPWMSDF	KVEFLRNELE	IPGQYDGRGK	PLPEYHVRIA	3720
	GFDERTVTMA	SLRRPKRIII	RGHDEREHFF	LVKGGEDLRQ	DQVEQLFQV	MNGILAQDSA	3780
	CSQRALQLRT	YSVVPMTSRL	GLIEWLENTV	TLKDLLLNTM	SQEEKAAVLS	DPRAPPCBYK	3840
60	DWLTKMSGKH	DVGAYMLMYK	GANRTETVTS	FRKRESKVPA	DLKRAFVRM	STSPFAFLAL	3900
	RSHPASSHAL	ICTSHWILGI	GDRHLNFMV	AMETGGVIGI	DFGHPAGSAT	QFLPVPELMP	3960
	FRLTRQFINL	LMFMKETGLM	YSIMVHALRA	FRSDPGLLTN	TMDVFKVEPS	FDWKNFEQKM	4020
	LKKGGSWIQE	INVAEKWYFP	RQKICYAKRK	LAGANPAVIT	CDELLLGHEK	APAFRDYVAV	4080
	ARGSKDHNR	AQEPESGLSE	ETQVKCLMDQ	ATDPNILGRT	WEGWEPWM		

Seq ID NO: 100 DNA sequence
Nucleic Acid Accession #: NM_000673
Coding sequence: 101-1225

70	1	11	21	31	41	51	
	ATGTGAAGGC	ACAAGCTGCT	GTTATATACA	ACAGAGTGAA	CTGAGCATCA	GTCAGAAAAA	60
	GTCATATGTT	GCAGAAATAC	AGATCCAAGA	CAAAGACAGG	ATGGGCACTG	CTGGAAGAA	120
	TATTAAATGC	AAAGCAGCTG	TGCTTTGGGA	GCAGAAGCAA	CCCTTCTCCA	TTGAGGAAAT	180
75	AGAAGTTGCC	CCACCAAAGA	CTAAAGAAGT	TCGCATTAA	ATTTTGGCCA	CAGGAATCTG	240
	TCGCACAGAT	GACCTATGTA	TAAAGGAAC	AATGGTGTC	AAGTTTCAG	TGATTGTGGG	300
	ACATGAGGCA	ACTGGGATG	TAGAGAGCAT	TGGAGAAGGA	GTGACTACAG	TGAACACAG	360
	TGACAAAGTC	ATCCCTCTCT	TCTGCCACA	ATGTAGAGAA	TGCAATGCTT	GTCGCAACCC	420
	AGATGGCAAC	CTTTGCATTA	GAGAGGATAT	TACTGGTCGT	GGAGTACTGG	CTGATGGCAC	480
80	CACCAGATTT	ACATGCAAGG	GCAACCAAGT	ACACCACCTC	ATGAACACCA	GTACATTATC	540
	CGAGTACACA	GTGGTGGATG	AATCTTCTGT	TGCTAAGATT	GATGATGCAG	CTCCTCTTGA	600
	GAAAGTCTGT	TAAATCTGCT	TGCGGTTTTC	CACTGGATAT	GGCGCTGCTG	TTAAACTGG	660
	CAAGGTCAAA	CCTGGTTCCT	CTTGGTCGT	CTTTGGCCTG	GGAGGAGTTG	GCCTGTCACT	720
	CATCATGGCG	TGTAAGTCAG	CTGGTGCATC	TAGGATCATT	GGGATTGACC	TCAACAAAGA	780
	CAAAATTTGAG	AAGGCCATGG	CTGTAGGTGC	CACGTAGTGT	ATCAGTCCCA	AGGACTCTAC	840
85	CAAAACCATC	AGTGAGGTGC	TGTGAGAAAT	GACAGGCAAC	AACGTGGGAT	ACACCTTTGA	900
	AGTTATTGGG	AGTATGAGAA	CATGATTGA	TGCCCTGGCA	TCCTGCCACA	TGAACATATG	960
	GACCAGCGTG	GTTGTAGGAG	TTCCCTCATC	AGCCAAGATG	CACCACTATG	ACCCGATGTT	1020

5
10
15
20

```

GCTCTTCACT GGACGCACAT GGAAGGGATG TGTCTTTGGA GGTTTGAAAA GCAGAGATGA 1080
TGTCCCAAAA CTAGTGACTG AGTTCTCTGGC AAAGAAAATT GACCTGGACC AGTTGATAAC 1140
TCATGTTTTA CCATTTTAAAA AAATCAGTGA AGGATTTGAG CTGCTCAATT CAGGACAAAG 1200
CATTGGAACG GTCCCTGACGT TTTGAGATCC AAAGTGGCAG GAGGTCTGTG TTGTCATGGT 1260
GAACTGGAGT TTCTCTTGTT AGAGTTCCCT CATCTGAAAT CATGTATCTG TCTCACAAT 1320
ACAAGCATAA GTAGAAGATT TGTGAAGAC ATAGAACCCT TATAAAGAAT TATTAACCTT 1380
TATAAACATT TAAAGTCTTG TGAGCACCTG GGAATTAGTA TAATAACAAT GTTAATATTT 1440
TTGATTTACA TTTTGTAAAG CTATAATTGT ATCTTTTAAG AAAACATACA CTGGGATTTC 1500
TATGTTGAAA TGGAGATTTT TAAGAGTTT AACCAGCTGC TGCAGATATA TAACTCAAAA 1560
CAGATATAGC GTATAAAGAT ATAGTAAATG CATCTCCAG AGTAATATTC ACTTAACACA 1620
TTGAAACTAT TATTTTITAG ATTTGAATAT AAATGTATTT TTTAAACACT TGTTATGAGT 1680
TAACTTGGAT TACATTTTGA AATCAGTTCA TTCCATGATG CATATTACTG GATTAGATTA 1740
AGAAAGACAG AAAAGATTAA GGGACGGGCA CATTTTTCAG CGATTAAAGAA TCATCATTAC 1800
ATAACTTGGT GAAAGTAAAA AAGTATATCA TATGGGTACA CAAGGCTATT TGCCAGCATA 1860
TATTAATATT TTAGAAAATA TTCTTTTGT AATACTGAAT ATAAACATAG AGCTAGAGTC 1920
ATATTATCAT ACTTATCATA ATGTTCAATT TGATACAGTA GAATTGCAAG TCCCTAAGTC 1980
CCTATTCACT GTGCTTAGTA GTGACTCCAT TTAATAAAAA GTGTTTTTAG TTTTAAACAA 2040
CTAAACCG

```

Seq ID NO: 101 Protein sequence:
Protein Accession #: NP_000664

25
30

```

1 11 21 31 41 51
MGTAGKVIK KAAVLWEQK PFSIEIEVA PPKTKEVRIK ILATGICRTD DHVIKGTMV 60
KFPVIVGHEA TGIVSIGEG VTTVKPGDKV IPLFLPQCRE CNACRNPDGN LCIRSDITGR 120
GVLADGTRF TCKGKPVHVF MNTSTPTEYT VVDESSVAKI DDAAPPEKVC LIGCGFSTGY 180
GAAVKTGKVK PGSTCVVFLG GVGGLSVIMG CKSAGASRII GIDLNKKDFE KAMAVGATEC 240
ISFKDSTKFI SEVLSEMTGN NVGYTFEIVG HLETMIDALA SCHMNYGTSV VVGVPSPAKM 300
LTYDPMLEF GRTNKGCVFG GLKSRDDVPK LVTFLAKKF DLDQLITHVL PFKKISEGFE 360
LLNSGQSIRT VLTF

```

Seq ID NO: 102 DNA sequence
Nucleic Acid Accession #: NM_006783.1
Coding sequence: 1..786

35
40
45
50

```

1 11 21 31 41 51
ATGGATTGGG GGACGCTGCA CACTTTCATC GGGGGTGTCA ACAACACTC CACCAGCATC 60
GGGAAGGTGT GGATCACAGT CATCTTTATT TTCCGAGTCA TGATCCTAGT GGTGGCTGCC 120
CAGGAAGTGT GGGGTGACGA GCAAGAGGAC TTGCTCTGCA ACACACTGCA ACCGGGATGC 180
AAAAATGTGT GCTATGACCA CTTTTTCCCG GTGTCCACA TCCGGCTGTG GGCCTCCAG 240
CTGATCTTGG TCTCCACCCC AGCGCTGCTG GTGGCCATGC ATGTGGCCTA CTACAGGCAC 300
GAAACCACTC GCAAGTTCAG GCGAGGAGAG AAGAGGAATG ATTTCAAAGA CATAGAGGAC 360
ATTAAAAAGC ACAAGGTTGG GATAGAGGGG TCGCTGTGGT GGACGTACAC CAGCAGCATC 420
TTTTTCCGAA CATCTTTTGA AGCAGCCTTT ATGTATGTGT TTTACTTCCT TTACAATGGG 480
TACCACCTGC CTTGGGTGTT GAAATGTGGG ATTGACCCCT GCCCAACCT TGTGACTGTC 540
TTTATTTCTA GGCCAACAGA GAAGACCGTG TTTACCATTT TTATGATTC TCGCTCTGTG 600
ATTTCATGTC TGCTTAACGT GGCAGAGTTG TGCTACCTGC TGCTGAAAGT GTGTTTTAGG 660
AGATCAAGA GAGCACAAGC GCAAAAAAAT CACCCCAATC ATGCCCTAAA GGAGAGTAAG 720
CAGAATGAAA TGAATGAGCT GATTTTCAGT AGTGGTCAAA ATGCAATCAC AGGTTTCCCA 780
AGCTAA

```

Seq ID NO: 103 Protein sequence:
Protein Accession #: NP_006774.1

55
60

```

1 11 21 31 41 51
MDWGLTLTFI GGVNKHSTSI GKVVITVIFI FRVMILVVAA QEVWQDEQED FVCNTLQPGC 60
KNVCYDHFFP VSHIRLWALQ LIPVSTPALL VAMHVAYYRH ETTRKFRRGE KRNDPKDIED 120
IKKKHVRIEG SLWWTYTSII FPRIIPEAAF MVVFFLYLNG YHLPWVLKCG IDPCPNLVDC 180
FISRPTKTV FTIFMISASV ICMLLNVAEL CYLLLVKCFR RSKRAQTQKN HPNHALKESK 240
QNMENELISD SQQNAITGFP S

```

Seq ID NO: 104 DNA sequence
Nucleic Acid Accession #: NM_020411
Coding sequence: 86-526

65
70
75
80

```

1 11 21 31 41 51
GGACCTGGGA AGGAGCATAG GACAGGGCAA GCGGGGATAA GGAGGGGCAC CACAGCCCTT 60
AAGGCACGAG GGAACCTCAC TGCGCATGCT CCTTTGGTGC CCACCTCAGT GCGCATGTTT 120
ACTGGGCGTC TTCCCATCGC CCCCTTCGCC AGTGTGGGGA ACGCGGCGGA GCTGTGAGCC 180
GGCGACTCGG GTCCCTGAGG TCTGGATTCT TTCTCCGCTA CTGAGACACG GCGGACACAC 240
ACAAACACAG AACACACAG CCAGTCCCAG GAGCCCAGTA ATGGAGAGCC CCAAAAAGAA 300
GAACACGAG CTGAAAGTCG GGATCCTACA CCTGGGCAGC AGACAGAAGA AGATCAGGAT 360
ACAGCTGAGA TCCAGTTCG CGACATGGAA GGTGATCTGC AAGAGCTGCA TCAGTCAAAC 420
ACCGGGGATA AATCTGGATT TGGGTTCGGG CGTCAAGGTG AAGATAATAC TAAAGAGGGA 480
ACACTGTAAA ATGCCAGAAG CAGGTGAAGA GCAACCACAA GTTTAAATGA AGACAAGCTG 540
AAACAACGCA AGCTGGTTTT ATATTAGATA TTTGACTTAA ACTATCTCAA TAAAGTTTTG 600
CAGCTTTTCA CAAAAAATAA AAAAAA

```

Seq ID NO: 105 Protein sequence:
Protein Accession #: NP_065144.1

1 11 21 31 41 51

MLLWCPPQCA CSLGVFPSPAP SPVWGTTRSC EPATRVPEVW ILSPLLRRHG HTQTQNHSTAS 60
PRSPVMESPK KKNQQLKVG I LHLGSRQKKI RIQLRSQCAT WKVICKSCIS QTPGINLIDL 120
SGVKVKIIFK EHKCKMPEAG EEQPPQV

Seq ID NO: 106 DNA sequence
Nucleic Acid Accession #: J04129
Coding sequence: 99-587

1 11 21 31 41 51
CATCCCTCTG GCTCCAGAGC TCAGAGCCAC CCACAGCCGC AGCCATGCTG TGCCTCCTGC 60
TCACCCTGGG CGTGGCCCTG GTCGTGTGGT TCCCGGCCAT GGACATCCCC CAGACCAAGC 120
AGGACCTGGA GCTCCCAAAG TTGGCAGGGA CCTGGCACTC CATGGCCATG GCGACCAACA 180
ACATCTCCCT CATGGCGACA CTGAAGGCCC CTCTGAGGGT CCACATCACC TCACTGTTGC 240
CCACCCCGGA GGACAACTTG GAGATCGTTC TGCCAGATG GGAGAACAAAC AGCTGTGTTG 300
AGAAGAAGGT CCTTGGAGAG AAGACTGGGA ATCCAAAGAA GTTCAAGATC AACTATACGG 360
TGGCGAACGA GGCCACGCTG CTCGATACTG ACTACGACAA TTTCTGTGTT CTCTGCCTAC 420
AGGACACCA CACCCCATC CAGAGCATGA TGTGCCAGTA CCTGGCCAGA GTCTCTGGG 480
AGGACGATGA GATCATGCAG GGATTCATCA GGGCTTTCAG GCCCTGCCCC AGGCACCTAT 540
GGTACTTGCT GGACTTGAAG CAGATGGAAG AGCCGTGCCG TTTCTAGCTC ACCTCGCCT 600
CCAGGAAGAC CAGACTCCCA CCCTTCCACA CCTCCAGAGC AGTGGGACTT CCTCTGCCCC 660
TTTCAAAGAA TAACCACAGC TCAGAAGACG ATGACGTGGT CATCTGTGTC GCCATCCCCT 720
TCTGTCTGCA CACCTGCACC ATTGCCATGG GGAGGCTGCT CCCTGGGGGC AGAGTCTCTG 780
GCAGAGGTTA TTAATAAACC CTTGGAGCAT G

Seq ID NO: 107 Protein sequence:
Protein Accession #: AAA60147

1 11 21 31 41 51
MDIPQTKQDL ELPKLAGTWH SMAMATNNIS LMATLKAPLR VHITSLLPTE EDNLEIVLHR 60
WENNSCVEKK VLGETGTGNPK KFKINYTVAN EATLLDSTDYD NFLFLCLQDT TTPIQSMCMQ 120
YLARVLVEDD EIMQGFIRAF RPLPRHLWYL LDLKQMEEPK RF

Seq ID NO: 108 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 48-794

1 11 21 31 41 51
TCCAGGCGAG CAGTTAGCCC GCCGCCGCCG TGTGTGTCCC CAGAGCCATG GAGAGAGCCA 60
GTCTGATCCA GAAGGCCAAG CTGGCAGAGC AGGCCGAACG CTATGAGGAC ATGGCAGCCT 120
TCATGAAGCA CCGCTGGAGG AAGGGCGAGG AGCTCTCCTG CGAAGAGCGA AACCTGCTCT 180
CAGTAGCCTA TAAGAACGTG GTGGGCGGCC AGAGGGCTGC CTGGAGGGTG CTGTCCAGTA 240
TTGAGCAGAA AAGCAACGAG GAGGGCTCGG AGGAGAAGGG GCCCGAGGTG CGTGAGTACC 300
GGGAGAAGGT GGAGACTGAG CTCAGGGCGG TGTGCCACAC CGTGTCTGGC CTGTGGGACA 360
GCCACCTCAT CAAGGAGGCC GGGGACGCCG AGAGCCGGGT CTTCTACCTG AAGATGAAGG 420
GTGACTACTA CCGCTACCTG GCCGAGGTGG CCACCGGTGA CGACAAGAAG CGCATCATTT 480
ACTCAGCCCG GTACGCTTAC CAGGAGGCCA TGGACATCAG CAAGAAGGAG ATGCCGCCCA 540
CCAACCCCTA CCGCTGGGCG CTGGCCCTGA ACTTTTCCGT CTTCCACTAC GAGATCGCCA 600
ACAGCCCGGA GGAGGCCATC TCTCTGGCCA AGACCACTTT CGACGAGGCC ATGGCTGATC 660
TGCAACCCCT CAGCGAGGAC TCCTACAAAG ACAGCACCCCT CATCATGCAG CTGTGCGAG 720
ACAACCTGAC ACTGTGGACG GCCGACAACG CCGGGGAAGA GGGGGGCGAG GCTCCCCAGG 780
AGCCCCAGAG CTGAGTGTGG CCGGCCACCG CCGCCCTCCG CCCCCTCCAG TCCCCACCC 840
TGCCGAGAGG ACTAGTATGG GGTGGGAGGC CCCACCTTTC TCCCTAGGCG GCTGTTCTTG 900
CTCCAAAGGT TCCCTGTGAG AGGACTGGC AGAGCTGAGG CCACCTGGGG CTGGGGATCC 960
CACTCTTCTT GCAGCTGTGG AGCGACCTA ACCACTGGTC ATGCCCCCAC CCCTGCTCTC 1020
CGCACCCGCT TCCCTCCGAC CCCAGGACCA GGCTACTTCT CCCCCTCTCT TGCTCTCCCTC 1080
CTGCCCTGTC TGCCCTGTAT CGTAGGAATT GAGGAGTGTG CGGCTTGTGT GCTGAGAACT 1140
GGACAGTGGC AGGGGCTGGA GATGGGTGTG TGTGTGTGTG TGTGTGTGTG TGTGTGTGTG 1200
CGCGCGCGCC AGTGCAAGAC CGAGATTGAG GGAAAGCATG TCTGTCTGGT GTGACCATGT 1260
TTCTCTCAA TAAAGTTCCC CTGTGACACT C

Seq ID NO: 109 Protein sequence:
Protein Accession #: NP_006133.1

1 11 21 31 41 51
MERASLIQKA KLAQEABERY DMAAFMKGAV EKGEELSCEE RNLLSVAYKN VVGGRRAAWR 60
VLSSIEQKSN EEGSEEGKPE VREYREKRET ELQGVCDTVL GLLDSHLIKE AGDAESRVFY 120
LKMKGDIYRY LAEVATGDDK KRIIDSARSA YQEAMDISKK EMPPTNPRL GLALNFSVPH 180
YEIANSPEEA ISLAKTTTDE AMADLHTLSE DSYKDSLTLM QLLRDNLTLW TADNAGEEGG 240
EAPQEPQS

Seq ID NO: 110 DNA sequence
Nucleic Acid Accession #: NM_000695
Coding sequence: 407-1564

1 11 21 31 41 51
CAGGAGTTGG TTTGGGAGCT GCCAGTCTCC TGGGAGGATC GCAGTCAGCA GAGCAGGGCT 60
GAGGCCTGGG GGTAGGAGCA GAGCCTGCGC ATCTGGAGGC AGCATGTCCA AGAAAGGGAG 120
TGGAGGTGCA GCGAAGGACC CAGGGGCAGA GCCCACGCTG GGGATGGACC CCTTCGAGGA 180
CACACTGCGG CGGCTGCTG AGGCCCTCAA CTGAGGGCGC ACGCGGCCGG CCGAGTTCCG 240
GGCTGCGCAG CTCCAGGGCC TGGGCCACTT CCTTCAAGAA AACAAGCAGC TTCTGCGCGA 300

CGTGTGGCC CAGGACCTGC ATAAGCCAGC TTTCGAGGCA GACATATCTG AGCTCATCCT 360
 TTGCCAGAAC GAGGTGACT ACGCTCTCAA GAACCTTCAG GCCTGGATGA AGGATGAACC 420
 ACGGTCCAGC AACCTGTCTA TGAAGCTGGA CTGCTCTTTC ATCTGGAAGG AACCTTTTGG 480
 CTTGGTCCCT ATCATCGCAC CCTGGAACCTA CCTATTGAAC CTGACCTCTG TGCTCCTGGT 540
 GGGCACCCTC CCGGAGGGA ATTGCGTGGT GCTGAAGCCG TCAGAAATCA GCCAGGGCAC 600
 AGAGAAGGTC CTGGCTGAGG TGCTGCCCA GTACCTGGAC CAGAGCTGCT TTGCGTGGT 660
 GCTGGGCGGA CCCCAGGAGA CAGGGCAGCT GCTAGAGCAC AAGTTGGACT ACATCTTCTT 720
 CACAGGAGAG CCTCGTGTGG GCAAGATTGT CATGACTGCT GCCACCAAGC ACCTGAAGCC 780
 TGTCACTCTG GAGCTGGGGG CCAAGAACCC CTGCTACGTG GACGACAACT GCGACCCCA 840
 GACCGTGGCC AACCGCTGG CCTGGTTCTG CTACTTCAAT GCCGGCCAGA CCTGCGTGGC 900
 CCCTGACTAC TCCCTGTGCA GCCCCGAGAT GCAGGAGAGG CTGCTGCCCG CCTGCAGAG 960
 CACCATCACC CGTTTCTATG GCGACGACCC CCAGAGCTCC CCAACCTGG GCCGCATCAT 1020
 CAACCAAGAA CAGTTCCAGC GGCTGCGGGC ATTGCTGGG TGCGGCCGCG TGGCCATTGG 1080
 GGGCCAGAGC AACAGAGAGC ATCGCTACAT CGCCCCACG GTGCTGTGGG ACGTGCAGGA 1140
 GACGAGAGCT GTGATGCAGG AGGAGATCTT CGGGCCATC CTGCCATCG TGAACGTGCA 1200
 GAGCGTGGAC GAGGCCATCA AGTTTATCAA CCGGAGGAG AAGCCCTGG CCTGTACGC 1260
 CTCTTCCAAC AGCAGACAGG TTGTGAACCA GATGCTGGAG CGGACCAAGC GCGGCAGCTT 1320
 TGGAGGCAAT GAGGGCTTCA CCTACATATC TCTGCTGTCC GTGCCATTGG GGGGAGTCGG 1380
 CCACAGTGGG ATGGGCGCGG ACCACGGCAA GTTCACTTC GACACCTTCT CCCACCAAGC 1440
 CACCTGCTGG CTGCGCCCTC CGGCGCTGGA GAAATTAAG GAGATCCGCT ACCCACCTTA 1500
 TACCGACTCC AACCCAGCAG GTTTACGCTG GGGCATGGGC TCCAGAGCT GCACCTCTCT 1560
 GTGAGCGTCC CACCCGCTCC CAACGGGTCA CACAGAGAAA CCTGAGTCTA GCCATGAGGG 1620
 GCTTATGTCT CCAACTCACA TTGTTCTCTC AGACCGCAGG CTCCCGCAGC CTCAGGTTGC 1680
 TGGAGCTGTC AACATGAGCG ATCTGCTCTG CCAGGGCTGC AAAGCAAGGT CTTGCTTCTA 1740
 TCTGGGGGAG GCTGCTGAG AGAGGCGGAG AGGCGCCAGA ACATGCCAGG TGTCTCTACT 1800
 CACCCACCCC ACTGGGAAAA CTGGGTTTG CCCTCTCGGT CAGGGTTGGC CAGGCCAGT 1860
 CACAGGGGCA GTGTACCCCT GGAATAATCA GTGCCCTGCC TTCTTAGGGG CATCAGCCCT 1920
 GAACGGTTGA GAGCGTGGAG CCCTCCAGGC CTTTGTCTCT CCCTCTAGGC ACACGCGCAC 1980
 TTCCACCTCT TCCCATCTCC AACTGCACCA GCACTGCCTC CCCCAGGGAT CCTCTCACAT 2040
 CCCCACCTGG TCTCTGCACC ACCCTCTGCG TTCAACCCGC ACCCTGCACT CACCCACAGC 2100
 AGCTCATCTC ACTGGGAAAA CTGGGTTTG CATCACTCCA CTGCACAGTG TTAGTGGGAC 2160
 CTGGGGGCAA GTCCCTTGAC TTCTCTGAGC CTCAGTTTCC TTATGTGAAA GTTGTGGGAA 2220
 CCAAAATGGA GTCACTTATG CCAAACTCTA ATAAATGGA GTCCGGGGGG CACATAGAAG 2280
 CCCTCACACA CACATGCCCG TAACAGGATT TATCACCAAG ACACGCTCGC ATGTAAAGAC 2340
 AGACACAGGG CGTATGGAAG AGCACGTCTT CAAAGACTGT AGTATTCAGC ATGAGCTGCA 2400
 GATGCTTACC TCCACGGGAA GTCTCCACCA GAAACCATC GCCAATCTCT GCGATCAGCT 2460
 TGTGACTTAC AAACCTTGTG TAAAGCTGCG TTACATGGAC TTCTGTCTCT TAAACGTTT 2520
 CCCTTGGCTG TGGCCCTCTG TGTATGCTG GGATCCTTCC AAGCACTCAT AGCCAGATA 2580
 GGAATCCTCT GCTCTCTCCA AATAAATTA TCTGTTT

Seq ID NO: 111 Protein sequence:
 Protein Accession #: NP_000686

1 11 21 31 41 51
 MKDEPRSTNL FMKLDVSFVW KEPFGLVLII APWNYPLNLT LVLLVGTLP A GNCVVLKPS 60
 ISQGTKEVLA EVLPQYLDQS CFAVVLGGPQ ETGQLLEHLK DYIFFTGSPP VGRIVMTAAT 120
 KHLTPVTLLE GSKNCPYVDD NCDPQTVANR VAWFCYFNAG QTCVAPDVVL CSPEMQERLL 180
 PALQSTITRF YGDDPQSSFN LGRIINQKQF QRLRALLGCG RVAIGGQSN SDRYIAPTVL 240
 VDQVETEPV QBEIPIPLP IVNVQSVDEA IKFINRQEPK LALYAFNSNR QVNVQMLBRT 300
 SSGSFQNGEG FTYISLLSVP FGGVGHSGMG RYHGKFTFDT FSHHRTCLLA PSGLEKLKEI 360
 RYPPYTDWNQ QLLRWGMGSQ SCTLL

Seq ID NO: 112 DNA sequence
 Nucleic Acid Accession #: NM_004456
 Coding sequence: 58-2298

1 11 21 31 41 51
 GAATTCGGGG CGACGCGCGG GAACAACGCG AGTCGGCGCG CGGGACGAAG AATAATCATG 60
 GGCACAGACTG GGAAGAAATC TGAGAAGGGA CCAAGTTTGT GCGCGGAAGC TGTAATATCA 120
 GAGTACATGC GACTGAGACA GCTCAAGAGG TTCAGACGAG CTGATGAAGT AAAGAGTATG 180
 TTATAGTTCCA ATCGTCAGAA AATTTTGGA AGAACGGAAA TCTTAAACCA AGAATGGAAA 240
 CAGCGAAGGA TACAGCCTGT GCACATCCTG ACTTCTGTGA GCTCATTGCG CGGGACTAGG 300
 GAGTGTTCGG TGACCAGTGA CTTGGATTTT CCAACACAAG TCATCCCATT AAAGACTCTG 360
 AATGCAAGTG CTTCAGTACC CATAATGTAT TCTTGGTCTC CCCTACAGCA GAATTTTATG 420
 GTGGAAGATG AAACGTGTTT ACATAACATT CCTTATATGG GAGATGAAGT TTTAGATCAG 480
 GATGCTACTT TCATTGAAGA ACTAATAAAA AATTATGATG GGAAGTACA CGGGGATAGA 540
 GAATGTGGGT TTATAAATGA TGAATTTTTT GTGGAGTTGG TGAATGCCCT TGGTCAATAT 600
 AATGATGATG ACGATGATGA TGATGGAGAC GATCCTGAAG AAAGAGAAGA AAAGCAGAAA 660
 GATCTGGAGG ATCACCAGGA TGATAAAGAA AGCCGCCAC CTGCGAAATT TCCTTCTGAT 720
 AAAATTTTGG AGGCCATTTC CTCAATGTTT CCAGATAAGG GCACAGCAGA AGAACTAAAG 780
 GAAAAATATA AAGAACTCAC CGAACAGCAG CTCCAGGCG CACTTCTCTC TGAATGTACC 840
 CCCAACATAG ATGGACCAAA TGCTAAATCT GTTCAGAGAG AGCAAGCTT ACTACTCTTT 900
 CATACGCTTT TCTGTAGGCG ATGTTTAAAA TATGACTGCT TCCTACATCC TTTTCTATGA 960
 ACACCCACAA CTTATAAGCG GAAGAACACA GAAACAGCTC TAGACAACAA ACCTTGTGGA 1020
 CCAAGTGTGT ACCAGCTGTT GGAGGGAGCA AAGGAGTTTG CTGCTGCTCT CACCGCTGAG 1080
 CGGATAAAGA CCCCACCAA ACCTCCAGGA GGCAGCAGAA GAGGACGGCT TCCCAATAAC 1140
 AGTAGCAGGC CCAGCACCCC CACCATTAAT GTGCTGGAAT CAAAGGATAC AGACAGTGAT 1200
 AGGGAAGCAG GGACTGAACG GGGGGGAGAG AACATGATA AAGAAGAAGA AGAGAAGAA 1260
 GATGAACACT CGAGCTCTTC TGAAGCAAA TCTCGGTGTC AAACACCAAT AAAGATGAAG 1320
 CCAAAATATT AAGCTCTCTG GAATGTGGAG TGGAGTGGT CTGAAGCCTC AATGTTTAGA 1380
 GTCTCATTTG GCACTTACTA TGACAATTTT TGTGCCATTG CTAGGTTAAT TGGGACCAAA 1440
 ACATGTAGAC AGGTGTATGA GTTTAGAGTC AAAGAATCTA GCATCATAGC TCCAGCTCCC 1500
 GCTGAGGATG TGGATACTCC TCCAAGGAAA AAGAAGAGGA AACACCGGTT GTGCGCTGCA 1560
 CACTGCAGAA AGATACAGCT GAAAAGGAGC GGCTCCTCTA ACCATGTTTA CAATATCAA 1620

	CCCTGTGATC	ATCCACGGCA	GCCTTGTGAC	AGTTGCTGCC	CTTGTGTGAT	AGCACAAAAT	1680
	TTTTGTGAAA	AGTTTTGTCA	ATGTAGTTCA	GAGTGTCAAA	ACCGCTTTCC	GGGATGCCGC	1740
	TGCAAAAGCAC	AGTGCAACAC	CAAGCAGTGC	CCGTGCTACC	TGGCTGTCCG	AGAGTGTGAC	1800
5	CCTGACCTCT	GTCTTACTTG	TGGAGCCGCT	GACCATGGG	ACAGTAAAAA	TGTGTCTCTG	1860
	AAGAACTGCA	GTATTTCAGC	GGGCTCCAAA	AAGCATCTAT	TGCTGGCACC	ATCTGACGTG	1920
	GCAGGCTGGG	GGATTTTAT	CAAAGATCCT	GTGCAGAAA	ATGAATTCAT	CTCAGAATAC	1980
	TGTGGAGAGA	TTATTCTCA	AGATGAAGCT	GACAGAAGAG	GGAAAGTGTA	TGATAAATAC	2040
	ATGTGCAGCT	TTCTGTTCAA	CTTGAACAA	GATTTGTGG	TGGATGCAAC	CCGCAAGGGT	2100
10	AACAAAATTC	GTTTTGCAAA	TCATTCGGTA	AATCCAACT	GCTATGCAAA	AGTTATGATG	2160
	GTTAAACGTTG	ATCACAGGAT	AGGTATTTT	GCCAGAGAG	CCATCCAGAC	TGGCGAAGAG	2220
	CTGTTTGTG	ATTACAGATA	CAGCCAGGCT	GATGCCCTGA	AGTATGTCGG	CATCGAAAAG	2280
	GAAATGGAAA	TCCCTTGACA	TCTGCTACCT	CCTCCCTCTC	CTCTGAAACA	GCTGCCTTAG	2340
	CTTCAGGAAC	CTCGAGTACT	GTGGGCAATT	TAGAAAAAGA	ACATGCAGTT	TGAAATTCTG	2400
15	AATTGCAAAA	GTACTGTAA	AATAATTTAT	AGTAATGAGT	TTAAAAATCA	ACTTTTATT	2460
	GCCTTCTCAC	CAGCTGCAAA	GTGTTTGTGA	CCAGTGAATT	TTTGCAATAA	TGCAGTATGG	2520
	TACATTTTTC	AACTTTGAAT	AAAGAATACT	TGAACCTGAA	AAAAAAAAAA	AAAAAA	

20 Seq ID NO: 113 Protein sequence:
Protein Accession #: NP_004447

	1	11	21	31	41	51	
25	MGQTGKKSEK	GPVCRWRKRVK	SEYMRRLRLK	RFRRRADEVKS	MFSSNRQKIL	ERTEILNQEW	60
	KQRRIQPVHI	LTSVSSIRGT	RECSVTSDDL	FETQVILPKT	LNAAVASVPI	YWSPLQONF	120
	MVEDETVLHN	IPYMGDEVLD	QGGTFIEELI	KNYDGKVHGD	RECGFINDEI	FVELVNALGO	180
	YNDDDDDDDG	DDPEEREKQ	KOLEDHRRDK	BSRPFRKFP	DKILEAISSM	FDPKGTAEEL	240
	KEKYKELTEQ	QLPGALNPEC	TPNIDGPNNA	SVQREQSLHS	FHTLFCRRCF	KYDCFLHPFH	300
	ATPNTYKRN	TETALDNKPC	GPQCYQHLEG	AKEFAAALTA	ERIKTPPKRP	GGRRRRLPN	360
30	NSSRPSTPTI	NVLESKDTDS	DREAGTETGG	ENNDKEEEK	KDETSSSSSEA	NSRCQTPIMK	420
	KPNIEPPENV	EWGABEASMP	RVLIGTYDYN	FCAIARLIGT	KTCRQVVEFR	VKESSIIAPA	480
	PAEDVDTPPR	KKKRKHRLWA	AHCRKIQLKK	DGSSNHVINY	QPCDHPRQPC	DSSCPCVIAQ	540
	NFCEKFCQCS	SECQNRFPFC	RCKAQCNTHQ	CPCYLAVREC	DPDLCLTCGA	ADHWDKSNVS	600
35	CKNCISIQRS	KHLLLLAPSD	VAGWIGIFIK	PVQKNFPISE	YCGEIIISQDE	ADRRGKVYDK	660
	YMCSEFLNLN	NDFVVDATRK	GNKIRFANHS	VNPNCYAKVM	MVNGDHRIGI	FAKRAIQTGE	720
	ELFVDYRYSQ	ADALKYVGIE	REMEIP				

40 Seq ID NO: 114 DNA sequence
Nucleic Acid Accession #: NM_001827
Coding sequence: 96-335

	1	11	21	31	41	51	
45	AGTCTCCGGC	GAGTTGTGTC	CTGGGCTGGA	CGTGGTTTGG	TCTGCTGCGC	CGCTCTTCG	60
	CGCTCTCGTT	TCATTTTCTG	CAGCGCGCCA	CGAGGATGGC	CCACAAGCAG	ATCTACTACT	120
	CGGACAAAGTA	CTTCGACGAA	CACACAGAGT	ACCGGCATGT	TATGTTACCC	AGAGAACTTT	180
	CCAAACAAGT	ACCTAAAACT	CATCTGATGT	CTGAAGAGGA	GTGGAGGAGA	CTTGGTGTCC	240
	AACAGAGTCT	AGGCTGGGTT	CATTACATGA	TTCATGAGCC	AGAACCACAT	ATTCTTCTCT	300
50	TTAGACGACC	TCTTCCAAAA	GATCAACAAA	AATGAAGTTT	ATCTGGGGAT	CGTCAAATCT	360
	TTTTCAAATT	TAATGTATAT	GTGTATATAA	GGTAGTATTC	AGTGAATACT	TGAGAAATGT	420
	ACAAATCTTT	GATCCATACC	GTGTCATGAG	CTGTATTCTT	CACAGCAACA	GAGCTCAGTT	480
	AAATGCAACT	GCAAGTAGGT	TACTGTAAAG	TGTTTAAGAT	AAAAGTTCTT	CCAGTCAGTT	540
	TTTCTCTTAA	GTGCCTGTTT	GAGTTTACTG	AAACAGTTTA	CTTTTGTTC	ATAAAGTTTG	600
55	TATGTTGCAT	TTAAAAAAA	AAAAAAA				

60 Seq ID NO: 115 Protein sequence:
Protein Accession #: NP_001818

	1	11	21	31	41	51	
60	MAHKQIYYS	KYFDEHYEYR	HVMLPRELSK	QVPKTHLMSE	EEWRRRLGVQ	SLGWVHYMIH	60
	EPEPHILLFR	RPLPKDQKQK					

65 Seq ID NO: 116 DNA sequence
Nucleic Acid Accession #: CAT cluster

	1	11	21	31	41	51	
70	TCAGACCTCA	TGAGTCACTT	GGACTCTTGA	GCCACCTCTG	GGGGTGGAGT	CTCTCTCCTG	60
	GCACTCTGGAC	CCTTGGTGCT	ATCGACGAAG	CTTGGGTGGG	GCTCTTAGCT	GCTATGTGCA	120
	AGAGGTGTGT	TCCAGGGAAA	GCCCCATATCT	CTCTGCAGAG	GTCAAGTGAA	AGCGACGGCC	180
	GCAGCCAACA	GAGTTCAAAA	TGCAGGCTTG	GAAAGTACAG	GGGGCTCTGT	GGAGGATGGG	240
	AAGGACTGAT	CCACATCCCC	ACCAGGAAGT	TAGCAGAAC	CCCCGCGTGC	CAACTGGACC	300
	CCTTGGAAAG	ACCTGGGCTCA	GGCTGGACCA	CCTCTTGAGA	GGGAGGAGCT	CTGGATTGGA	360
75	TCAAGAATTC	TTTGCTGAGC	ATGGTGCCTC	ATGCCTATAA	TACCAACACT	TTGGGAGGCC	420
	AGTGTGGGAG	GATCTCTTGA	GCCAGGAGT	TCAAGACTAG	CCTGGGCAAC	ACAGAGAGAA	480
	CCCATCTCTA	AAATAATAAT	AATAATAAAA	TAAAAAATTA	GCAGGGCATG	GTGGCATGTG	540
	CCTGTAGTTC	CAGCTACCCA	GAGGGCTGAG	GCAAGAGGAT	GGCTGGAGCC	TGGGATGTTG	600
	AGGCTGCAAT	GAACTGTGAT	TACCCCACTG	CACTCCAGCC	TGGGCAAAAG	AGCGAGAGAA	660
80	CCTGTCTCAA	ATAATAATAA	TAATAATAAT	CTTATTTTGG	AGAATAAAGA	GACCTCTGGA	720
	TTTGAGGTGC	CATTTGGGTA	GAAAGAAAAG	ACGTTTACAC	CGAGAAATAG	TCTGTGTTGC	780
	CCTGAAGGAG	CAGAGGGATG	CATCGCTGGA	GGTGACCTAC	AGTTGAAGAA	GACTCATTAT	840
	GACAGACCTT	GTCCTTCTTC	CTTGTGGAAA	GTGTTTCTCT	TGCTGTCTACT	GCTCATGAGA	900
	CTCTTCCCCC	TCCCTGTCCC	AGGGAACCAA	AGGGCTTTCT	ACCACACCTT	TTCTTGCCCC	960
85	CGCCCTCCCA	TGTCTGCTGT	GCCTTTGTAC	TCAGCAATTC	TTGTTTGTCT	CATTATCTTC	1020
	CAGCCGGATA	CAGAGTGAAT	AGTTAACCCAC	ACTTAGGTCA	AATAGGATCT	AAATTTTGTG	1080
	TCCTGCTCCG	TGTAAGAGAG	CCAGTGTTTG	TGTGTTGCAA	GCAGCCTTGG	AATAGTAATC	1140

WO 02/086443

PCT/US02/12476

5
10
15

```
CTTCTCATT GTTTGGGATC TGGCCACCAA GTTCCAGAAT GATACACGGA TCAGTGCAGA 1200
AGTTCATCAG GCTCTCGGAC CTTAGGGCTG TTGAGAGAAG GTTCAGCAGC AGAACTGATG 1260
GTGAAGGCTC GTGTTCTCCA TCCTCAACTT TCTTTGCTTC GATCATACAC AAGAATACAT 1320
TTGGAAGGGC AAAAAATGAA CACTGTCGTT CATTGCAGCC GTGTTTTGTG ACACAGATGC 1380
ACAGTCTGCT GTGAAGACCT TCTCTCAAGT GGCATTTTGG AGTCCATGCC AGATCATGGT 1440
GCTTCTAGAG AGACTGACAG CTATCAGGGG TTGTGGCACT TAGTGAGGAC TCTCTCCCC 1500
CAGTGTGTGC TGATGACACA TACACACCTG ACAATAGCTT GAGTCTTCTC TGTTCCTTTT 1560
ACTCTGTAGC CAACATACAC ATGATTTAAA ACCCTTTCTA AATATCTATC ATGGTTTCATC 1620
CTTGTCACAA TCAGAGTCA GAGCTATTG TACTTCATTA TTATTTCCAA GGCAGATAGT 1680
TGGCTTTCTT TTTGCAAAAA TAATTAAAGT TTTTGTATGT TGCAAAAAAA AAAAAAAA 1740
AAACAAAAAA
```

Seq ID NO: 117 DNA sequence
Nucleic Acid Accession #: BC012178.1
Coding sequence: 204-2285

20
25
30
35
40
45
50
55
60

```
1 11 21 31 41 51
| | | | |
CTTCTCTCCC GCGCGCTGG GCGCGCGCT CCGCTGCTGT TGCTCCATTG GCGCGTTTTT 60
TGGCGGCTGG CTCCTCTCCG CTGCCGGCTG CTCCTCGACC AGGCCTCCTT CTCAACCTCA 120
GCGCGCGGCG CGACCCCTTC CGGCACCCTC CCGCCCCGTC TCGTACTGTC GCCGTCACCG 180
CCGCGGCTCC GGCCTTGGCC CCGATGGCTC TGTGCAACGG AGACTCCAAG CTGGAGAATG 240
CTGGAGGAGA CCTTAAGGAT GGCCACCACC ACTATGAAGG AGCTGTTGTC ATTCTGGATG 300
CTGGTGTCTA GTACGGGAAA GTCATAGACC GAAGAGTGAG GGAAGTGTTC GTGCAGTCTG 360
AAATTTTCCC TCTGGAAACA CCAGCATTTC CTATAAAGGA ACAAGGATTC CGTGCTATTA 420
TCATCTCTGG AGGACCTTAA TCTGTGTATG CTGAAGATGC TCCCTGGTTT GATCCAGCAA 480
TATTCACATAT TGGCAAGCCT GTTCTTGAAA TTGTCTATGG TATGCAGATG ATGAATAAGG 540
TATTTGGAGG TACTGTGCAC AAAAAAAGTG TCAGAGAAGA TGGAGTTTTC AACATTAGTG 600
TGGATAATAC ATGTTCATTA TTCAGGGGCC TTCAGAAGGA AGAAGTTGTT TTGCTTACAC 660
ATGGAGATAG TGTAGACAAA GTAGCTGATG GATTCAAGGT TGTGGCACGT TCTGGAAACA 720
TAGTAGCAGG GATACCTAAA GAATCTAAAA AGTTATATGG AGCACAGTTC CACCCTGAAG 780
TTGGCCTTAC AGAAATCTGA AAGTAATATC TGAAGAATTT CCTTATGAT ATAGCTGGAT 840
GCAGTGAAC CTTCACCTGT CAGAACAGAG AACTTGAGTG TATTCGAGAG ATCAAAGAGA 900
GAGTAGGCAC GTCAAAAGTT TTGTTTTTAC TCAGTGGTGG AGTAGACTCA ACAGTTTGTA 960
CAGCTTTGCT AAATCGTGCT TTGAACCAAG AACAAAGTCT TGCTGTGCAC ATTGATAATG 1020
GCTTTATGAG AAAACGAGAA AGCCAGTCTG TTGAAGAGGC CCTCAAAAAG CTTGGAATTC 1080
AGGTCAAAGT GATAATCTCT GCTCATCTCT TCTACAATGG AACAAACAAC CTACCAATAT 1140
CAGATGAAGA TAGAACCCCA GTGAAAAGAA TTAGCAAAAC GTTAAATATG ACCCAAGTCT 1200
CTGAAGAGAA AAGAAAAATC ATTGGGGATA CTTTGTGTTA GATTGCCAAT GAAGTAATTTG 1260
GAGAAATGAA CTGTAAACCA GAGGAGGTTT TCCTTGCCCA AGGTACTTTA CGGCCTGATC 1320
TAATTGAAGG TCCATCCCTT GTTGCAAGTG GCAAAGCTGA ACTCATCAA ACCCATCACA 1380
ATGACACAGA GCTCATCAGA AAGTTGAGAG AGGAGGGAAA AGTAATAGAA CCTCTGAAAG 1440
ATTTTCATPA AGATGAAGTG AGAATTTTGG GCAGAGAACT TGGACTTCCA GAAGAGTTAG 1500
TTTCCAGGCA TCCATTTCCA GGTCTTGGCC TGGCAATCAG AGTAATATGT GCTGAAGAAC 1560
CTTATATTGG TAAGGACTTT CCTGAAACCA ACAATATTTT GAAAATAGTA GCTGATTTTT 1620
CTGCAAGTGT TAAAGAGCCA CATACCTTAT TACAGAGAGT CAAAGCCTGC ACAACAGAG 1680
AGGATCAGGA GAGACTGATG CAAATTACCA GTCTGCATTC ACTGAATGCC TTCTTGCTGC 1740
CAATTAAGAC TGAAGTGTG CAGGGTGACT GTCTGTTCTA CAGTTACGTG TGTGGAATCT 1800
CCAGTAAAGA TGAACCTGAC TGGGAATCAC TTATTTTCTT GGCTAGGCTT ATACCTCGCA 1860
TGTGTACAAA CGTTAACAGA GTTGTTTATA TATTTGGCCC ACCAGTTAAA GAACCTCCTA 1920
CAGATGTGTAC TCCCACTTTC TTGACACACG GGGTGCTCAG TACTTTACGC CAAGCTGATT 1980
TTGAGGCCCA TAACATCTCT AGGAGTCTG GGTATGCTGG GAAAATCAGC CAGATGCCGG 2040
TGATTTTGAC ACCATTACAT TTTGATCGGG ACCCACTTCA AAAGCAGCCT TCATGCCAGA 2100
GATCTGTGGT TATTCGAAAC TTTATTACTA GTGACTTCAT GACTGGTATA CTGCAACAC 2160
CTGGCAATGA GATCCCTGTA GAGGTGGTAT TAAAGATGGT CACTGAGATT AAGAAGATTC 2220
CTGGTATTTT TCGAATTATG TATGACTTAA CATCAAAGCC CCCAGGAAC ACTGAGTGGG 2280
AGTAATAAAC TTCTGTCTCT ATTAATAA
```

Seq ID NO: 118 Protein sequence:
Protein Accession #: AAH12178.1

65
70
75
80

```
1 11 21 31 41 51
| | | | |
MALCNGDSKL ENAGGDLKDG HHHYEGAVVI LDAGAQYGVK IDRRVRELTV QSEIFPLETP 60
AFAIKEQGFRI AIISGGPNS VYAEADPWFD PAIFTYIKPV LGICYGMQMM NKVFGGTVHK 120
KSVREDGVFN ISVDNTCSLF RGLQKEVVVL LTHGDSVDKV ADGFKVVAR S GNIVAGIANE 180
SKKLYGAQFH PEVLGTENGK VILKNFLYDI AGCSGTFTVQ NRELECIREI KERVTGTSKVL 240
VLLSGGVNST VCTALLNRAL NQEQVIAVHI DNGFMRKRES QSVEEALKKL GIQVKVINAA 300
HSFYNGTTTL PISDEDRTFR KRISKTLNMT TSPEEKRII GDTFVKIANE VIGEMNLKPE 360
EVFLAQGTLR PDLIESASLV ASGKAELIKT HHNDTELIRK LREEGKVIEP LKDPHKDEV 420
ILGRELGLPE ELVSRHPFPG PGLAIRVICA EEPYICKDFP ETNNILKIVA DFSASVKKP 480
TLLQRVKACT TEEDQELMQ ITSLSLNAF LLPIKTVGVQ GDGRSYSYVC GISSKDEPDW 540
ESLIFLARLI PRMCHNVNRV VYIFGPPVKE PPTDVTPTFL TTGVLSTLRQ ADPEAHNLR 600
ESGYAGKISQ MPVILTPLHF DRDPLQKPS CQRSVVIRTF ITSDFMTGIP ATPGNEIPVE 660
VVLKMTVEIK KIPGISRIMY DLTSKPPGTT ENE
```

Seq ID NO: 119 DNA sequence
Nucleic Acid Accession #: NM_006500.1
Coding sequence: 27..1967

85

```
1 11 21 31 41 51
| | | | |
ACTTGGCTCT GCGCCTCCGG CCAAGCATGG GGCTTCCCAG GCTGGTCTGC GCCTTCTTGC 60
TCGCCGCTGT CTGCTGCTGT CCTCGCTCG CGGGTGTCGC CGGAGAGGCT GAGCAGCCTG 120
CGCCTGAGCT GGTGGAGGTG GAAGTGGGCA GCACAGCCCT TCTGAAGTGC GGCTCTCCC 180
AGTCCCAAGG CAACCTCAGC CATGTCGACT GGTTTTCTGT CCACAAGGAG AAGCGGACGC 240
```


	TCATCTTCGG	TGTGCGCCAG	GGCCAGGGCC	AGAGCGAACC	TGGGGAGTAC	GAGCAGCGGC	300
	TCAGCCTCCA	GGACAGAGGG	GCTACTCTGG	CCCTGACTCA	AGTCACCCCC	CAAGACGAGC	360
	GCATCTTCTT	GTGCCAGGGC	AAGCGCCCTC	GGTCCCAGGA	GTACCGCATC	CAGCTCCGCG	420
5	TCTACAAAGC	TCCGGAGGAG	CCAAACATCC	AGGTCAACCC	CCTGGGCATC	CCTGTGAACA	480
	GTAAGGAGCC	TGAGGAGGTC	GCTACCTGTG	TAGGGAGGAA	CGGGTACCCC	ATTCTCAAG	540
	TCATCTGGTA	CAAGAAATGGC	CGGCCTCTGA	AGGAGGAGAA	GAACCGGGTC	CACATTTCAGT	600
	CGTCCCAGAC	TGTGGAGTCG	AGTGGTTTGT	ACACCTTGCA	GAGTATTCTG	AAGGCACAGC	660
	TGGTTAAAGA	AGACAAAGAT	GCCCACTTTT	ACTGTGAGCT	CAACTACCGG	CTGCCAGTGT	720
10	GGAAACCAT	GAAGGAGTCC	AGGGAAGTCA	CCGTCCCTGT	TTTCTACCCG	ACAGAAAAG	780
	TGTGGCTGGA	AGTGGAGCCC	GTGGGAATGC	TGAAGGAAGG	GGACCGCGTG	GAATCAGGT	840
	GTCTGGCTGA	TGGCAACCTT	CCACCACACT	TCAGCATCAG	CAAGCAGAAC	CCCAGCAGCA	900
	GGGAGGCAGA	GGAAAGAGACA	ACCAACGACA	ACGGGCTCCT	GGTGTGCGAG	CCTGCCCGGA	960
	AGGAACACAG	TGGGCGCTAT	GAATGTCAGG	CCTGGAACTT	GGACACCATG	ATATCGCTGC	1020
15	TGAGTGAACC	ACAGGAACTA	CTGGTGAAC	ATGTGTCTGA	CGTCCGAGTG	AGTCCCGCAG	1080
	CCCCGTAGAG	ACAGGAAGGC	AGCAGCCTCA	CCCTGACCTG	TGAGGCAGAG	AGTAGCCAGG	1140
	ACCTCGAGTT	CCAGTGGCTG	AGAGAAGAGA	CAGACCAAGT	GCTGGAAAGG	GGGCGCTGTC	1200
	TTCAAGTGCA	TGACCTGAAA	CGGGAGGCAG	GAGGCGGCTA	TGCTGCGGTG	GGCTCTGTGC	1260
	CCAGCATACG	CGGCTCTGAC	CGCACACAGC	TGGTCAAGCT	GGCCATTTT	GGCCCCCTTT	1320
20	GGATGGCATT	CAAGGAGAGG	AAGGTGTGGG	TGAAGAGAAA	TATGGTGTGT	AATCTGTCTT	1380
	GTGAAGCGTC	AGGGCAGCCC	CGGCCACACA	TCTCTGGAAA	CGTCAACGGC	ACGGCAAGTG	1440
	AACAAGAGCA	AGATCCACAG	CGAGTCTCTG	GCACCTGAAA	TGTCCTCGTG	ACCCCGGAGC	1500
	TGTTGGAGCA	AGGTGTTGAA	TGCACGGCCT	CCAACGACCT	GGGCAAAAAC	ACCAGCATCC	1560
	TCCTTCTGCA	GGCTCTCAAT	TAAACACACC	TCACACACAG	CTCCACACAC	ACCACTGGCC	1620
25	TCAGCACTTC	CACTGCCAGT	CCTCATACCA	GAGCCACACG	CACCTCCACA	GAGAGAAAGC	1680
	TGCCGGAGCC	GGAGAGCCGG	GGCGTGGTCA	TCGTGGCTGT	GATTGTGTGC	ATCCTGGTCC	1740
	TGGCGGTGCT	GGGGCTGTCT	CTCTATTTC	TCTATAAGAA	GGGCAAGCTG	CCGTGCAGGC	1800
	GCTCAGGAAA	GCAGGAGATC	ACGCTGCCCC	CGTCTCGTAA	GACCGAAGCT	GTAGTTGAAG	1860
	TTAAGTCAGA	TAACTGCCCA	GAAGAGATGG	GCCTCTGACA	GGGCAGCAGC	GGTGACAAGA	1920
30	GGGCTCCGGG	AGACCAGGGA	GAGAAATACA	TCGATCTGAG	GCATTAGCCC	CGAATCACTT	1980
	CAGCTCCCTT	CCCTGGCTGG	ACCATTCCCA	GCTCCCTGCT	CACCTCTCTC	TCAGCCAAAG	2040
	CCTCCAAAGG	GACTAGAGAG	AAGCCTCCTG	CTCCCTCAC	CTGCACACCC	CCTTTCAGAG	2100
	GGCCACTGGG	TTAGGACCTG	AGGACCTCAC	TTGGCCCTGC	AAGCCGCTTT	TCAGGGAACA	2160
	GTCCACCACC	ATCTCTCCCA	CGTTGAGTGA	AGCTCATCCC	AAGCAAGGAG	CCCCAGTCTC	2220
35	CCGAGCGGGT	AGGAGAGTTT	CTTGACAGAC	GTGTTTTTTC	TTTACACACA	TTATGGCTGT	2280
	AAATACCTGG	CTCTGTCAG	CAGCTGAGCT	GGGTAGCCTC	TCTGAGCTGG	TTTCTGCCC	2340
	CAAAGGCTGG	CTTCCACCAT	CCAGGTGCAC	CAGTGAAGTG	AGGACACACC	GGAGCCAGGC	2400
	GGCTGCTCAT	GTTGAAGTGC	GCTGTTTACA	CCCGCTCCGG	AGAGCACCCC	AGCGGCATCC	2460
	AGAAGCAGCT	CGCTGTGTGC	TGCCACCACC	CTCCTGCTCG	CCTCTTCAAA	GTCTCTGTGT	2520
40	ACATTTTTTC	TTTGGTCAGA	AGCCAGGAAC	TGGTGTCAAT	CCTTAAAGA	TACGTGCCGG	2580
	GGCCAGGTGT	GGTGGCTCAC	GCCTGTAATC	CCAGCACTTT	GGGAGGCCGA	GGCGGGCGGA	2640
	TCACAAAGTC	GAGTACGAGAC	CATCCTGGCT	AACACGGTGA	AACCTGTGCT	CTACTAAAAA	2700
	TACAAAAAAA	AATAGCTAG	CGGTAGTGGT	TGGCACCTAT	AGTCCAGACT	ACTCGGAAGG	2760
	CTAAGAGGAG	GAATGCTAT	AGATCCAGGA	GGTGGAGCTT	GCAGTGAGTG	GAGACCGTGC	2820
45	CACTGCATCT	CAGCTGGGCG	AACACAGCGA	GACTCCGTCT	CGAGGAAAAA	AAAAGAAAAA	2880
	ACGCGTACCT	GCGGTGAGGA	AGCTGGGCGC	TGTTTTTCAG	TTGAGGTGAA	TTAGCCTCAA	2940
	TCCCGTGTTT	CACCTGTCTC	CATAGCCCTC	TTGATGGATC	ACGTAAAGCT	GAAAGGCAGC	3000
	GGGGAGCAGA	CAAGATGAG	GTCTCACTG	TCCTTCATGG	GGATTAAAGC	TATGGTTATA	3060
	TTAGCACCAA	ACTTCTACAA	ACCAAGCTCA	GGGCCCAAC	CTAGAAAGGG	CCCAATGAG	3120
50	AGAAATGAT	TTAGGGATGG	AAAACGGGGC	CTGGCTAGAG	CTTCGGGTGT	GTGTGTCTGT	3180
	CTGTGTGTAT	GCATACATAT	TGTGTATAT	ATGGTTTGT	CAGGTGTGTA	AATTTGCAAA	3240
	TTGTTTCTCT	TATATATGTA	TATATATATA	TATATGAAAA	TATATATATA	TATGAAAAAT	3300
	AAAGCTTAAT	TGTCCCAGAA	AATCATACAT	TGCTTTTTTA	TTCTACATGG	GTACCACAGG	3360
	AACCTGGGGG	CCTGTGAAAC	TACAACCAAA	AGGCACACAA	AACCGTTTCC	AGTTGGCAGC	3420
55	AGAGATCAGG	GGTTACCTCT	GCTTCTGAGC	AAATGGCTCA	AGCTCTACCA	GAGCAGACAG	3480
	CTACCCTACT	TTTCAGCAGC	AAAACGTCCC	GTATGACGCA	GCACGAAGGG	CCTGGCAGGC	3540
	TGTTAGCAGG	AGCTATGTCC	CTTCTATATG	TTTCCGTCCA	CTT		

Seq ID NO: 120 Protein sequence:
Protein Accession #: NP_006491.1

	1	11	21	31	41	51	
65	MGLPRIVCAF	LLAACCCCPR	VAGVPGEAEO	PAPELVEVEV	GSTALLKCOL	SQSQGNLSHV	60
	DWFSVHKEKR	TLIFRVRQGG	QSEPGGEYEQ	RLSLQDRGAT	LALTQVTFQD	ERIFLCQGR	120
	PRSQEYRIQL	RVYKAPBEPN	IQVNPGLGIPV	NSKEPEEVAT	CVGRNGYPIPI	QVIWYKNGRP	180
	LKBEENRVIH	QSSQTVSSSG	LYTLQSLILKA	QLVKEDKDAQ	FYCLNRYLRL	SGNHMKESRE	240
70	VTVPVFPTE	KVWLEVEFVG	MLKEGDRVEI	RCLADGNPPP	HFSISKQNPFS	TREABEETTN	300
	DNGVLVLEPA	RKEHSGRYEC	QAWNLDTMIS	LLSEPOELLV	NYVSDVRVSP	AAPERQEGSS	360
	LTLTCEABSS	QDLFQWLRE	ETDQVLERGP	VLQLHDLKRE	AGGGYRCVAS	VPSIPGLNRT	420
	QLVKLAIFGP	PWMAFKERKV	WVKENMVLNL	SCBASGHPRP	TISWNVNGTA	SEQDQDPQRV	480
	LSTLNLVLT	ELLETVBECT	ASNDLGKNTS	ILFLELVNLT	TLTPDSNTTT	GLSTSTASPH	540
75	TRANSTSTER	KLPEPESRGV	VIVAVIVCIL	VLAVLGAVLY	FLYKKGKLPC	RRSGKQETIL	600
	PFSRKTELVV	EVKSDKLPPE	MGLLQSSGD	KRAPGDQGEK	YIDLRH		

Seq ID NO: 121 DNA sequence
Nucleic Acid Accession #: NM_018306
Coding sequence: 60-671

	1	11	21	31	41	51	
80	ATAGTCTACA	CAGAGCTCCC	CTTGCTGCCC	AGACAAGCTG	AAGGACCACA	GGAAAAGCCA	60
	TGGAGACTTC	AGCATCTCTC	TCCAGCCTC	AGGACAACAG	TCAAGTCCAC	AGAGAAACAG	120
85	AAGATGTAGA	CTATGGAGAG	ACAGATTTC	ACAAGCAAGA	CGGGAAGGCT	GGACTCTTTT	180
	CCCAAGAAAC	ATATGAGAGA	AACAAGTCTT	CTTCTCTCTC	CTTCTCTTCC	TCCTCATCTC	240
	CCTCATCTTC	TTCATCTCTC	TCCTCTCTCAG	GTCTTGGGCA	TGGGGAGCCT	GACGTTTTGA	300

WO 02/086443

PCT/US02/12476

5
10
15
20

```

AGGATGAGCT TCAACTCTAT GGAGATGCTC CTGGAGAGGT GGTACCCTCT GGGGAATCAG 360
GACTCCGAAG GAGAGGCTCT GACCCAGCAA GTGGAGAAGT GGAGGCCTCT CAGTTAAGAA 420
GACTGAATAT AAAGAAAGAT GATGAGTTT TCCATTTCGT CCTCTGTGC TTTGCCATCG 480
GGGCCTTGCT GGTGTGTTAT CACTATTACG CAGACTGGTT CATGTCTCTT GGGGTCCGCC 540
TGCTCACCTT CGCTCCCTTG GAAACCGTTG GCATCTACTT CGGACTAGTG TACCGTATCC 600
ACAGCGTCTT CCAAGGCTTC ATCCCTCTCT TCCAGAAAGT TAGGCTGACA GGGTTCAGGA 660
AGACTGACTG AGGCCACTTC CAGGTGGGCA GCAGAGGCAG GCCCAGTGT GACCACCACT 720
GCGACCCCTG AGCCCAACAG GGCAGAGCAG CATTCTGAGA GACGCACAGG AGACCAAGCC 780
AGACCAATAA ACAGAACACT TTTCTTCCA TGTGCTCTGA ATGTTGGCAC CAGCCCGGCC 840
AGGGGCATCT CATTGTTGGCA GTACTGCTGT GCAACCCAGC TGCAAGGATG GAAGGCAGAG 900
GGTGGGTGTG GGGCCTGAGG CTTCACAGTA CCTGGACCAG CAGGAAGATT CTGGGAGGTC 960
ACTGCTCTCA GAGGACAGCA AGGGACCCCTG AGCTCTGCAA GCTGTGATCT GTCTGGGTTT 1020
ATGTTTTTTC TCAAATCCCA GGCTATCTGC ATGCGCTCTC AGGTGCTACC GAGCCATCCT 1080
GGGAGAGATG GATGGTCCAC TGCTTTGAGG CAGGGAGCCA TCGGGCTGGG GCCCTTGGT 1140
GAACTGTATG CAGGTAAGAT GCTGAGGACT AAAACCATTT TTTTTCACCC CAAAAAATAA 1200
GGCAGGAAAA TGATCTCAG AAACCTAAATG GCAGCCAGGC ATGGGGGCTC ACGACTGTAA 1260
TCCTCGCACT TTGGGAGGCT CAGGCTAAGG GTGCGCTTGA GCTGAGAGTT CAAGACCAAC 1320
CTGGGCAACA TAGTGAGACC CCATCTCTTA CAATTTTTTT TTAATGACCA AATGTGGCGG 1380
TACATACCTG TACATACCTG CGGTTCACAG TACTCAAGAG GCTGAGGCAG GAGGACTGCT 1440
TGAGCCCAAG AGTTCAGGGC TGCACTGAGG TACGATCAAG CCACTGCACT CCAGCCTGGG 1500
CGACAGAGCA AGATCGTTTC TCTAAAAAT

```

25 Seq ID NO: 122 Protein sequence:
Protein Accession #: NP_060776

30

```

1 11 21 31 41 51
| | | | |
METSASSSQP QDNSQVHRET EDVDYGETDF HKQDGKAGLF SQEQYERNKS SSSSFSSSSS 60
SSSSSSSSSS FPHGHEFDVL KDEQLQYGDA PGEVVPSSGBS GLRRRGSDPA SGEVEASQLR 120
RLNIKKDDEF GHFVLCLCPAI GALLVCYHY ADWFMSLGVG LLTFASLETV GIYFLVLYRI 180
HSVLQGFPL FQKRLTGFR KTD

```

35 Seq ID NO: 123 DNA sequence
Nucleic Acid Accession #: BC022542
Coding sequence: 243..896

40
45
50
55
60
65
70

```

1 11 21 31 41 51
| | | | |
ACTTGGTCCC AGCCGATAAA TCTGGGGCAG CGCGCGGTAG GAGCTGCGGG CGGCCAGGCC 60
CCTTCCTGCG TCCGCACTCG QCCCGCGCGG CCCCTCTCGG GCGTCCGGCT TCCGGCGTCC 120
TGGCGGCTCG GGTGGCGGCG GTTCGGGCGG CCGCCTGCGT GCTCCTCGGG GCGGCGACGG 180
GGCTCACGCG CGGCGCGCGC ACGGCCTTCA CCGCGCGCGG CTCTGACGCC GGCATAAGGG 240
CCATGTGTTC TGAATTTATT TTGAGGCAAG AAGTTTGTAA AGATGGTTTC CACAGAGACC 300
TTTTAATCAA AGTGAAGTTT GGGGAAAGCA TTGAGGACTT GCACACGTGC CGTCTCTTAA 360
TTAAACAGGA CATTCCTGCA GACTTTATG TGGATCCGTA TGAGTTGGCT TCATTACGAG 420
AGAGAAACAT AACAGAGGCA GTGATGGTTT CAGAAAAATT TGATATAGAG GCCCTTAAT 480
ATTTGTCCAA GAGTCTTGAA GTTCTCATTT ATGCCAGACG AGATTACAGG TGCATTGACT 540
GTTTTCAGAC CTTTTTGCCT GTGCACTGCC GCTATCATCG GCCGCACAGT GAAGATGGAG 600
AAGCCTCGAT TGTGGTCAAT AACCCAGATT TGTGTATGTT TTGTGACCAA GAGTTCCTGA 660
TTTTGAAGAT CTGGGCTCAC TCAGAAAGTG CAGCCCTCTG TGCTTTGGAT AATGAGGATA 720
TATGCCAATG GAACAAGATG AAGTATAAAT CAGTATATAA GAATGTGATT CTACAAGTTC 780
CAGTGGGACT GACTGTACAT ACCTCTCTAG TATGTTCTGT GACTCTGCTC ATTACAATCC 840
TGTGCTCTAC ATTGATCCTT GTAGCAGTTT TCAAATATGG CCATTTTTC CTATAAGTTT 900
TATGTAGTTA AATGCTCTCT AGAAACCTAA ATAAGATCTA TTAATTTCTG ACGAGAGGTG 960
TTCTTTCTAGA ATTAATTACT TTTATCTTTT GTCTTCATTT GTGGCCAAAA TTATGTTTAC 1020
TAGAGGAAAT TTGGGATCAT TCTCAGCTAA TTCCAAATG TAGTGCTCTA TTGCATGGAT 1080
CCTTGGTAAT CCTCAAGCAT CAGATGCCAT AAGGGGAAAC TTAATTTCTG TAAATTAATG 1140
TTTATTTTGT GAGAAGTGCA TTTATCTTCA TTTGGGGTAG AAAAATTATT TCTTTATGTA 1200
GTAGAGACAA ATTATTCTCA TTTTGCAAGT ACITTTCAAT TAAGCTACAA ATTGAGAAAA 1260
COGTTATAAA TAAGAATAAA ATAGGCCAGG CACAGTGGCT CACACCTGTA ATCCAGCAC 1320
TTTGGGAGGC CGAGGTGGGC GGATCACCAG AGGTCAAGAG TTTGAGACCA GCTTGGTGAA 1380
ACCTGTCTC TACTAAAAAT ACAAAAGTTA GCTGGGGCTG GTGGTGGGCA TCTGTAGTCC 1440
CAGCTAATTG GAAGGGTGAG GCGGGAGGAT CGCTTGAACC TGGGAGGCGG AGGTTCACAG 1500
GAGCCAAGAT CGCACACTG CACTACAGCC TGGGCGACAG AACGAGACCC TGTCTCCAAA 1560
GGAAAAACAA AAAAGAAGAA TAAATAATT TGGATGAAAA TCATGTTTAT TTAATAGTA 1620
ATGTCATGAG ACTATTAAAG ATGTGCCAGA GTTTCATGA AAATCATTAA AGTAGGACAG 1680
CTAAGAAATT AATATTAATA TAAAAATTAT TGATAATCTT AAATTATTGA TTATTCCTTA 1740
ACGCACTCCA TTCTCTTTT ACATTTTATC ATGTTTCTTT TGAATATATG AATTGGCAAA 1800
GGACTTGATG AAACGTAGTA CTAAGATTG GTACAGAGTA TGTGAGGAAG ACAACTCAGA 1860
TTGCCATTTT AAATAAAGTT GTACATGAAC AAAAAAAAAA AAAAAA

```

75 Seq ID NO: 124 Protein sequence:
Protein Accession #: AAH22542

80

```

1 11 21 31 41 51
| | | | |
MCSEIILRQE VLKDGPHRDL LIKVKFGESI EDLHTCRLLI KQDIPAGLYV DPYELASLRE 60
RNITEAVMVS ENPDIEAPNY LSKSEVLIY ARRSQCIDC FQAFPLVHCR YHRPHSEGE 120
ASIVVMNPD LMFCDQAGSR RMIRFRPDSF DKTIEFPILK CWAHSEVAAP CALENEDICQ 180
WNMKYKSVY KNVILQVPVG LTVHTSLVCS VTLITILCS KKKKK

```

85 Seq ID NO: 125 DNA sequence
Nucleic Acid Accession #: NM_004994.1
Coding sequence: 20..2143

```

1      11      21      31      41      51
|      |      |      |      |      |
AGACACCTCT GCCCTCACCA TGAGCCTCTG GCAGCCCTG GTCTGTGTGC TCCTGTGTGCT 60
5 GGGCTGTGTC TTTGTGCCCC CCAGACAGCG CCAGTCCACC CTTGTGCTCT TCCCTGGAGA 120
CCTGTAGAAC AATCTCACCG ACAGGACAGT GGCAGAGGAA TACCTGTACC GCTATGGTTA 180
CACTCGGGTG GCAGAGATGC GTGGAGAGTC GAAATCTCTG GGGCCTGCGC TGCTGCTTCT 240
CCAGAAGCAA CTGTCCCTGC CCGAGACCGG TGAGCTGGAT AGCGCCACGC TGAAGGCCAT 300
GCGAACCCCA CGGTGCGGGG TCCCAGACCT GGCAGATTG CAAACCTTTG AGGGCGACCT 360
10 CAAGTGGCAC CACCACAACA TCACCTATTG GATCCAAAC TACTCGGAAG ACTTGCCTCG 420
GGCGGTGATT GACGACGCTT TTGCCCGCGC CTTGCGACTG TGGAGCGCGG TGACGCCGCT 480
CACCTTCACT CGCTGTACA GCGGGGAGCG AGACATCGTC ATCCAGTTTG GTGTGCGGGA 540
GCACGAGAC GGGTATCCCT TCGACGGGAA GGACGGGCTC CTGGCACACG CCTTCTCTCC 600
TGGCCCGCGC ATTACGGGAG ACGCCCATTT CGACGATGAC GAGTTGTGGT CCCTGGGCAA 660
15 GGGCGTCTGT GTTCCAATCT GGTTTGGAAA CGCAGATGGC GCGGCTGCC ACTTCCCCTT 720
CATCTTGGAG GGCCGCTCCT ACTCTGCTTG CACCACCGAC GGTGCTCCG ACGGCTTGCC 780
CTGGTGCAGT ACCACGGGCA ACTACGACAC CGACGACCGG TTTGGCTTCT GCCCAGCGA 840
GAGACTCTAC ACCCGGGAGC GCAATGTGTA TGGGAAACCC TGCCAGTTTC CATTCATCTT 900
CCAAGGCCAA TCCTACTCCG CCTGCACCAC GGACGGTCCG TCCGACGGCT ACCGTGGTG 960
20 CGCCACCACC GCCAATACG ACCGGGACAA GCTCTTCCGC TTCTGCCGA CCCGAGCTGA 1020
CTCGACGGTG ATGGGGGGCA ACTCGCGGGG GGAGCTGTGC GTCTTCCCTT TCACTTTCTT 1080
GGGTAAAGAG TACTCGACTT TACCAAGGGA GGGCCGCGGA GATGGGCGCC TGTGGTGC 1140
TACCACCTCG AACTTTGACA GCGACAAGAA GTGGGGCTTC TGCCCGGACC AAGGATACAG 1200
TTTGTCTCTC GTGGCGGGC ATGAGTTCCG CCACGCGCTG GGCTTAGATC ATTCTCAGT 1260
25 GCGGAGGCG CTATGTACC CTATGTACC GTTCACTGAG GGGCCCCCTT TGCATAAGGA 1320
CGACGTGAAT GGACATCCGC ACCTCTATGG TCCTCGCCTT GAACCTGAGC CACGGCCTCC 1380
AACCAACACC ACCACGGGCA CACGGCTCC CCGACGGTCC TGCCCCACCG GACCCCCAC 1440
TGTCCACCCC TCAGAGCGGC CCACAGCTGG CCCCACAGGT CCCCCTCAG CTGGCCCCAC 1500
AGTCCGCCCC ACTGCTGGCC CTCTACGGC CACTACTGTG CCTTGGAGTC CGGTGGACGA 1560
30 TGCTTGAAC GTGAACATCT TCGACGCCAT CGCGGAGATT GGAACACAGC TGTATTGT 1620
CAAGATGGG AAGTACTGGC GATTCTCTGA GGGCAGGGGG AGCGGGCGCG AGGGCCCTT 1680
CCTTATCGCC GACATGGTGC CCGCGCTGCC CCGCAAGCTG GACTCGGTCT TTGAGGAGCC 1740
GCTCTCAAG AAGCTTTTCT TCTTCTCTGG CGCCAGGTG TGGGTGTACA CAGGCGGCTC 1800
GGTGTGGGC CCGAGGCGTC TGGACAAGCT GGGCCTGGGA GCCGACGTGG CCCAGGTGAC 1860
35 CGGGGCCCTC CGGAGTGGCA GGGGGAAGAT GCTGCTGTTT AGCGGGCGGC GCCTCTGAG 1920
GTTGAGCTG AAGCGGCAGA TGGTGGATCC CCGGAGCGCC AGCGAGGTGG ACCGGATGTT 1980
CCCCGGGGTG CCTTTGGACA CGCACGACGT CTTCAGTAC CGAGAGAAAG CCTATTTCTG 2040
CCAGGACCGC TTCTACTGGC GCGTGAGTTC CCGAGTGTAG TTGAACAGG TGAACCAAGT 2100
GGGTACGTG ACCTATGACA CCTGACATG CCTGAGGAC TAGGGCTCCC GTCTGCTTT 2160
40 GCAGTGCCAT GTAAATCCCC ACTGGGACCA ACCCTGGGGA AGGAGCCAGT TTGCGGATA 2220
CAACTGGTA TTCTGTCTG GAGGAAAGGG AGGAGTGGAG GTGGGCTGGG CCTCTCTTCT 2280
TCACCTTTGT TTTTGTGG AGTGTTCTTA ATAAACTTGG ATTCCTAAC CTTT

```

Seq ID NO: 126 Protein sequence:
Protein Accession #: NP_004985.1

```

1      11      21      31      41      51
|      |      |      |      |      |
MSLWQPLVLV LVLVLCFFAA PRQRQSTLVL FPGDLRLNLT DRQLAEYLY RYGYTRVAEM 60
50 RGESKSLQPA LLLQLQLSL PETGELDSAT LKAMRTPRCG VPDLGRFOTF EGDLLKWHHN 120
ITYWIQYSE DLPRVIDDA FARAFALWSA VTPLTPTRVY SRDADIVIOF GVAEHGDOYP 180
FDGKDGLLAH AFPFGPIQG DAHPDDDELW SLGKGVVPT RFGNADGAAC HFPFIFEGRS 240
YSACTTGRS DGLFWCSTTA NYDTRDFRFP CPSERLYTRD GNADGKPCQF PFIFQGGSYS 300
ACTTDRSDG YRWCAATTANY DRDLFGFCP TRADSTVMGG NSAGELCVFP PTFLGKEYST 360
CTSEGRDGR LWCATTSNFD SDKWKGFCDP QGVSLFLVAA HEFGHALGLD HSSVPEALMY 420
55 PMYRFTGPP LHKDDVNGIR HLYGPRPEPE PRPFTTTTPO PTAPPTVCPT GPPTVHPSER 480
PTAGPTGPPS AGPTGPTAG PSTATTVPLS PVDDACNVNI FDAIAEIGNQ LYLFPKDGKYW 540
RFSEGRGSRP QGFPLIADKW PALPRKLDSV FEELSKKLF PFSGRQVWVY TGA SVLGP RR 600
LDKLGADV AQTGALRSR RGMMLFSGR RLWRFDVKAQ MVDPRSASEV DRMPFPGVPLD 660
60 THDVFQYREK AYPQDRPYW RVSSRSELNQ VDQGVYVTD ILQCPED

```

Seq ID NO: 127 DNA sequence
Nucleic Acid Accession #: NM_004181
Coding sequence: 32-670

```

1      11      21      31      41      51
|      |      |      |      |      |
GCAGAAATAG CCTAGGGAGA TCAACCCGGA GATGCTGAAC AAAGTGCTGT CCCGCTGGG 60
GGTGCCTGGC CAGTGGCGCT TCGTGGACGT GCTGGGGCTG GAAGAGGAGT CTCTGGGCTC 120
GGTGCCAGCG CCTGCCTGCG CGCTGCTGCT GCTGTTTCCC CTCACGCCCC AGCATGAGAA 180
CTTCAGGAAA AAGCAGATTG AAGAGCTGAA GGGACAAGAA GTTAGTCTTA AAGTGTACTT 240
CATGAAGCAG ACCATTGGGA ATTCCTGTGG CACAATCGGA CTATTACAGC CAGTGGCCAA 300
TAATCAAGAC AAACCTGGAT TTGAGGATGG ATCAGTTCTG AAACAGTTTC TTTCTGAAAC 360
AGAGAAAATG TCCCTGAAG ACAGAGCAAA ATGCTTTGAA AAGAATGAGG CCATACAGGC 420
AGCCCATGAT GCCGTGGCAC AGGAAGGCCA ATGTCGGGTA GATGACAAGG TGAATTTCCA 480
75 TTTTATTCTG TTTAACCAAG TGGATGGCCA CCTCTATGAA CTTGATGGAC GAATGCCTTT 540
TCCGGTGAAC CATGGCCCA GTTCAGAGGA CACCCTGCTG AAGGACGCTG CCAAGGTGTG 600
CAGAGAATTC ACCAGCGGTG AGCAAGGAGA AGTCCGCTTC TCTGCCGTGG CTCTCTGCAA 660
GGCAGCCTAA TGCTCTGTGG GAGGACTTT GCTGATTTC CCTCTTCTCT TCAACATGAA 720
AATATATACC CCCCATGCAG TCTAAAATGC TTCAGTACT GTGAAACACA GCTGTTCTTC 780
80 TGTCTGCGC AACGCGCTTC CCTCAGCCA CACCAGGCA CTTAAGCACA AGCAGAGTGC 840
ACAGCTGTCC ACTGGGCCAT TGTGGTGTGA GCTTCAGATG GTGAAGCATT CTCCCCAGTG 900
TATGTCTTGT ATCCGATATC TAACGCTTTA AATGGCTACT TTGGTTTCTG TCTGTAAAGT 960
AAGACCTTGG ATGTGGTTAT GTTGTCTTAA AGAATAAATT TTGCTGATAG TAGC

```

Seq ID NO: 128 Protein sequence:
Protein Accession #: NP_004172

1	11	21	31	41	51	
MLNKVLSRLG	VAGQWRFVDV	LGLEEESLGS	VPAPACALLL	LFPLTAQHEN	FRKKQIEELK	60
GQEVSPKVYF	MKQTIGNSCG	TIGLIHAVAN	NQDKLGFEDG	SVLKQFLSET	EKMSPEDRAK	120
CFEKNEAIQA	AHDAVAQEGG	CRVDDKVNPH	FILFNNVDGH	LYELDGRMPF	PVNHGASSED	180
TLLKDAAKVC	REFTEREQGE	VRFSAVALCK	AA			

Seq ID NO: 129 DNA sequence
Nucleic Acid Accession #: NM_000213
Coding sequence: 127-5385

1	11	21	31	41	51	
CGCCCGCGCG	CTGCAGCCCC	ATCTCCTAGC	GGCAGCCCGAG	GCGCGGAGGG	AGCGAGTCCG	60
CCCCGAGGTA	GGTCCAGGAC	GGGCGCACAG	CAGCAGCCGA	GGCTGGCCGG	GAGAGGGAGG	120
AAGAGGATGG	CAGGGGCCAG	CCCCAGCCCA	TGGGCCAGGC	TGCTCCTGGC	AGCCTTGATC	180
AGCGTCAGCC	TCTCTGGGAC	CTTGGCAAAC	CGCTGCAAGA	AGGCCCCAGT	GAAGAGCTGC	240
ACGAGGTGTG	TCCGTGTGGA	TAAGGACTGC	GCCTACTGCA	CAGACGAGAT	GTTCAGGGAC	300
CGCGCGTGCA	ACACCCAGGC	GGAGCTGTCT	GCCGCGGGCT	GCCAGCGGGA	GAGCATCGTG	360
GTCAATGGAGA	GCAGCTTCCA	AATCACAGAG	GAGACCCAGA	TTGACACCCAC	CCTGGCGGCG	420
AGCCAGATGT	CCCCCAAGG	CCTGCGGGTC	CGTCTGCGGC	CCGGTGAGGA	GCGGCATTTC	480
GAGCTGGAGG	TGTTTGAAGC	ACTGGAGAGC	CCCCTGGACC	TGTACATCCT	CATGGACTTC	540
TCCAACCTCA	TGTCGATGA	TCTGGACAAC	CTCAGAAGA	TGGGCGAGAA	CCTGGCTCGG	600
GTCTTGAGCC	AGCTCACCAG	CGACTACACT	ATTGGATTGT	GCAAGTTTGT	GGACAAAGTC	660
AGCGTCCGCG	AGACGGACAT	GAGGCCTGAG	AAGCTGAAGG	AGCCCTGGCC	CAACAGTGAC	720
CCCCCTCTCT	CCTTCAAGAA	CGTCATCAGC	CTGACAGAAG	ATGTGGATGA	GTTCGGGAAT	780
AAACTGCAGG	GAGAGCGGAT	CTCAGGCAAC	CTGGATGCTC	CTGAGGGCGG	CTTCGATGCC	840
ATCCTGCAGA	CAGCTGTGTG	CACGAGGGAC	ATTGGCTGGC	GCCGCGCAGC	CACCCACCTG	900
CTGGTCTTCT	CCACCGAGTC	AGCCTTCCAC	TATGAGGCTG	ATGGCGCCAA	CGTGCTGGCT	960
GGCATCATGA	GCGCAACGA	TGAACGGTGC	CACCTGGACA	CCACGGGCAC	CTACACCCAG	1020
TACAGGACAG	AGGAATACCC	GTCCGTGCCC	ACCCCTGGTG	GCCTGTCTGC	CAAGCACAAAC	1080
ATCATCCCCA	TCTTTGCTGT	CACCAACTAC	TCCTATAGCT	ACTACAGAGAA	GCTTCACACC	1140
TATTTCCCTG	TCTCTCACT	GGGGGTGCTG	CAGGAGGACT	CGTCCACAT	CGTGAGCTG	1200
CTGGAGGAGG	CCTTCAATCG	GATCCGCTCC	AACCTGGACA	TCCGGGCCCT	AGACAGCCCC	1260
CGAGGCCTTC	GGACAGAGGT	CACCTCCAAG	ATGTTCCAGA	AGACGAGGAC	TGGGTCTTTT	1320
CACATCCGGC	GGGGGGAGCT	GGGTATATAC	CAGGTGCAGC	TGCGGGCCCT	TGAGCACGTG	1380
GATGGGACGC	ACGTGTGCCA	GCTGCGGGAG	GACCAGAAAG	GCAACATCCA	TCTGAAACCT	1440
TCCTTCTCCG	ACGGCCTCAA	GATGGACGCG	GGCATCATCT	GTGATGTGTG	CACCTGCGAG	1500
CTGCAAAAG	AGGTGCGGTC	AGCTCGCTGC	AGCTTCAACG	GAGACTTCGT	GTGCGGACAG	1560
TGTGTGTGCA	GCGAGGGCTG	GAGTGGCCAG	ACCTGCAACT	GCTCCACCGG	CTCTCTGAGT	1620
GACATTTCAGC	CCTGCTCTGC	GGAGGGCGAG	GACAAGCCGT	GCTCCGCGCG	TGGGGAGTGC	1680
CAGTGCGGGC	ACTGTGTGTG	TACGGCGGAA	GGCCGCTACG	AGGTCAGTTT	CTGCGAGTAT	1740
GACAACTTCC	AGTGTCCCCG	CACCTCCGGG	TTCTCTGCA	ATGACCGAGG	ACGCTGCTCC	1800
ATGGGCCAGT	GTGTGTGTGA	GCCTGGTTGG	ACAGGCCCAA	GCTGTGACTG	TCCCTCAGC	1860
AATGCCACCT	GCATCGACAG	CAATGGGGGC	ATCTGTAATG	GACGTGGCCA	CTGTGAGTGT	1920
GGCGGCTGCC	ACTGCCACCA	GCAGTGCCTC	TACACGGACA	CCATCTGCGA	GATCAACTAC	1980
TGGCGGATGC	TCCCGGGGCT	CTCGAGGAC	CTACGCTCCT	CGGTGCAATG	CCAGGCGTGC	2040
GGCACCGGCG	AGAGAAGAGG	GCGCACGTGT	GAGGAATGCA	ACTTCAAGGT	CAAGATGGTG	2100
GACGAGCTTA	AGGAGCGCGA	GAGGTGGTGT	GTGCGCTGCT	CCTTCCGGGA	CGAGGATGAC	2160
GACTGCACCT	ACAGCTACAC	CATGGAAGGT	GACGGCGCCC	CTGGGCCCAA	CAGCACTGTC	2220
CTGGTGACCA	AGAGAAGGGA	CTGCCCTCCG	GGCTCCTTCT	GGTGGCTCAT	CCCCCTGCTC	2280
CTCCTCCTCC	TGCGCTCTCT	GGCCCTGCTA	CTGCTGCTAT	GCTGGAAGTA	CTGTGCCTGC	2340
TGCAAGGCTC	GCCTGGCACT	TCTCCGCTGC	TGCAACCGAG	GTCAATGGT	GGGCTTTAAG	2400
GAAGACCAT	ACATGTCTGG	GGAGAACCTG	ATGGCTCTG	ACCACTTGG	CACGCCCATC	2460
CTGCGCAGCG	GGAACTCAA	GGGCGGTGAC	GTGGTCCGCT	GGAGGTTCAC	CAACAACATG	2520
CAGCGGCTCG	GCTTTGGCAC	TCATGCCGCG	AGCATCAACC	CCACAGAGCT	GGTGCCTTAC	2580
GGCTGTGCTT	TGCGCTTGGC	CGGCTTTTGC	ACCGAGAACC	TGCTGAAGCC	TGACACTCGG	2640
GAGTGCGCCC	AGCTGCGCCA	GGAGGTGGAG	GAGAACCCTGA	ACGAGGTCTA	CAGGCAGATC	2700
TCCGGTGTAC	ACAACTTCCA	CGAGACCAAG	TTCCGGCAGC	AGCCCAATGC	CGGGAAGGAG	2760
CAAGACCAAC	CCATTGTGGA	CACAGTGTCT	ATGGCGCCCC	GCTCGGCCAA	GCCGGCCCTG	2820
CTGAAGCTTA	CAGAGAAGCA	GGTGAACACG	AGGGCCTTCC	ACGACCTCAA	GGTGGCCCCC	2880
GGCTACTACA	CCCTCACTGC	AGACCAGGAC	GCCCCGGGCA	TGGTGGAGTT	CCAGGAGGGC	2940
GTGGAGCTGG	TGGAGCTACG	GGTGCCCTTC	TTTATCCGGC	CTGAGGATGA	CGACGAGGAG	3000
CAGCTGCTGG	TGGAGGCTAT	CGACGTGCCC	GCAGGCACTG	CCACCTTCGG	CGCGCGCTGC	3060
GTAACATCA	CCATCATCAA	GGAGCAAGCC	AGAGACGTGG	TGTCTTGTGA	GCAGCTGAG	3120
TTCTCGTCA	CCGCGGGGGA	CCAGGTGGCC	CGCATCCCTG	TCATCCGGCG	TGTCTGGAC	3180
GGCGGGAAGT	CCCAGGTCTC	CTACCGCACA	CAGGATGGCA	CCGCGCAGGG	CAACCGGAC	3240
TACATCCCGG	TGGAGGGTGA	GCTGTGTTTC	CAGCCTGGGG	AGGCCTGGAA	AGAGCTGCAG	3300
GTGAAGCTCC	TGGAGCTGCA	AGAAGTTGAC	TCCCTCCTGC	GGGGCCGCCA	GGTCCGCGGT	3360
TTCCAGTCC	AGCTCAGCAA	CCCTAAGTTT	GGGGCCCAAC	TGGGCCAGCC	CCACTCCACC	3420
ACCATCATCA	TCAGGGACCC	AGATGAACCTG	GACCGGAGCT	TCACGAGTCA	GATGTTGTCA	3480
TCACAGCCAC	CCCCTCACGG	CGACCTGGGC	GCCCCGCGAG	ACCCCAATGC	TAAGGCCGCT	3540
GGGTCCAGGA	AGATCCATT	CAACTGGCTG	CCCCCTTCTG	GCAAGCCAAT	GGGGTACAGG	3600
GTAAAGTACT	GGATTCAAGG	TGACTCCGAA	TCCGAAGCCC	ACCTGCTCGA	CAGCAAGGTG	3660
CCCTCAGTGG	AGCTCACCAA	CCTGTACCCG	TATTGCGACT	ATGAGATGAA	GGTGTGCGCC	3720
TACGGGGCTC	AGGGCGAGGG	ACCCTACAGC	TCCCTGGTGT	CCTGCGGCAC	CCACAGGAA	3780
GTGCCACAGC	AGCCAGGGCG	TCTGGCCTTC	AATGTGCTCT	CCTCCACGGT	GACCCAGCTG	3840
AGCTGGGCTG	AGCCGGCTGA	GACCAACGGT	GAGATCACAG	CCTACGAGGT	CTGCTATGGC	3900
CTGGTCAACG	ATGACCAACG	ACCTATTGGG	CCCATGAAGA	AAGTGTCTGT	TGACAAACCT	3960
AAGAACCGGA	TGCTGTATAT	TGAGAACCTT	CGGGAGTCCC	AGCCCTACCG	CTACACGGTG	4020
AAGGGCGCGA	AGCCGATGTC	CATCCCATC	ATCCCTGACA	TCCCTATCGT	GGACGCCAG	4080
CAGCCCAAGA	AGCCGATGTC	CATCCCATC	ATCCCTGACA	TCCCTATCGT	GGACGCCAG	4140
AGCGGGGAGG	ACTACGACAG	CTTCCTTATG	TACAGCGATG	ACGTTCTACG	CTCTCCATCG	4200
GGCACCAGGA	AGCCAGCGGT	CTCCGATGAC	ACTGAGCACC	TGGTGAATGG	CCGGATGGAC	4260
TTTGCTTCC	CGGCGAGCAC	CAACTCCCTG	CACAGGATGA	CCACGACGAG	TGCTGCTGCC	4320
TATGGCACCC	ACCTGAGCCC	ACACGTGCCC	CACCGCGTGC	TAAGCACATC	CTCCACCTTC	4380

	ACACGGGACT	ACAACTCACT	GACCCGCTCA	GAACACTCAC	ACTCGACCAC	ACTGCCGAGG	4440
	GACTACTCCA	CCCTCACTCT	CGTCTCTCTC	CACGACTCTC	GCCTGACTGC	TGGTGTGCCC	4500
	GACACGCCCA	CCCGCCTGGT	GTTCTCTGCC	CTGGGGCCCA	CATCTCTCAG	AGTGAGCTGG	4560
5	CAGGAGCCGC	GGTGCAGGCG	GCCGCTGCAG	GGCTACAGTG	TGGAGTACCA	GCTGCTGAAC	4620
	GGCGGTGAGC	TGCATCCGCT	CAACATCCCC	AACCTCGCCC	AGACCTCGGT	GGTGTGGGAA	4680
	GACCTCTGCG	CCAAACCACT	CTACGTGTTT	CGCGTGCGGG	CCCAGAGCCA	GGAAGGCTGG	4740
	GGCCGAGAGC	GTGAGGGTGT	CATCACCATT	GAATCCCAGG	TGACCCCGCA	GAGCCCACTG	4800
	TGTCCCTGCG	CAGGCTCCGC	CTTCACTTTG	AGCACTCCCA	GTGCCCCAGG	CCCGCTGGTG	4860
10	TTCATGCCCC	TGAGCCGAGA	CTCGCTGCAG	CTGAGCTGGG	AGCGGCCACG	GAGGCCCAAT	4920
	GGGGATATCG	TGGCTACCTT	GGTGACCTGT	GAGATGGCCC	AAGGAGGAGG	GCCAGCCACC	4980
	GCATTCCGGG	TGGATGGAGA	CAGCCCCGAG	AGCCGGCTGA	CCGTGCCGGG	CCTCAGCGAG	5040
	AACGTGCCCT	ACAAGTTCAA	GGTGACAGCC	AGGACCACTG	AGGGCTTCGG	GCCAGAGCGC	5100
	GAGGGCATCA	TCACCATAGA	GTCCACAGAT	GGAGGACCCT	TCCCGCAGCT	GGGCAGCCGT	5160
15	GCCGGGCTCT	TCCAGCACCC	GCTGCAAAAG	GAGTACAGCA	GCATCACACC	CACCCACACC	5220
	AGCGCCACCG	AGCCCTTCTT	AGTGGATGGG	CCGACCCCTG	GGGCCACGCA	CCTGGAGGCA	5280
	GGCGGCTCCC	TCACCCGCGA	TGTGACCCAG	GAGTTTGTGA	GCCGGACACT	GACCCACGCA	5340
	GGAAACCTTA	GCACCCACAT	GGACCAACAG	TTCTTCCAAA	CTTGACCGCA	CCCTGCCCCA	5400
	CCCCGCGCAT	GTCCCACTAG	CGCTCTCTCC	GACTCCTCTC	CCGGAGCCTC	CTCAGCTACT	5460
20	CCATCCTTGC	ACCCCTGGGG	GCCAGCCCA	CCCGCATGCA	CAGAGCAGGG	GCTAGGTGTC	5520
	TCTTGGGAGG	CATGAAGGGG	GCAAGGTCCG	TCTCTGTGG	GCCCAACACT	ATTGTAAACC	5580
	AAAGAGCTGG	GAGCAGCAC	AGGACCCAGC	CTTTGTTCTG	CACCTAATAA	ATGGTTTTGC	5640
	ACTG						

25 Seq ID NO: 130 Protein sequence:
Protein Accession #: NP_000204

	1	11	21	31	41	51	
30	MAGPRPSPNA	RLLLAALISV	SLSGTLANRC	KKAPVKSCTE	CVRVDKDCAY	CTDEMFRDRR	60
	CNTQAEELAA	GQQRSEIVVM	ESSFQITEET	QIDTTLRRSQ	MSPQGLRVRL	RPGEERHFEL	120
	EVFEPLSEFV	DLVILDMFSN	SMDDLDNLK	KMGQNLARVL	SQLTSDYTTIG	FGKFVDKVS	180
	PQTDNRPEKL	KEPWNSDDPP	FSFKNVISLT	EDVDEFNRKL	QGERISGNLD	APEGGFDAIL	240
35	QTAVCTRDIG	WRPDSHTLLV	FSTESAFHYE	ADGANVLAGE	MSRNDERCHL	DTTGTYYTQYR	300
	TQDYPSPVTL	VRLLAKHNII	PIPAVTNYSY	SYYEKLHTYF	FVSSLGLVLQE	DSSNIVELLE	360
	BAFNIRIRNL	DIRALDSPRG	LRTTEVTSKMF	QKTRTGSFHI	RRGEVGIYQV	QLRALEHVDG	420
	THVQQLPDEQ	KGNHKLKPSF	SDGLKMDAGI	ICDVCTCELO	KEVRSARCSF	NGDFVCGQCV	480
	CSEGWSGQTC	NCSGTSLSDI	QCCLREGEDK	PCSGRGECQC	GHCVCYGEGR	YEQFCEYDN	540
40	FQCPRTSGFL	CNDRGRCSMG	QCVCEPGWTG	PSCDCPLSNA	TCIDSNGGIC	NGRGHCECGR	600
	CHCHQQLSLT	DTICEINYS	IHPGLCEDLR	SCVQCQAWGT	GEKKGRTCEE	CNFKVKMVDL	660
	LKRAEIVVVR	CSPRDEDDDC	TYSYTMEDGD	APGPNSTVLV	HKKDCPPGS	FWWLIPLLLL	720
	LLPLALLLLL	LCKWKYCACCK	ACLLALLPCCN	RGHMVGFKE	HYMLRENLM	SDHLDTPLMR	780
	SGNLKRGDVR	RGWVNTNMQR	PQFATHAASI	NPTLVPYGL	SLRLARLCTE	NLLKPDTRER	840
45	AQLRQVEVEN	LNEVYRQISG	VHKLQQTFR	QQPNAGKKQD	HTIVDTVLMA	PRSAKPALLK	900
	LTEKQVEQRA	FHDLKVAPGY	YTLADQDAR	GMVEFQEGVE	LVDVRVPLFI	RPEDDDEKQL	960
	LVEAIDVPAG	TATLGRRLVN	ITIIKEQARD	VVSFEQPEFS	VSRGDQVARI	PVIRRVLDGG	1020
	KSQVSYRTQD	GTAGQNRDVI	PVEGELLFPQ	GEAWKELQVK	LLELQVDSL	LRGRQVRRFH	1080
	VQLSNPKFGA	HLGQPSSTTI	IIRDPELDR	SFTSQMLSSQ	PPPHGLDLAG	QNPNAKAAGS	1140
50	RKIHFNMWLP	SGKPMGYRVK	YNIQGDSESE	AHLDSKVPS	VELTNLYPYC	DYEMKVCAYG	1200
	AQGEQPYSSL	VSCRTHQVEP	SEPGRLAFNV	VSTVTQLSW	AEPAETNGEI	TAYEVCYGLV	1260
	NDDNRPIGFM	KKVLVDNPKN	RMLLIENLRE	SQPYRYTVKA	RNGAGWGPER	EAIINLATQP	1320
	KRPMISIPPI	DIPIVDAQSG	EYDVSFLMYS	DDVLRSPSGS	QRPSVSDDT	HLVNGRMDFA	1380
	FFGSTNSLHR	MTTISAAAYG	THLSPHVPHR	VLSTSSLTTR	DYNSLTRSEH	SHSTTLPRDY	1440
55	STLTSVSSH	SRLTAGVPDT	PTRLVFSALG	PTSLRVSWQE	PRCERPLQGY	SVEYQLLNGG	1500
	ELHRLNIPNP	AQTSVVVEDL	LPNHYSVPRV	RAQSQEGWGR	EREGVITIES	QVHPQSPLCP	1560
	LPGSAFTLST	PSAPGPLVFT	ALSPDSLQLS	WERFRPNNGD	IVGYLVTCME	AQGGGPATAF	1620
	RVDGDSPESR	LTVPGISENV	PYKFKVQART	TEGFGPEREG	IITIESQDGG	PPFQLGSRAG	1680
60	LFQHPLQSEY	SSITTTHTSA	TEPFLVDGPT	LGAQHLEAGG	SLTRHVTTQEF	VSRTLTTSST	1740
	LSTHMDQQFF	QT					

Seq ID NO: 131 DNA sequence
Nucleic Acid Accession #: BC004372
Coding sequence: 132..2231

65	1	11	21	31	41	51	
	CCTCGTGCCG	CGGACCCAG	CCTCTGCCAG	GTTCCGGTCCG	CCATCCTCGT	CCCGTCTCTC	60
	GCCGCGCCCT	GCCCGCGGCC	CAGGGATCCT	CCAGCTCCTT	TGCGCCGCGC	CCTCCGTTGG	120
70	CTCCGGACAC	CATGGACAAG	TTTTGGTGGC	ACGCAGCCTG	GGGACTCTGC	CTCGTGCCGC	180
	TGAGCCTGGC	GCAGATCGAT	TGAAATATAA	CCTGCCGCTT	TGCAGGTGTA	TTCCACGTGG	240
	AGAAAAATGG	TCGCTACAGC	ATCTCTCGGA	CGGAGGCGCG	TGACCTCTGC	AAGGCTTTCA	300
	ATAGCACCTT	GCCCACAATG	GCCAGATGG	AGAAAGCTCT	GAGCATCGGA	TTTGAGACCT	360
	GCAGGTATGG	GTTTCATAGAA	GGGCATGTGG	TGATTCCTCG	GATCCACCCC	AACTCCATCT	420
75	GTGCAGCAAA	CAACACAGGG	GTGTACATCC	TCACATCCAA	CACCTCCCAG	TATGACACAT	480
	ATTGCTTCAA	TGCTTCAGT	CCACCTGAAG	AAGATTGTAC	ATCAGTCACA	GACCTGCCCA	540
	ATGCCTTTGA	TGGACCAATT	ACCATAACTA	TTGTAAACCG	TGATGGCACC	CGCTATGTCC	600
	AGAAAGGAGA	ATACAGAAGC	AATCCTGAAG	ACATCTACCC	CAGCAACCC	ACTGATGATG	660
	ACGTGAGCAG	CGGCTCTCC	AGTGAAAGGA	GCAGCACTTC	AGGAGGTTAC	ATCTTTTACA	720
80	CCTTTTCTAC	TGTACACCCC	ATCCAGACCG	AAGACAGTCC	CTGGATCACC	GACAGCACAG	780
	ACAGAAATCC	TGCTATCCAG	ACGTCTTCAA	ATACCATCTC	AGCAGGCTGG	GAGCCAAATG	840
	AAGAAATGA	AGATGAAAGA	GACAGACACC	TCAGTTTTC	TGGATCAGGC	ATTGATGATG	900
	ATGAAGATTT	TATCTCCAGC	ACCATTTCAA	CCACACCAAG	GGCTTTTGAC	CACACAAAAC	960
	AGAACCAGGA	CTGGAACCC	TGGAACCCAA	GCCATTCAAA	TCGGGAAGTG	CTACTTCAGA	1020
85	CAACCACAA	GATGATCTGAT	GTAGACAGAA	ATGGACCAAC	TGCTTATGAA	GGAAACTGGA	1080
	ACCCAGAAC	ACATCTCTCC	CTCATTCACC	ATGAGCATCA	TGAGGAAGAA	GAGACCCACA	1140
	ATTCTACAAG	CACAATCCAG	GCAACTCCTA	GTAATACAAC	GGAAGAAACA	GCTACCCAGA	1200
	AGGAACAGTG	GTTTGGCAAC	AGATGGCATG	AGGGATATCG	CCAAACACCC	AGAGAAGACT	1260

CCCATTCCGAC AACAGGGGACA GCTGCAGCCT CAGCTCATAC CAGCCATCCA ATGCAAGGAA 1320
 GGACAACACCC AAGCCCAGAG GACAGTTTCTT GGACTGATTT CTTCACCCCA ATCTCACACC 1380
 CCATGGGACG AGGTCAATCAA GCAGGAAGAA GGATGGATAT GGACTCCAGT CATAGTACAA 1440
 CGCTTCAGCC TACTGCAAT CCAACACAG GTTTGGTGGG AGATTGGAC AGGACAGGAC 1500
 CTCTTTCAAT GACAAACGAG CAGAGTAATT CTCAGAGCTT CTCTACATCA CATGAAGGCT 1560
 TGGAAAGAAG TAAAGACCAT CCAACAACCT CTACTCTGAC ATCAAGCAAT AGGAATGATG 1620
 TCACAGGTGG AAGAAGAGAC CCAATCATTT CTGAAGGCTC AACTACTTTA CTGGAAGGTT 1680
 ATACCTCTCA TTACCCACAC ACGAAGGAAA GCAGGACCTT CATCCAGTG ACCTCAGCTA 1740
 AGACTGGGTC CTTTGGAGTT ACTGCAGTTA CTGTTGGAGA TTCCAACCTT AATGTCAATC 1800
 GTTCCTTATC AGGAGACCAA GACACATTCC ACCCCAGTGG GGGGTCCCAT ACCACTCATG 1860
 GATCTGAATC AGATGGACAC TCACATGGGA GTCAAGAAGG TGGAGCAAAC ACAACCTCTG 1920
 GTCCTATAAG GACACCCCAA ATTCCAGAAT GGCTGATCAT CTGGGATCC CTCTTGGCCT 1980
 TGGCTTTGAT TCTTGCAATT TGCAATTGAG TCAACAGTCG AAGAAGGTGT GGGCAGAAGA 2040
 AAAAGCTAGT GATCAACAGT GGCAATGGAG CTCTGGAGGA CAGAAAGCCA AGTGGACTCA 2100
 ACGGAGAGGC CAGCAAGTCT CAGGAAATGG TGCATTTGGT GAACAAGGAG TCGTCAGAAA 2160
 CCTCAGAGCA GTTTATGACA CTGATGGAGA CAAGGAACCT GCAGAATGTG GACATGAAGA 2220
 TTGGGGTGTA ACACCTACAC CATTATCTTG GAAAGAAACA ACCGTTGGAA ACATAACCAT 2280
 TACAGGGAGC TGGGACACTT AACAGATGCA ATGTGCTACT GATTGTTTCA TTGCGAATCT 2340
 TTTTTCAGCAT AAAATTTTCT ACTCTTAAAA AAAAAA AAAAAA

Seq ID NO: 132 Protein sequence:
 Protein Accession #: AAH04372

1 11 21 31 41 51
 MDKFWHHAAM GLCLVPLSLA QIDLNITCRF AGVFHVEKNG RYISIRTEAA DLCKAFNSTL 60
 PTMAQMEKAL SIGPETCRYG PIEGHVVIPR IHPNSICAA NTGVYILTSN TSQYDTCYFN 120
 ASAPPEEDCT SVTDLPNAFD GPITITIVNR DGTTRYVQKE YRTNPEDIYP SNPTDDVSS 180
 GSSSERSSTS GGYIFYFYST VHPIDEDSP WITDSTRIP ATSTSSNTIS AGWEPNEENE 240
 DERDRHLSFS GSGIDDDDF ISSTISTTFR AFDHTKQND WTQWNPESHN PEVLQTTTR 300
 MTDVDRNGTT AYGNNWNPFA HPLIHHEHH EEEETPHSTS TIQATPSSTT EBTATQKEQ 360
 FGNRNHEGYR QTPREDSHST TGTAAASAHT SHPMQGRITP SPEDSSWTD FNPISHPMGR 420
 GHQAGRRMDM DSSHSTTLQP TANPNTGLVE DLDRTGPLSM TTQSSNSQSP STSHEGLEED 480
 KDHPPTTSLT SNNRNDVTGG RRDPNHSEGS TTLLEGYTSY YPHTKESRTF LPVTSKATGS 540
 FGVTAVTVGD SNNVNVNLSL GDQDTFHPSS GSHTTHGSES DGHSHGSEQE GANTTSGPIR 600
 TPQIPFWLLI LASLLALALI LAVCIAVNSR RRCGQKKKLV INSGNGAVED RKPSGLNGEA 660
 SKSQEMVHLV NKSSSETPDQ FMTADETRNL QNVDMKIGV

Seq ID NO: 133 DNA sequence
 Nucleic Acid Accession #: NM_002882
 Coding sequence: 150-755

1 11 21 31 41 51
 CGAGGTTCCG GTCTGCGGCG GGAGGGAAGA GCGGGCGGGC GGGAGGCGCC GCGCCAGAC 60
 GCGGAGGAA GGAGCTACGA GTAGCCGCGG AGAGGCGCGG GAGCCAGCGA CGACCCAGCC 120
 AGCCGAGCCG CCGCCGCGCG CGCGCCCCCA TGGCGGCGCG CAAGGACACT CATGAGGACC 180
 ATGATACTTC CACTGAGAAT ACAGACGAGT CCAACCATGA CCTCAGTTT GAGCCAATAG 240
 TTTCTCTTCC TGAGCAAGAA ATTAAACAC TGGAAGAAGA TGAAGAGGAA CTTTTTAAAA 300
 TCGCGGCAAA GATTGTCGGA TTTGCCTCTG AGAACGATCT CCCAGATGG AAGGAGCGAG 360
 GCACCTGGTGA CGTCAAGCTC CTGAAGCACA AGGAGAAAGG GGGCATCCG CTCTCATGC 420
 GGAGGGACAA GACCTCAAG ATCTGTGCCA ACCACTACAT CACGCGGATG ATGGAGCTGA 480
 AGCCCCAAGC AGGTAGCGAC CGTGCCCTGG TCTGGAACAC CCACGCTGAC TTCGCCGACG 540
 AGTGCCCCAA GCCAGAGCTG CTGGCCATCC GCTTCTGAA TGCTGAGAA GCACAGAAAT 600
 TCAAAACAAA GTTTGAAGAA TGCAAGAAAG AGATCGAAGA GAGAGAAAAG AAAGCAGGAT 660
 CAGGCAAAAA TGATCATGCC GAAAAAGTGG CGGAAAAGCT AGAAGCTCTC TCGGTGAAGG 720
 AGGAGACCAA GGAGGATGCT GAGGAGAAGC AATAAATCGT CTTATTTTAT TTTCTTTTCC 780
 TCTCTTCTCT TTCCTTTTTT TAAAAAATTT TACCCTGCCC CTCTTTTTCG GTTTGTTTTT 840
 ATTCTTTCAT TTTTACAGG GACGTTATAT AAAGAACTGA ACTC

Seq ID NO: 134 Protein sequence:
 Protein Accession #: NP_002873

1 11 21 31 41 51
 MAAAKDTHED HDTSTENTDE SNHDPQFEPI VSLPEQEIKT LEEDEEELPK MRKLFRFAS 60
 ENDLPEWKER GTGDVKLLKH KEKGAIKLLM RRDKTLKICA NHYITPMEL KPNAGSDRAW 120
 VNNTHADPAD ECPKPELLAI RFLNAENAQK PKTKPEECRK EIEEREKKAG SKNDHAEKV 180
 AEKLEALSVK EETKEDAEK Q

Seq ID NO: 135 DNA sequence
 Nucleic Acid Accession #: NM_000077.2
 Coding sequence: 277-742

1 11 21 31 41 51
 CCAACCTGG GCGCACTTCA GGTGTGCCAC ATTCTGCTAAG TGCTCGGAGT TAATAGCACC 60
 TCCTCCGAGC ACTCGCTCAC GCGGTCCCCT TGCTCGGAAA GATACCGCGG TCCCTCCAGA 120
 GGATTTGAGG GACAGGGTCC GAGGGGGCTC TTCCGCCAGC ACCGAGGAA GAAAGAGGAG 180
 GGGCTGGCTG GTACCCAGAG GGTGGGGCGG ACCGCGTGCG CTGCGCGGCT GCGGAGAGGG 240
 GGAGAGCAGG CAGCGGGCGG CGGGGAGCAG CATGAGGCGG GCGGCGGGGA GCAGCATGGA 300
 GCCTTCGGCT GACTGGCTGG CCACGGCCCG GCGCCGGGGT CGGGTAGAGG AGGTGCGGGG 360
 GCTGCTGGAG GCGGGGGCGC TGCCCAACGC ACCGAATAGT TACGGTCCGA GGCCGATCCA 420
 GGTATGATG ATGGGCAGCG CCCGAGTGGC GGAGCTGCTG CTGCTCCACG GCGCGGAGCC 480

CAACTGCGCC GACCCCGCCA CTCTCACCG ACCCGTGCAC GACGCTGCCC GGGAGGGCTT 540
 CCTGGACACG CTGGTGGTGC TGCACCGGGC CGGGGCGCGG CTGGACGTGC GCGATGCTCG 600
 GGGCGGTCTG CCGGTGGACC TGGCTGAGGA GCTGGGCCAT CGGATGTGCG CACGGTACCT 660
 GCGCGCGGCT GCGGGGGGCA CCAGAGGCAG TAACCATGCC CGCATAGATG CCGCGGAAGG 720
 TCCCTCAGAG ATCCCGGATT GAAAGAACCA GAGAGGGTCT GAGAAACCTC GGGAAACTTA 780
 GATCATCAGT CACCGAAGGT CCTACAGGGC CACAACCTGC CCGGCCACAA CCCACCCGCG 840
 TTTGCTAGTT TTCAATTAGA AATAGAGCT TTTAAAAATG TCCTGCCTTT TAACGTAGAT 900
 ATATGCTTTC CCCCACTACC GTAAATGTCC ATTTATATCA TTTTATATAT ATTCTTATAA 960
 AAATGTAAAA AAGAAAAACA CCGCTTCTGC CTTTCTACTG TGTGGAGTTT TTCTGGAGTG 1020
 AGCACTACAG CCGTAAGCGC ACATTCATGT GGGCATTTCG TGGAGGCTTC GCAGGCTCCG 1080
 GAAGCTGTG ACTTCATGAC AAGCATTTTG TGAACTAGGG AAGCTCAGGG GGGTTACTGG 1140
 CTTCTCTTGA GTCACACTGC TAGCAAATGG CAGAACCAAA GCTCAATAAA AAATAAAATA 1200
 ATTTTCATTC ATTCACTC

Seq ID NO: 136 Protein sequence:
 Protein Accession #: NP_000068.1

1 11 21 31 41 51
 MEPAAGSSME PSADWLATAA ARGVEEVRA LLEAGALPNA PNSYGRRIQ VMMGSRVA 60
 ELLLLHGAEP NCDPATLTR FVHDAAREGF LDTLVVLHRA GARLDVRDAW GRLPVDLAEZ 120
 LGHRDVARYL RAAAGGTRGS NHARIDAAEG PSDIPD

Seq ID NO: 137 DNA sequence
 Nucleic Acid Accession #: NM_058196.1
 Coding sequence: 104-421

1 11 21 31 41 51
 TGTGTGGGGG TCTGCTTGGC GGTGAGGGGG CTCTACACAA GCTTCTCTTC CGTCATGCGG 60
 GCCCCACCCC TGGCTCTGAC CATTCTGTTC TCTCTGGCAG GTCATGTAGA TGGGCAGCGC 120
 CCGAGTGGCG GAGCTGCTGC TGCTCCACCG CCGGAGCCCC AACTGCGCGG ACCCGCCAC 180
 TCTCACCCGA CCGGTGCACG ACGCTGCCCG GGAGGGCTTC CTGGACACGC TGGTGGTGCT 240
 GCACCGGGCC GGGGCGGGC TGGACGTGCG CGATGCTTGG GGCCGTCTGC CCGTGGACCT 300
 GGCTGAGGAG CTGGGCCATC GCGATGTGCG ACGGTACCTG CCGCGGGCTG CCGGGGGCAC 360
 CAGAGCGAGT AACCATGCCG CATAGATGCG CCGGAAGGT CCCTCAGACA TCCCGGATTG 420
 AAAGAACCAG AGAGGCTCTG AGAAACCTCG GGAACCTTAG ATCATCAGTC ACCGAAGGTC 480
 CTACAGGGCC ACAACTGCCC CCGCCACAC CCACCCCGCT TCGTAGTTT TCATTAGAA 540
 AATAGAGCTT TTAATAATGT CCTGCCTTTT AACGTAGATA TAAGCCTTCC CCCACTACCG 600
 TAAATGTCCA TTTATATCAT TTTTATATA TTCTTATAAA AATGTAAAAA AGAAAAACAC 660
 CGCTTCTGCG TTTTCACTGT GTTGGAGTTT TCTGGAGTGA GCACTCACGC CTAAGCGCA 720
 CATTATGTG GGCATTTCCT GCGAGCCTCG CAGCCTCCGG AAGCTGTGCA CTTATGACA 780
 AGCATTTTGT GAACTAGGGA AGCTCAGGGG GGTACTGGC TTCTCTTGG TCACTATGCT 840
 AGCAATGGC AGAACCAAG CTCAATAAA AATAAAATA TTTTCATTCA TTCACTC

Seq ID NO: 138 Protein sequence:
 Protein Accession #: NP_478103.1

1 11 21 31 41 51
 MMGSRVAE LLLHGAEPN CADPATLTRP VHDAAREGFL DTLVVLHRA ARLDVRDAW 60
 RLPVDLAEEL GHRDVARYLR AAAGGTRGSN HARIDAAEGP SDIPD

Seq ID NO: 139 DNA sequence
 Nucleic Acid Accession #: NM_058197.1
 Coding sequence: 272-684

1 11 21 31 41 51
 CCCAACCTGG GGGCACTTCA GGTGTGCCAC ATTGCTAAG TGCTCGGAGT TAATAGCACC 60
 TCCTCCGAGC ACTCGCTCAC GCGGTCCCTC TGCTTGGAAA GATACCGCGG TCCCTCCAGA 120
 GGAATTTGAG GACAGGGTGC GAGGGGGCTC TTCGCGCAGC ACCGGAGGAA GAAAGAGGAG 180
 GGGCTGGCTG GTCACAGAG GGTGGGGCGG ACCGCTGCGG CTGGCGGGCT GCGGAGAGGG 240
 GGAGAGCAGG CAGCGGGCGG CCGGGAGCAG CATGGAGCCG CGCGCGGGGA GCAGCATGGA 300
 GCCGGCGCGG GGGAGCAGCA TGGAGCCTTC GGCTGACTGG CTGGCCACGG CCGCGGGCCG 360
 GGGTGGGTA GAGGAGGTGC GGGCGCTGCT GGAGGCGGGG GCGCTGCCCA ACGCACCGAA 420
 TAGTTACGGT CGGAGGCCGA TCCAGTGGG TAGAAGTCT GCAGCGGGAG CAGGGGATGG 480
 CCGGCGACTC TGGAGGACGA AGTTTGACAG GGAATTGGAA TCAGGTAGCG CTTGATTCT 540
 CCGGAAAAAG GGGAGGCTTC CTGGGGAGTT TTCAGAGGGG GTTTGTAATC ACAGACCTCC 600
 TCCTGGCGAC GCCCTGGGGG CTTGGGAAAC CAAGGAAGAG GAATGAGGAG CCACGCGCGT 660
 ACAGATCTCT CGAATGCTGA GAAGATCTGA AGGGGGGAAC ATATTGTAT TAGATGGAAG 720
 TCATGATGAT GGGCAGCGCC CGAGTGGCGG AGCTGCTGCT GCTCCACGGC GCGGAGCCCA 780
 ACTGCGCGCA CCCCGCCACT CTCACCCGAC CCGTGCACGA CGCTGCCCGG GAGGGCTTCC 840
 TGGACACGCT GGTGGTGTG CACCGGGCGG GGGCGCGGCT GGAAGTGGCG GATGCTTGGG 900
 GCGCTCTGCC CGTGGACCTG GCTGAGGAGC TGGGCCATCG CGATGTGCA CGGTACCTGC 960
 GCGCGGCTGC GGGGGGCACC AGAGGCAGTA ACCATGCCCG CATAGATGCC GCGGAAGGTC 1020
 CCTCAGACAT CCGGATTTGA AAGAACCCAG GAGGCTCTGA GAAACCTCGG GAACTTAGAT 1080
 CATCAGTCAC CGAAGGTCTT ACAGGGCCAC AACTGCCCCC GCCACAACCC ACCCGGCTTT 1140
 CGTAGTTTTC ATTTAGAAAA TAGAGCTTTT AAAAATGTCC TGCTTTTAA CGTAGATATA 1200
 TGCTTCCCCC CACTACCGTA AATGTCCATT TATATCATT TTTATATAT CTTATAAAAA 1260
 TGTAAAAAAG AAAAACACCG TTCTGCTCTT TCTACTGTGT TGGAGTTTTC TGGAGTGAGC 1320
 ACTACGCGCC TAAGCGCACA CTTATGTGGG CATTCTTTCG GAGCCTCGCA GCCTCCGGAA 1380
 GCTGTGACT TCATGACAAG CATTTTGTGA ACTAGGGAAG CTCAGGGGGG TTAAGTGGCT 1440
 CTCTTGAGTC AACTGTGTAG CAAATGGCAG AACCAGAGCT CAAATAAAAA TAAAAAATT 1500

Seq ID NO: 140 Protein sequence:
Protein Accession #: NP_478104.1

1	11	21	31	41	51	
MEPAAGSSME	PAAGSSMEPS	ADWLATAAAR	GRVEEVALL	EAGALPNAPN	SYGRRPIQVG	60
RRSAAGAGDG	GRLNRTKFPAG	ELESGSASIL	RKKGRLPGEF	SEGVCNHRPP	PGDALGAWET	120
KEEE						

Seq ID NO: 141 DNA sequence
Nucleic Acid Accession #: NM_058195.1
Coding sequence: 163-684

1	11	21	31	41	51	
CCTCCCTACG	GGCGCCTCCG	GCAGCCCTTC	CCGCGTGC	AGGGCTCAGA	GCGTTCCTGA	60
GATCTTGGAG	GTCCGGGTGG	GAGTGGGGGT	GGGGTGGGGG	TGGGGGTGAA	GGTGGGGGGC	120
GGGCGCGCTC	AGGGAAGGCG	GGTGC	GGGGGGCG	AGATGGGCAG	GGGGCGGTGC	180
GGGGTCCCA	GTCTGCAATT	AAGGGGGCAG	GAGTGGCGCT	GCTCACCTCT	GGTGCCAAAG	240
GGGGGGCAG	CGGCTGCCGA	GCTCGGCCCT	GGAGGCGCG	AGAACATGGT	GCGCAGGTTT	300
TTGGTGACCC	TCGGGATTTC	GCGCGCGTGC	GGCCCGCGCG	GAGTGAGGGT	TTTCTGTGGT	360
CACATCCCGC	GGCTCACGGG	GGAGTGGGCA	GCGCCAGGGG	CGCCCGCGCG	TGTGGCCCTC	420
GTGCTGATGC	TACTGAGGAG	CCAGCGTCTA	GGGCAGCAGC	CGCTTCTTAG	AAGACCAAGT	480
CATGATGATG	GGCAGCGCCC	GAGTGGCGGA	GCTGCTGCTG	CTCCACGGCG	CGGAGCCCAA	540
CTGCGCGGAC	CCCGCCACTC	TCACCCGACC	CGTGACGAC	GCTGCCCGGG	AGGGCTTCTT	600
GGACACGCTG	GTGGTGCTGC	ACCGGGCGCG	GGCGCGGCTG	GACGTGCGCG	ATGCTTGGGG	660
CCGTCTGCCC	GTGGACCTGG	CTGAGGAGCT	GGCCATCGC	GATGTGCGAC	GGTACCTGCG	720
CGCGGCTGCG	GGGGGCACCA	GAGGCAGTAA	CCATGCCCGC	ATAGATGCCG	CGGAAGGTCC	780
CTCAGACATC	CCCGATTGAA	AGAACCAGAG	AGGCTCTGAG	AAACCTCGGG	AAACTTAGAT	840
CATCAGTCA	CGAAGGTCTT	ACAGGGCCAC	AACTGCCCCC	GCCCAACCC	ACCCCGCTTT	900
CGTAGTTTTT	ATTAGAAAA	TAGAGCTTTT	AAAAATGTCC	TGCCTTTTAA	CGTAGATATA	960
TGCCTTCCCC	CACTACCGTA	AATGTCCATT	TATATCATTT	TTTATATATT	CTTATAAAAA	1020
TGTAAAAAAG	AAAAACACCG	CTTCTGCCTT	TTCACTGTGT	TGGAGTTTTC	TGGAGTGAGC	1080
ACTCAGCCCC	TAAGCGCACA	TTCACTGTGG	CATTCTTGCG	GAGCCTCGCA	GCCTCGGAAA	1140
GCTGTGAGCT	TCATGACAAG	CATTCTGTGA	ACTAGGGAAG	CTCAGGGGGG	TTACTGGCTT	1200
CTCTTGAGTC	ACACTGCTAG	CAATGGCAG	AACCAAGCT	CAATAAAAA	TAAATAAATT	1260
TTCATTCAATT	CACTC					

Seq ID NO: 142 Protein sequence:
Protein Accession #: NP_478102.1

1	11	21	31	41	51	
MGRGRCVGPS	LQLRQEWRC	SPLVPKGGAA	AABLGPGGGE	NMVRRLVLT	RIRACGPPR	60
VRVFFVHPR	LTGEWAIPA	PAVALVLM	LRSQRLGQPP	LPRRPHDDG	QRPSSGAAAA	120
PRRGAQLRRP	RHSHPTRARR	CPGGLPGHAG	GAAPGRGAAG	RARCLGPSAR	GPG	

Seq ID NO: 143 DNA sequence
Nucleic Acid Accession #: NM_018131
Coding sequence: 412..1107

1	11	21	31	41	51	
GAAATGTCAC	ACTTAAAGAC	ATCAGTGGAT	GAAATCACAA	GTGGGAAAGG	AAAGCTGACT	60
GATAAAGAGA	GACAGAGACT	TTTGGAGAAA	ATTGAGTCC	TTGAGGCTGA	GAAGGAGAAG	120
AATGCTTATC	AACTCACAGA	GAAGGACAAA	GAAATACAGC	GACTGAGAGA	CCAAGTGAAG	180
GCAGATATA	GTACTACCGC	ATTGCTTGAA	CAGCTGGAAG	AGACAACGAG	AGAAGGAGAA	240
AGGAGGGAGC	AGGTGTTGAA	AGCCTTATCT	GAAGAGAAAG	ACGTATTGAA	ACAACAGTTG	300
TCTGCTGCAA	CCTCAGCAAT	TGCTGAACTT	GAAAGCAAAA	CCAATACACT	CCGTTTATCA	360
CAGACTGTGG	CTCCAACCTG	CTTCAACTCA	TCAATAAATA	ATATTATGTA	AATGGAAAATA	420
CAGCTGAAAG	ATGCTCTGGA	GAAAAATCAG	CAGTGGCTCG	TGTATGATCA	GCAGCGGGAA	480
GTCTATGTAA	AAGGACTTTT	AGCAAAAGATC	TTTGTGTTGG	AAAAGAAAAC	GGAAACAGCT	540
GCTCATTCAC	TCCACAGCA	GACAAAAAAG	CCTGAATCAG	AAGGTTATCT	TCAAGAAGAG	600
AAGCAGAAAT	GTTACAACGA	TCTCTTGGCA	AGTGCAAAAA	AAGATCTTGA	GGTTGAACGA	660
CAAAACATAA	CTCAGCTGAG	TTTTGAACTG	AGTGAATTC	GAAGAAAATA	TGAAGAAACC	720
CAAAAAGAAG	TTCACAATTT	AAATCAGCTG	TTGTATTAC	AAAGAAAGGC	AGATGTGCAA	780
CATCTGGAAG	ATGATAGGCA	TAAACAGAG	AAGATACAAA	AACTCAGGGA	AGAGAATGAT	840
ATTGTAGGG	GAAAACCTGA	AGAAGAGAAG	AAGAGATCCG	AAGAGCTCTT	ATCTCAGGTC	900
CAGTCTCTTT	ACACATCTCT	GCTAAAGCAG	CAAGAAGAAC	AAACAAGGGT	AGCTCTGTTG	960
GAACAACAGA	TGCAGGCATG	TACTTTAGAC	TTTGAAATG	AAAAACTCGA	CCGTCAACAT	1020
GTGCAGCATC	AATTGCATGT	AATTCTTAAG	GAGCTCCGAA	AAGCAAGAAA	AAATAACACA	1080
GTTGGAATCC	TGAAACAGC	TTCAATGAGT	TGCCATCACA	GAGCCATTAG	TCACTTTCCA	1140
AGGAGAGACT	GAAAACAGAG	AAAAAGTTGC	CGCCTCACCA	AAAAGTCCCA	CTGCTGCACT	1200
CAATGGAAGC	CTGGTGGAAAT	GTCCCAAGTG	CAATATACAG	TATCCAGCCA	CTGAGCATCG	1260
CGATCTGCTT	GTCCATGTGG	AATACTGTTT	AAAGTAGCAA	AATAAGTATT	TGTTTGTATA	1320
TTAAAAGATT	CAATACTGTA	TTTTCTGTTA	GCTTGTGGGG	ATTTTGAATT	ATATATTTCA	1380
CATTTTGCAAT	AAAATGCTCT	ATCTACCTTT	GACACTCCAG	CATGCTAGTG	AATCATGTAT	1440
CTTTTAGGCT	GCTGTGCATT	TCTCTTGGCA	GTGATACCTC	CCTGACATGG	TTTATCATCA	1500
GGCTGCAATG	ACAGAATGTG	GTGAGCAGCG	TCTACTGAGA	TACTAACATT	TTGCACTGTC	1560
AAAATACTTG	GTGAGGAAAA	GATAGCTCAG	GTTATTGCTA	ATGGGTTAAT	GCACCAGCAA	1620
GCAAAATATT	TATGTTTTCG	GGGGTTTGA	AAAATCAAG	ATAATTAAAC	AAGGATCTTA	1680
ACTGTGTTGG	CATTTTATAT	CCAAGCACTT	AGAAAACCTA	CAATCCTAAT	TTTGTATGCC	1740
ATTGTTAAGA	GGTGGTGATA	GATACTATTT	TTTTTTCATA	TTGTATAGCG	GTTATTAGAA	1800

AAGTTGGGGA TTTTCTTGAT CTTTATGCT GCTTACCATT GAAACTTAAC CCAGCTGTGT 1860
 TCCCCAATCT TGTCTGCGC ACGAAACAGT ATCTGTTTGA GGCATAATCT TAAGTGGCCA 1920
 CACACAATGT TTTCTCTTAT GTTATCTGGC AGTAACTGTA ACTTGAATTA CATTAGCACA 1980
 TCTGCTTAG CTAAATTTGT TAAAATAAAC CCAATGTAGCC CTCTCATTGT 2040
 ATTGACAGTA TTTTAGTTAT TTTTGGCATT CTAAAGCTG GGCAATGTAA TGATCAGATC 2100
 TTTGTTTGTG TGAACAGTA TTTTATACA TGCTTTTGT AAACCAAAAA CTTTAAAT 2160
 TCTCAGGTT TTCTAACATG CTTACCACTG GGCTACTGTA AATGAGAAAA GAATAAAATT 2220
 ATTTAATGTT TT

Seq ID NO: 144 Protein sequence:
 Protein Accession #: NP_060601

1 11 21 31 41 51
 | | | | |
 MBIQLKDALE KNQQLVVDQ QREVVYVGLL AKIPELEKKT ETAHSLPQQ TKKPESEGYL 60
 QEEKQKCYND LLASAKKDL ESRQTITQLS FELSEFRKY EETQKEVHNL NQLLYSQRRA 120
 DVQHLEDDRH KTKIKLRE ENDIARGKLE BEKKRSEELL SQVQSLYTSL LKQSEQTRV 180
 ALLEQQMQAC TLDPENEKLD RQHVQHLHV ILKELRKARK NNTVGILETA S

Seq ID NO: 145 DNA sequence
 Nucleic Acid Accession #: NM_001168
 Coding sequence: 50..478

1 11 21 31 41 51
 | | | | |
 CCGCCAGATT TGAATCGCGG GACCCGTGCG CAGAGGTGGC GCGCGCGGCA TGGGTGCCCC 60
 GACGTTGCCC CCTGCCTGGC AGCCCTTTCT CAAGGACCAC CGCATCTCTA CATTCAAGAA 120
 TGGGCCCTTC TTGGAGGCTG CGCCTGTCAC CCCGGAGCGG ATGGCCGAGG CTGGCTTCAT 180
 CCACTGCCCC ACTGAGAACG AGCCAGACTT GGCCAGTGT TTCTTCTGCT TCAAGGAGCT 240
 GGAAGGCTGG GAGCCAGATG ACGACCCCAT AGAGGAACAT AAAAAGCATT CGTCCGTTG 300
 CGCTTTCCTT TCTGTCAAGA AGCAGTTTGA AGAATTAACC CTTGGTGAAT TTTTGAAGCT 360
 GGACAGAGAA AGAGCCAAGA ACAAAATTGC AAAGGAAACC AACAATAAGA AGAAAGAAAT 420
 TGAGGAAACT GCGAAGAAAG TGCCCGTGC CATCGAGCAG CTGGCTGCCA TGGATTGAGG 480
 CCTCTGGCCG GAGCTGCTGT GTCCAGAGT GGCTGCACCA CTTCCAGGGT TTATTCCCTG 540
 GTGCCACCAAG CCTTCTCTGT GGCCTTGA CAATGTCTTA GGAAAGGAGA TCAACATTTT 600
 CAAATTAGAT GTTCAACTG TGCTCCTGTT TTGTCTTGAA AGTGGCACA GAGGTGCTTC 660
 TGCCGTGACA GCGGTGCTG CTGGTAACAG TGGCTGCTTC TCTCTCTCTC TCTCTTTTTT 720
 GGGGGCTCAT TTTTGTCTTT TTGATTCCCG GGCTTACCAG GTGAGAAAGT AGGGAGGAAG 780
 AAGGCAGTGT CCTTTTGTCT AGAGCTGACA GCTTTGTTCG CGTGGGAGCA GCCTTCCACA 840
 GTGAATGTGT CTGGAACCTCA TGTGTGTGAG GCTGTACAG TCCTGAGTGT GGACTTGGCA 900
 GGTGCTGTT GAATCTGAGC TGCAAGTTCC TTATCTGTCA CACCTGTGCC TCCTCAGAGG 960
 ACAGTTTTTT TGTGTGTGTG TTTTGTGTT TTTTGTGTT GGTAGATGCA TGACTTGTGT 1020
 GTGATGAGAG AATGGAGACA GAGTCCCTGG CTCCTTACT GTTTAACAAC ATGGCTTCTT 1080
 TATTTTGTGT GAATGTGTAA TTCACAGAAT AGCACAAGT ACAATTAAAA CTAAGCACAA 1140
 AGCAATCTTA AGTCAATGGG GAACCGGGT GAACCTCAGG TGATGAGGA GACAGAATAG 1200
 AGTGATAGGA AGCGTCTGGC AGATACTCCT TTGCACTGT CTGTGTGATT AGACAGGCCC 1260
 AGTGAGCGCG GGGGCACATG CTGGCCGCTC CTCCTCAGA AAAAGGCAGT GGCCTAAATC 1320
 CTTTTTAAAT GACTTGGCTC GATGCTGTGG GGGACTGGCT GGGCTGCTGC AGGCGGTGTC 1380
 TCTGTGAGCG CAACCTTTCAC ATCTGTACAG TTCTCCACAC GGGGAGAGA CGCAGTCCCG 1440
 CAGGTTCCCG GCTTCTCTTG GAGGAGCAG CTCCGCGAGG GCTGAAGTCT GGCCTAAGAT 1500
 GATGGATTGT ATTGCGCTC CTCCCTGTCA TAGAGCTGCA GGGTGGATTG TTACAGCTTC 1560
 GCTGGAAACC TCTGGAGTGC ATCTCGGCTG TTCTGAGAA ATAAAGGCC TGTCATTTT

Seq ID NO: 146 Protein sequence:
 Protein Accession #: NP_001159

1 11 21 31 41 51
 | | | | |
 MGAPTLPFAW QPFLKDHRI TFIKNWPFLEG CACTPERMAE AGFIHCPTEN EPDLAQCFPC 60
 FKELEGWEED DDPIEEHKKH SSGCAFLSVK KQFBEELTGE FLKLDREKAK NKIAKETNNK 120
 KKEFBETAKK VRAIBQLAA MD

Seq ID NO: 147 DNA sequence
 Nucleic Acid Accession #: NM_014176.1
 Coding sequence: 127-720

1 11 21 31 41 51
 | | | | |
 GCGCGCAGCG CTGGTACCCC GTTGGTCCGC GCGTTGCTGC GTTGTGAGGG GTGTCAGCTC 60
 AGTGATCCCC AGGCAGCTCT TAGTGTGGAG CAGTGAACCTG TGTGTGGTTC CTCTACTTGT 120
 GGGATCATGC AGAGAGCTTC ACGTCTGAAG AGAGAGCTGC ACATGTTAGC CACAGAGCCA 180
 CCCCCAGGCA TCACATGTTG GCAAGATAAA GACCAATGG ATGACCTGCG AGCTCAAATA 240
 TTAGGTGGAG CCAACACACC TTATGAGAAA GGTGTTTTTA AGCTAGAAGT TATCATTCCT 300
 GAGAGGTACC CATTGTGAAC TCCTCAGATC CGATTCTCA CTCCAATTTA TCATCCAAAC 360
 ATTGATCTG CTGGAAGGAT TTGTCTGGAT GTTCTCAAT TGCCACCAAA AGGTGCTTGG 420
 AGACCATCCC TCAACATGCG AACTGTGTTG ACCTCTATT AGCTGCTCAT GTCAGAACCC 480
 AACCCGTATG ACCCGCTCAT GGCTGACATA TCCTCAGAA TTAATATAA TAAGCCAGCC 540
 TTCCTCAAGA ATGCCAGACA GTGGACAGAG AAGCATGCAA GACAGAAACA AAAGGCTGAT 600
 GAGGAAGAGA TGCTTGATAA TCTACCAGAG GCTGGTGACT CCAGAGTACA CAACTCAACA 660
 CAGAAAAGGA AGGCCAGTCA GCTAGTAGGC ATAGAAAAGA AATTTCATCC TGATGTTTAG 720
 GGGACTTGTG CTGTTTATGC TTAGTTAATG TGTCTTTTGC CAAGGTGATC TAAGTTGCTC 780
 ACCTGAATTT TTTTGTAAAT TATATTGAT GACATAATTT TTGTGTAGTT TATTTATCTT 840
 GTACATATGT ATTTTGAAT CTTTTAAACC TGAAAAATAA ATAGTCATTT AATGTTGAAA 900

Seq ID NO: 148 Protein sequence:
 Protein Accession #: NP_054895.1

1	11	21	31	41	51	
MQRASRLKRE	LHMLATEPPF	GITCWQDKDQ	MDDLRAQILG	GANTPYEKGV	FKLEVIIPER	60
YPFEPPQIRF	LTPIYHPNID	SAGRICLDVL	KLPPKGAWRP	SLNIATVLTS	IQLLMSEPNP	120
DDPLMADISS	EFKYNKPAFL	KNARQWTEKH	ARQKQRADEE	EMLDNLPEAG	DSRVHNSTQK	180
RKASQLVIGIE	KKFHFEDV					

Seq ID NO: 149 DNA sequence
 Nucleic Acid Accession #: NM_003812
 Coding sequence: 224-2722

1	11	21	31	41	51	
TCCTCTGCGT	CCCCCCCCCG	GAGTGGCTGC	GAGGCTAGGC	GAGCCGGGAA	AGGGGGCGCC	60
GCCAGAGCCC	GAGCCCCGCG	CCCCGTGCCC	CGAGCCCGGA	GCCCCCTGCC	CGCGGCGGCA	120
CCATGCGCGC	CGAGCCGCGC	TGACCGGCTC	CGCCCGCGGC	CGCCCGCAG	CTAGCCCGGC	180
GCTCTGCGCG	GCCACACGGA	GCGCGCGCCG	GGAGCTATGA	GCCATGAAGC	CGCCCGGCAG	240
CAGCTGCGCG	CAGCCGCCCC	TGGCGGGCTG	CAGCCTTGCC	GGCGCTTCCT	CGGCGCCCCA	300
ACGCGGCCCC	GCCGGGCTCG	TGCCTGCCAG	CGCCCCGGCC	CGCACGCGCC	CCTGCGCGCT	360
GCTTCTCGCT	CTTCTCTGTC	TGCCTCCGCT	CGCCCGCTCG	TCCCGGCCCC	GCGCCTGGGG	420
GGCTGCTGCG	AATGGGTTGT	CGCATTGGAA	TGAAACTGCA	GAAAAAATT	TGGGAGTCCT	480
GGCAGATGAA	GACAAATCAT	TGCAACAGAA	TAGCAGCAGT	AATATCAGTT	ACAGCAATGC	540
AATGCAGAAA	GAAATCACAC	TGCCTTCAAG	ACTCATATAT	TACATCAACC	AAGACTCGGA	600
AAGCCCTTAT	CACGTTCTTG	ACACAAAGGC	AAGACACCAG	CAAAAACATA	ATAAGGCTGT	660
CCATCTGGCC	CAGGCAAGCT	TCCAGATTGA	AGCCTTCGGC	TCCAAATTC	TTCTTGACCT	720
CATACTGAAAC	TCTAGGTTGT	TGCTTCTGTA	TTATGTGGAG	ATTCACTACG	AAAATGGGAA	780
ACCACAGTAC	TCTAAGGGTG	GAGAGCACTG	TTACTACCAT	GGAAGCATCA	GAGGCGTCAA	840
AGACTCCAA	TGGGCTCTGT	CAACCTGCAA	TGGACTTCAT	GGCATGTTTG	AAGATGATAC	900
CTTCGTGTAT	ATGATAGAGC	CACTAGAGCT	GGTTCATGAT	GAGAAAAGCA	CAGGTCGACC	960
ACATATAATC	CAGAAAACCT	TGGCAGGACA	GTATTCTAAG	CAATGAAGA	ATCTCACTAT	1020
GGAAAGAGGT	GAGCAAGTGC	CCTTCTCTCT	TGAAATTACAG	TGGTTGAAAA	GAAGGAAGAG	1080
AGCAGTGAAT	CAATCAGGTG	GTATATTGTA	AGAAATGAAA	TATTTGGAAC	TTATGATTGT	1140
TAATGATCAC	AAACGCTATA	AGAAGCATCG	CTCTTCTCAT	GCACATACCA	ACAACTTTGC	1200
AAAGTCCGTG	GTCAACCTTG	TGGATTCTAT	TTACAAGGAG	CAGCTCAACA	CCAGGGTTGT	1260
CTGTTGGGCT	TATAGAGACCT	GGACTGAGAA	GGATCAGATT	GACATCACCA	CCAACCTGT	1320
GCAGATGCTC	CATGAGTTCT	CAAAATACCG	GCAGCGCATT	AAGCAGCATG	CTGATGCTGT	1380
GCACCTCATC	TGCGGGGTGA	CATTCTACTA	TAAGAGAAGC	AGTCTGAGTT	ACTTTGGAGG	1440
TGTCTGTTCT	CGCACAGAGG	GAGTTGGTGT	GAATGAGTAT	GGTCTTCCAA	TGGCAGTGGC	1500
ACAAGTATTA	TGCGAGAGCC	TGGCTCAAAA	CCTTGGAAATC	CAATGGGAAC	CTTCTAGCAG	1560
AAAGCCAAAA	TGTGACTGCA	CAGAATCCTG	GGGTGGCTGC	ATCATGGAGG	AAACAGGGGT	1620
GTCCCACTTC	CGAAAATTTT	CAAAATGCGC	CATTTTGGAG	TATAGAGACT	TTTTACAGAG	1680
AGGAGGTGGA	GCCTGCCTTT	TCAACAGGCC	AACAAAGCTA	TTTGAGCCCA	CGGAATGTGG	1740
AAATGGATAC	GTGGAGAGCTG	GGGAGGAGTG	TGATTGTGGT	TTTCATGTGG	AATGCTATGG	1800
ATTATGCTGT	AAGAAATGTT	CCCTCTCCAA	CGGGGCTCAC	TGCAGCGACG	GGCCCTGCTG	1860
TAACAATACC	TCATGTCTTT	TTCAAGCCAG	AGGGTATGAA	TGCCGGGATG	CTGTGAACGA	1920
GTGTGATATT	ACTGAATATT	GTACTGGAGA	CTCTGGTCAG	TGCCCAACCA	ATCTTCATAA	1980
GCAAGACGGA	TATGATGCA	ATCAAAATCA	GGGCGCTGCT	TACAATGGCG	AGTGCAAGAC	2040
CAGAGACAA	CAGTGTGAGT	ACATCTGGGG	AACAAAGGCT	GCAGGGTCTG	ACAAGTTCTG	2100
CTATGAAAAG	CTGAATACAG	AAGGCACTGA	GAAGGGAAGC	TGCGGGGAAGG	ATGGAGACCG	2160
GTGGATTGAG	TGCAGCAATC	ATGATGTGTT	CTGTGGATTG	TTACTCTGTA	CCAATCTTAC	2220
TGAGGCTCCA	CGTATTGGTC	AACCTCAGGG	TGAGATCATT	CCAACTTCCT	TCTACCATCA	2280
AGGCCGCGTG	ATTGACTGCA	GTGGTGCCCA	TGTAGTTTAA	GATGATGATA	CGGATGTGGG	2340
CTATGTAGAA	CATGTGAACG	CATGTGGCCC	GTCTATGATG	TGTTTAGATG	GGAAAGTGCCT	2400
ACAAATTCAA	GCCCTAAATA	TGAGCAGCTG	TCCACTCGAT	TCCAAGGGTA	AAGTCTGTTC	2460
GGGCCATGGG	GTGTGTAGTA	ATGAAGCCAC	CTGCATTGTT	GATTTACCT	GGGAGGGGAC	2520
AGATTGAGT	ATCCGGGATC	CAGTTAGGAA	CCTTCACCCC	CCCAAGGATG	AAGGACCCAA	2580
GGGTCTTAGT	GCCACCAATC	TCATAATAGG	CTCCATCGCT	GGTGCCATCC	TGGTAGCAGC	2640
TATTGTCTCT	GGGGGACACG	GCTGGGGATT	TAAAAATGTC	AAGAAGAGAA	GGTTGATGCC	2700
TACTCAGCAA	GGCCCCATCT	GAATCAGCTG	CGCTGGATGG	ACACCGCCTT	GCACTGTTGG	2760
ATTCTGGGTA	TGACATACTC	CGAGCAGTGT	TACTGGAATC	ATTAAGTTTG	TAAACAAAAC	2820
CTTTGGGTGG	TAATGACTAC	GGAGCTAAAG	TGGGGGTGAC	AAGGATGGGG	TAAAGAAAAA	2880
CTGTCTCTTT	TGGAATAAAT	GTCAAAGAAC	ACCTTTTACC	ACCTGTGAGT	AAACGGGGGA	2940
GGGGGCAAAA	GACCATGCTA	TAAAAAGAAC	TGTTCCAGAA	TCTTTTTTTT	TCCTTAATGG	3000
ACGAAGGAAC	AACACACACA	CAAAAATTAA	ATGCAATAAA	GGAATCATT	AAAA	

Seq ID NO: 150 Protein sequence:
 Protein Accession #: NP_003803

1	11	21	31	41	51	
MKPPGSSSRQ	PPLAGCSLAG	ASCGPQRGPA	GSVPASAPAR	TPPCRLLLV	LLLPLLAASS	60
RPRAWGAAAP	SAPHWNCTAE	KNLGVLADED	NTLQONSSSN	ISYSNAMQKE	ITLPSRLIYY	120
INQDSESPYH	VLDTKARHQQ	KHNKAVHLAQ	ASFQIEAFGS	KFILDLLINN	GLLSSDYVEI	180
HYENGKPYYS	KGGHPCYHYG	SIRGVKDSKV	ALSTCNLHGG	MFEDDTFVYM	IEPLBLVHDE	240
KSTGRPHIIQ	KTLAQYYSKQ	MKNLTMERGD	QNPFLSELQW	LKRRKRAVNP	SRGIFPEEMKY	300
LELMIVNDHK	TYKKHRSSEA	HTNNFAKSVV	NLVDSIYKEQ	LNTRVVLVAV	ETWTEKDQID	360
ITINPVQMLH	EFKRYRRIK	QHADAHLIS	RVTFFHYKRS	LSYFGGVCSR	TRGVGVNEYG	420
LPMVAQVLIS	QSLAQNLGIQ	WEPSSRKPKC	DCTESWGGCI	MEETGVSHSR	KPSKCSILEY	480
RDPLQRRGGA	CLFNRPTKLF	EPTCEGNGYV	EAGEECDCGF	HVECYGLCKC	KCSLSNGAHC	540
SDGFCQNNWS	CLFQPRGYEC	RDVAVNECDIT	EYCTGDSGQC	PPNLHKQDGY	ACNQNGGRCY	600
NGECKTRDNQ	CQYINGTKAA	GSDKFCYEKL	NTEGTEKGNC	GKGDWRVIQC	SKBDVFCGFL	660

WO 02/086443

LCNLNTRAFR IGQLQGEIIP TSFYHQGRVI DCSGARHVLD DTDVGYVED GTPCGPSMMC 720
LDRKCLQIQAL LNMSSCLPDS KGKVCSEGHV CSNEATCICD FTWAGTDCSI RDPVRNLHPP 780
KDEGPKGPSA TNLIGSIAG AILVAAIVLG GTGWGPKNVK KRRFDPTQQG PI

PCT/US02/12476

Seq ID NO: 151 DNA sequence
Nucleic Acid Accession #: NM_023915
Coding sequence: 250-1326

1 11 21 31 41 51
GGCAGCAGGG TTTGCTTTTC ATGCTTTACC AGAAAAATCCA CTTCCTGCC GACCTTAGTT 60
TCAAAGCTTA TTCTTAATTA GAGACAAGAA ACCTGTTTCA ACTTGAAGAC ACCGTATGAG 120
GTGAATGGAC AGCCAGCCAC CACAATGAAA GAAATCAAAC CAGGAATAAC CTATGCTGAA 180
CCCAGCCTC AATGTCCTCC AAGTGTCTTC TGACACGCAT CTTTGCTTAC AGTGCAATC 240
15 AACTGAAGAA TGGGGTTCAA CTTGACGCTT GCAAAATTAC CAAATAACGA GCTGCACGGC 300
CAAGAGAGTC ACAATTGAGG CAACAGGAGC GACGGGCCAG GAAAGAACAC CACCTTTCAC 360
AATGAATTG ACACAATTGT CTGCGCGGTG CTTTATCTCA TTATATTGT GGCAGCATC 420
TTGCTGAATG GTTTAGCAST GTGATCTTC TTCCACATTA GGAATAAAC CAGCTTCATA 480
TTCTATCTCA AAAACATAGT GGTGTCAGAC CTCATAATGA CGCTGACATT TCCATTTCGA 540
20 ATAGTCCATG ATGCAGGATT TGGACCTTGG TACTTCAAGT TTATTCTCTG CAGATACACT 600
TCAGTTTGT TTTATGCAAA CATGTATACT TCCATCGTGT TCCTTGGGCT GATAAGCATT 660
GATCGCTATC TGAAGGTGGT CAAGCCATT GGGGACTCTC GGATGTACAG CATAACCTTC 720
ACGAAGGTTT TATCTGTTTG GTTTTGGGTG ATCATGGCTG TTTTGTCTTT GCCAAACATC 780
25 ATCCTGACAA ATGGTCAGCC AACAGAGGAC AATATCCATG ACTGCTCAA ACTTAAAGT 840
CCTTTGGGGG TCAAATGGCA TACGGCAGTC ACCTATGTGA ACAGCTGCTT GTTTGTGGCC 900
GTGCTGGTGA TTCTGATCGG ATGTTACATA GCCATATCCA GGTACATCCA CAAATCCAGC 960
AGGCAATTCA TAAGTCAGTC AAGCCGAAAG CGAAAACATA ACCAGAGCAT CAGGGTTGTT 1020
GTGGCTGTGT TTTTACCTG CTTTCTACCA TATCACTTGT GCAGAATTCC TTTTACTTTT 1080
30 AGTCACTTAG ACAGGCTTTT AGATGAATCT GCACAAAAA TCCTATATTA CTGCAAGAA 1140
ATTACACTTT TCTGTCTGCG GTGTAATGTT TGCTGGATC CAATAATTTA CTTTTCATG 1200
TGTAGGTGTC TTTCAAGAA GCTGTTCAA AAATCAAATA TCAGAACAG GAGTGAAAGC 1260
ATCAGATCAC TGCAAGTGT GAGAAGATCG GAAGTTCGCA TATATTATGA TTACACTGAT 1320
GTGTAGGCCT TTTATTGTTT GTTGAATCG ATATGTACAA AGTGTAAATA AATGTTTCTT 1380
35 TTCATTATCC TTAATAAAAA AA

Seq ID NO: 152 Protein sequence:
Protein Accession #: NP_076404

1 11 21 31 41 51
MGFNLTLAKL PNNELHGGES HNSGNRSDGP GKNTTLHNEF DTIVLPVLYL IIFVASILLN 60
GLAVWTFPHI RNKTSFIPLY KNIVVADLIM TLTFPFRIVH DAGFGPWYFK FILCRYTSVL 120
45 FYANMYTSIV FLGLISIDRY LKVVKPPGDS RMYSTFTKV LSVCVWVIMA VLSLPNIILT 180
NQOPTEDNIH DCSKLKSPLG VKWHTAVTYV NSCLFVAVLV ILIGCYIAIS RYIHKSSRQF 240
ILQSSSRKRKH NQSIIRVVAV FFTCFLPYHL CRIPPTFSHL DRLLDESAQK ILYYCKEITL 300
FLSACNVCLD PIIVFFMCRS FSRRLFKKSN ITRSESIRS LQSVRRSEVR IYYDYTDV

Seq ID NO: 153 DNA sequence
Nucleic Acid Accession #: D80008.1
Coding sequence: 149-739

1 11 21 31 41 51
GTTCCGCGCC AAAGCGCGGA CGCGAGGCCG AGGCGAGAGC CTGGCGCTGT AGGACTAGAA 60
CGAAAGGAGT GAGGGCGCGA GAGCCAGAT ACCATTTTGG CGTGAGAGCT GGTGGTTGGC 120
AAGGCCGCGG GAGTGGGAAG CGTCCGCCAT GTTCTGCGAA AAAGCCATGG AACTGATCCG 180
CGAGCTGCAT CGCGCGCCCG AAGGGCAACT GCCTGCCTTC AACGAGGATG GACTCAGAGA 240
AGTTCTGGAG GAGATGAAG CTTTGTATGA ACAAACCAG TCTGATGTGA ATGAAGCAAA 300
60 GTTCAGGTGA CGAAGTGATT TGATACCAAC TATCAAATT CGACACTGTT CTCTGTTAAG 360
AAATCGACGC TGCACGTAG CATACCTGTA TGACCGCTTG CTTGCGATCA GAGCACTCAG 420
TTGGGAATAT GGTAGCGTCT TGCCAAATGC ATTACGATT CACATGGCTG CTGAAGAAAT 480
GGAGTGGTTT AATAATTATA AAGATCTCT TGCTACTTAT ATGAGGTCAC TGGGAGGAGA 540
TGAAGGTTTG GACATTACAC AGGATATGAA ACCACCAAAA AGCCTATATA TTGAAGTCCG 600
65 GTGTCTAAAA GACTATGGAG AATTGAAAT TGATGATGGC ACTTCAGTCC TATTAATAAA 660
AAATAGCCAG CACTTTTAC CTCGATGGAA ATGTGAGCAG CTGATCAGAC AAGGAGTCTC 720
GGAGCACATC CTGTCAATG CATGCGCCGA GGCACCTCCA GGCCTTCACT AACTCATGGA 780
CTCCTCTGTA CTCACCTCTC CCACCACTCC CTTCACTTCC CTCTTTGATT TTAGAAGCTA 840
TAGACATTGT TTAAGATAAC TAAGAAACT TGGCTAAGAA GTATAATTG CTAACATTAT 900
70 AGGACTTTCT TTTTATAAT TTGTACACTA TTCTTCTTAC TCTTTTGGG TTTTGGTTTT 960
GTTTGTAGA GACTGTCTCA CTATGTTGCC CAAGCTGGTC TCAAACCTCT GGCCTCAAGC 1020
AGTCTCTCCA CCTTAGCTTC TCAAAGTGT GAGATCACAG GCGTGAGCCA CTGCACCCG 1080
CCCTACTCC TTTTCTAAT AAGCTGTATC TGTAATCACA GCATTCTAC AGTGTGTACA 1140
75 GTGTGTTTTT TAAATGAAG TAAACATGGT TACATTTGAA TCTCTTAAAT AAGCAGTCAC 1200
TTGGCTGGAC AGGAGAAGG TAGATCCTGT GTGTCTTGT TCTGGTCAT GTGTATTGTA 1260
CAAGCTAGAG AGCTGAATT CTGAGATACA CATTTCAAA TCACATGCAA GTGAAGATGA 1320
TGGTCTGTAG AAATTTTCAG TATATATAAT GTTTAATGAC ATACTAATT ATCATCTGGC 1380
TATTTGGGAA GGAAGGACAC ACATGGATT TGACATTTT CACCATGGTG GCTGGTGTGG 1440
CTTGTGGCTA TGGGTGATC ACCAGTATCA CCACCTTGA AGGGAGCAGT GAAATTTGGG 1500
80 CTAGAGAAGG AACTTTGATC AGTTTCCCT GAGATTGAGA TTGACTGAAA AGTCACATGA 1560
AGAGTTGATT GTCTTTTAA GGTATGTTT AAACAGCTGA CATTTTAAAT TTTGATGAAA 1620
TCCAGTTTAT TCGTTTGTTC TTTTATGCTT TGGGTGTTGC ATCCGAGAAA TCTTTCCCA 1680
TCCCAAGATC ACAATTTTTT TTCTTTTTTA CTCTAGAAAG TGTATATAAT TTAAGCTTTA 1740
TACTTTGGTC TATGACCCGT TTTTTTTTTT GTTTTGTGTT GTTTTTCGT TTGTTTCTTT 1800
85 GTTTTGAGAT GAGAGTCTGT TCTGTCAACC AGGCTGGGGT GCAGTGGGGT GATCTTGGCT 1860
CACTGCAATC TCTATCCCT GGGTCAAGT GATTCTCTTG TCTCAGCCTC CCAAGTAGCT 1920
GGGATTACAG GCACAGGCCG CCAGCCCTGG CTAATTTTTG TATTTTTAGT AGAGACAGAG 1980

5	TTTTACCATG	TTGGCCAGGC	TGGTTTCAAA	CTCCTGACCT	CAAGTGACCC	ACCTTGGCCT	2040
	CCCAAAGTTT	TGGGATTACA	AGTGTGGGCC	ACCGCGGCCA	GCCTATGATC	CATTTTGAAT	2100
	GAATTTTATA	TATGGTGCNA	GGTGTCAATC	CACCTTCACT	TTTCTTGGG	AATATAGATA	2160
	TCCAGCTGTT	TCACCTACCAT	TTTTTGAAAG	GACTGCCCTT	TGCTCTATCA	CCTTTGCATT	2220
	TTTGTAAAA	AGTAGTTGTC	AATGTATATG	TGGGTTTATT	TCAGGACTCT	GTTTTGTTC	2280
	ATTGACCTGT	TTTTCTCTCC	TGAATGCCAA	TACCATATTT	GTATGTAGTG	TATGTAATTT	2340
	TCTAATAATT	CTTGAAACAG	ATAGTATTAA	TGTGTCTAT	TTTTGTCTGT	GTTTGTATTT	2400
	TTGTAGAGA	TGGGTTTCA	CCGTGTTGGC	CAGGCTGTGT	TGAACTCCTG	AGCTAAAGCA	2460
10	ATACACTTGC	CTCGTCTCTC	CCATGTGCTG	GGATTACAGG	CGTGAGCCTT	GGTGCTGGCC	2520
	CAGTGATCCA	CATTCTCTTT	TGAGATTGTT	TTTGGCTATG	TTAAGTCCTT	TGCTTTTGAT	2580
	GTGAAATTG	GGAACAGGCA	GGGTGTGGTG	GCTTATGCCT	GTAATCCTAG	AACCTTGGGA	2640
	GGCTTAGATG	GGTGGATCAC	TTGAGCTCAG	GAGTTCCAGA	CCAGCCCGGG	CCTATGGCAA	2700
	AACTCCGTCT	CTACAAAAAA	TAGAAAAAAT	TAGCCAGGTG	TGGTGGTGCA	TGCTGTAGT	2760
15	CACAGTTACA	CGGCGAGCTG	AGGTGGGAGG	ATCACTTGAA	CCCCAGAGGT	CAAGACTGCA	2820
	GTGAGCTGAG	ATCACACAC	TGTACTCCAG	CCTGGGTGAC	AAAGTGAGAC	TCTATCTCAA	2880
	AAAGAAATTA	GGATCAATTT	TGCAATTTCT	ACAAACAACA	CAACAAAAAC	CCCTGTTGGG	2940
	CACCTTGATT	GAGATTGCAT	TGAATTTATA	TAAACTGTT	GGGAGAAATT	ACATCTTAAT	3000
	AATATTGAGT	TTCTGCGCCT	ATAACAAGG	TCTGTCTTCC	TAGGTATTAA	TGTTTGTCT	3060
20	TCTATTCTC	TTAATAATCT	TTTGTAGTTT	TCAGTGATCA	GGTCTACCAT	GTGAGCATT	3120
	CATAGTTTG	ATGCTAAATG	GTATTTTAAA	ATTTCAAATT	CTAACCACCT	GTTGCTAGTA	3180
	AATAGAAATA	CAATTGATGT	TGAACCTGTA	TCCTTCAGCC	TTGCTAAACT	GTGAGTTCTC	3240
	ATGGTGTGTT	TGTAAATTAC	ATCAACAGTC	ATGTGTTCTA	TGAATAAAGA	GTTTTACTCC	3300
	TTC						

Seq ID NO: 154 Protein sequence:
Protein Accession #: BAA11503.1

30	1	11	21	31	41	51	
	MFCEKAMELI	RELHRAPEQG	LPAFNEGLR	QVLEEMKALY	EQNQSDVNEA	KSGGRSDLIP	60
	TIKPRHCSLL	RNRCTVAYL	YDRLLRIRAL	RWEYGSVLPN	ALRFHMAAEE	MEWFNNYKRS	120
	LATYMRSLGG	DEGLDITQDM	KPKKSLYIEV	RCLKDYGEFE	VDDGTSVLLK	KNSQHFPLRW	180
	KCEQLIRQGV	LEHILS					

Seq ID NO: 155 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 149-709

40	1	11	21	31	41	51	
	GTTCGGCGCC	AAAGCGCGGA	GCGGAGGCCG	AGGCGAGAGC	CTGGCGCTGT	AGGACTAGAA	60
	CGAAAGGAGT	GAGGCGCCGA	GAGCCCAGAT	ACCATTTTGG	CGTGAGAGCT	GGTGGTTGGC	120
	AAGGCCGCGG	GAGTGGGAAG	CGTCCGCCAT	GTTCTGCGAA	AAAGCCATGG	AACGTATCCG	180
	CGAGCTGCAT	CGCGCGCCCG	AAGGGCAACT	GCCTGCCTTC	AACGAGGATG	GACTCAGACA	240
45	AGTTCGAGG	GAGATGAAG	CTTTGTATGA	ACAAAACCCAG	TCTGATGTGA	ATGAAGCAAA	300
	GTCAAGTGGG	CGAAGTGATT	TGATACCAAC	TATCAAATTT	CGACACTGTT	CTCTGTTAAG	360
	AAATCGACGC	TGCCTGTAG	CATACCTGTA	TGACCGCTTG	CTTCGGATCA	GAGCACTCAG	420
	ATGGGAATAT	GGTAGCGTCT	TGCCAAATGC	ATTACGATTT	CACATGGCTG	CTGAAGAAAT	480
	GGAGTGGTTT	AATAATTATA	AAGATCTCT	TGCTACTTAT	ATGAGGTGAC	TGGGAGGAGA	540
50	TGAAGGTTTG	GACATTACAC	AGGATATGAA	ACCACCAAAA	AGCCTATATA	TTGAAGCTGG	600
	ATGCAGTGGC	GCGATCTCGG	CTCAACCTGC	AACCTCCACC	TCCCAGGTTT	ACCTCAACTG	660
	CACCTCCAC	CTCCAGCTG	CGGTGTCTAA	AAGACTATGG	AGAAATTTGAA	GTGTATGATG	720
	GCACTTCAGT	CCTATTAAAA	AAAAATAGCC	AGCACTTTTT	ACCTCGATGG	AAATGTGAGC	780
	AGCTGATCAG	ACAAGGAGTC	CTGGAGCACA	TCTGTCTATG	ACCATGCGCC	GAGGCACTTC	840
55	CAGGCTTCAC	TCAACTCATG	GACTCCTCTG	TACTCACTCT	CTCCACCACT	CCCTTCACCT	900
	CCCTCTTTGA	TTTTAGAGC	TATAGACATT	GTTTAAAGATA	ACTAAGAATA	CTTGCTAAG	960
	AAGTATAATT	TGCTAACTAT	TAAAGACTTT	CTTTTTTTAA	TGTTGTACAC	TATTTCTTCT	1020
	ACTCTTTTTT	GGTTTGGTTT	TGTTTGTGA	GAGACTGTCT	CACATATGTT	CCCAAGCTGG	1080
	TCTCAAATCT	CTGGCCTCAA	GCACTCTCTC	CACCTTAGCT	TCTCAAAGTG	TTGAGATCAC	1140
60	AGGCGTGAAG	CACGTGACCC	CGCCCTTACT	CTTTTTTCTA	ATAAGCTGTA	TCTGTAATCA	1200
	CAGCATTCCT	ACAGTTGTTA	CAGTGTGTTT	TTTAAATGAA	AGTAAACATG	GTACATTGTT	1260
	AATCTCTTAA	ATAAGCAGTC	ACTTGGCTGG	ACAGGAAGAA	GGTAGATCCT	GTGTGCTTGG	1320
	TTTTCTGGTC	ATGTGTATTG	TACAAGCTAG	AGAGCTGAAT	TTCTGAGATA	CACATTTTCA	1380
	AATCAGATGC	AAGTGAAGAT	GAGGTCTGT	AGAAATTTTC	AGTATATATA	ATGTTTAAATG	1440
65	ACATACATA	TTATCATCTG	GCTATTTGGG	AAGGAAGGAC	ACACATGGAT	TTTGACATT	1500
	TCCACCATTG	TGGCTGTGTG	GGCTTGTGGC	TATGGGGTGA	TCACCAGTAT	CACCACCTTG	1560
	GAAGGGGACA	GTGAAATTTG	GGCTAGAGAA	GGAACTTTGT	ACAGTTTTC	CTGAGATTCA	1620
	GATTGACTGA	AAAGTCACAT	GAAGAGTTGA	TTGTCTTTTA	ATGGTATGTT	TTAAACAGCT	1680
	GACATTTTAA	ATTTTGTATGA	AATCCAGTTT	ATTCTGTTGT	TCITTTATGC	TTTGGGTGTT	1740
70	GCATCCGAGA	AATCTTTTCC	CATCCCAAGA	TCACAATTTT	TTTTCTTTT	TACTTCTAGA	1800
	AGTGTATATA	TTTTAAGCTT	TATACITTTG	TCTATGACCC	GTTTTTTTTT	TTGTTTTGTT	1860
	TTGTTTTTTC	GTTTGTCTCT	TTGTTTTGAG	ATGGAGTCTT	GTTCTGTAC	CCAGGCTGGG	1920
	GTGCACTGGC	GTGATCTTGG	CTCACTGCAA	TCTCTATCCC	CTGGGTTCAA	GTGATCTCT	1980
	TGTCTCAGCC	TCCCAAGTAG	CTGGGATTAC	AGGCACAGGC	CGCCACGCC	GGCTAATTTT	2040
75	TGTATTTTAA	GTAGAGACAG	AGTTTACCA	TGTTGGCCAG	GCTGGTTTCA	AACTCCTGAC	2100
	CTCAAGTGAC	CCACTTGGC	CTCCCAAAGT	TTTGGGATTA	CAAGTGTGGG	CCACCGCGGC	2160
	CAGCCTATGA	TCCATTTTGA	ATGAATTTT	TATATGGTGC	AAGGTGTCAA	TCCACCTTCA	2220
	CTTTTTCTTG	GGAATATAGA	TATCCAGCTG	TTTCACTACC	ATTTTGTGAA	AGGACTGCC	2280
	TTTGCTCTAT	CACCTTTGCA	TTTTTGTATA	AAAGTAGTTG	TCAATGTATA	TGTGGGTTTA	2340
80	TTTCAGGACT	CTGTTTGTG	CCATTGACCT	GTTTTCTCT	CCTGAATGCC	AATACCATAT	2400
	TTGTATGTAG	TGTATGTAAT	TTTCTAATAA	TTCTTGAAAC	AGATAGTATT	AATGTGTCAT	2460
	ATTTTGTCTG	TTGTTGTAT	TTTTTGTAGA	GATGGGGTTT	CACCGTGTG	GCCAGGCTGT	2520
	GTGAACTCC	TGAGCTAAAG	CAATACACTT	GCCTCGTCT	CCCCATGTGC	TGGGATTACA	2580
	GGCGTGAGCC	TTGTGTCTGG	CCCAAGTGAC	CACATTTCTT	TTTGAGATTT	GTTTTGGCTA	2640
85	TGTTAAGTCC	TTTGTCTTTG	ATGTGAAATT	TGGGAACAGG	CAGGGGTGTG	TGGCTTAGTA	2700
	CTGTAATCCT	AGAACTTTGG	GAGGCCTAGA	TGGGTGGATC	ACTTGAGCTC	AGGAGTTCCA	2760
	GACCAGCCCG	GGCCTATGGC	AAAACCTCCG	CTCTACAAAA	AATAGAAAAA	ATTAGCCAGG	2820

TGTGGTGGTG CATGCCCTGA GTCACAGTTA CACGGCAGGC TGAGGTGGGA GGATCACTTG 2880
 AACCCAGAG GTCAGAGCTC CAGTGAGCTG AGATCACACC ACTGTACTCC AGCCTGGGTG 2940
 ACAAGTGGAG ACTCTATCTC AAAAAGAAAT TAGGATCAAT TTGTCAATTT CTACAACAAC 3000
 AACACAAAA ACCCTGTTG GGCACCTTGA TTGAGATTGC ATTGAATTTA TATAAACTG 3060
 TTGGGAGAAAT TGACATCTTA ATAATATTGA GTCTTCTGGC CTATAACAA GGTCTGTCTT 3120
 CCTAGGTATT AATGTTTGT CTCTATTTC TCTTAATAAT CTTTTGTAGT TTTCAGTGT 3180
 CAGGTCTACC ATGTCAGCAT TTCATAGTTT TGATGCTAAA TGGTATTTTA AAATTTCAA 3240
 TTCTAACAC TTGTGCTAG TAAATAGAAA TACAATTGAT GTTGAACCTG TATCCTTCAG 3300
 CCTGTCTAAA CTGTGAGTTC TCATGGTGT TTTGTAAATT ACATCAACAG TCATGTGTTC 3360
 TATGAATAAA GAGTTTACT CCTTC

Seq ID NO: 156 Protein sequence:
Protein Accession #: Bos sequence

1 11 21 31 41 51
 MFCEKAMELI RELHRAPEQG LPAPNEDGLR QVLEEMKALY EQNQSDVNEA KSGGRSDLIP 60
 TIKFRHCSLL RNRRCTVAYL YDRLLRIRAL RWEYGSVLEN ALRFHMAAEE MEWFNNYKRS 120
 LATYMRSLGG DEGLDIQDM KPKKSLYIEA GCSGAISAQP ATSTSQVHLN CNLHLPGPVS 180
 KRLWRI

Seq ID NO: 157 DNA sequence
Nucleic Acid Accession #: Bos sequence
Coding sequence: 148-621

1 11 21 31 41 51
 TTCCGGCCCA AAGCGCCGAG CGGAGGCCGA GCGGAGAGCC TGGCGCTGTA GGACTAGAAC 60
 GAAAGGAGTG AGGCGCCGAG AGCCAGATA CCATTTTGGC GTGAGAGCTG GTGGTTGGCA 120
 AGGCGCGCGG AGTGGGAGAG GTCCGCCATG TTCTGCGAAA AAGCCATGGA ACTGATCCGC 180
 GAGCTGCATC GCGCGCCCGA AGGCAACTG CCTGCCTTCA ACGAGGATGG ACTCAGACAA 240
 GTTCTGGAGG AGATGAAGAG TTTGTATGAA CAAAACCACT CTGATGTGAA TGAAGCAAA 300
 TCAGGTGACG GAAGTGATTT GATACCAACT ATCAAATTTG GACACTGTTC TCTGTTAAGA 360
 AATCGACGCT GCACTGTAGC ATACCTGTAT GACCGCTTGC TTCGATCAG AGCACTCAGA 420
 TGGGAATATG GTAGCGTCTT GCCAAATGCA TTACGATTTC ACATGGCTGC TGAAGAAGTC 480
 CGGTGTCTAA AAGACTATGG AGAATTGAA GTTGATGATG GCACCTCAGT CCTATTAAAA 540
 AAAAAAGACC AGCACTTTT ACCTCGATGG AAATGTGAGC AGCTGATCAG ACAAGGAGTC 600
 CTGGAGCACA TCCTGTCTAG ACCATGCGCC GAGGCACTTC CAGGCTTCAC TCAACTCATG 660
 GACTCCTCTG TACTCACTCT CTCCACCCT CCCTTCACCT CCCTCTTTGA TTTTAGAAGC 720
 TATAGACATT GTTTAAGATA ACTAAGAATA CTGGCTAAG AAGTATAATT TGCTAACTAT 780
 TAAGGACTTT CTTTTTTTAA TGTGTACAC TATTCTTCTT ACTCTTTTTT GGTTTTGGTT 840
 TTGTTTTGTA GAGACTGTCT CACTATGTG CCCAAGCTGG TCTCAAACCT CTGGCCTCAA 900
 GCAGTCTCC CACTTGTACT TCTCAAAGT TTGAGATCAC AGGCGTGAGC CACTGCACCC 960
 GCGCCCTACT CTTTTTTCTA ATAAGCTGTA TCTGTAATCA CAGCATTCCT ACAGTTGTTA 1020
 CAGTGTGTTT TTTAAATGAA AGTAAACATG GTTACATTTC AATCTCTTAA ATAAGCAGTC 1080
 ACTTGCTGGG ACAGGAAGAA GGTAGATCCT GTGTGCTTGT TTTTCTGGTC ATGTGTATTG 1140
 TACAAGTATG AGAGCTGAAT TTCTGAGATA CACATTTTCA AATCAGATGC AAGTGAAGAT 1200
 GATGCTCTGT AGAATTATTC AGTATATATA ATGTTTAATG ACATACTAAT TTATCATCTG 1260
 GCTATTTGGG AAGGAAGGAC ACACATGGAT TTGTCACATT TCCACCATGG TGGCTGGTGT 1320
 GGCTGTGGG TATGGGGTGA TCACCAGTAT CACCCTTTG GAAGGGGACA GTGAATTTGG 1380
 GGCTAGAGAA GGAACCTTGT ACAGTTTTC CTGAGATTCA GATTGACTGA AAAGTCACAT 1440
 GAAGAGTTGA TTGTCTTTA ATGGTATGTT TTAACACAGT GACATTTTAA ATTTTGATGA 1500
 AATCCAGTTT ATTCGTTTGT TCTTTTATGC TTTGGGTGTT GCATCCGAGA AATCTTTTCC 1560
 CATCCCAAGA TCACAAATTT TTTTCTTTT TACTCTAGA AGTGTATATA TTTTAAGCTT 1620
 TATACTTTGG TCTATGACCC GTTTTTTTT TTGTTTGTGT TTGTTTTTTC GTTTGTTTCT 1680
 TTGTTTGGAG ATGGAGTCTT GTTCTGTAC CCAGGCTGGG GTGCGTGGC GTGATCTTGG 1740
 CTCACGTCAA TCTCTATCCC CTGGGTCAA GTGATCTCT TGTCTCAGCC TCCCAGTAG 1800
 CTGGGATTAC AGGCACAGGC CGCCACGCCCT GGCTAATTTT TGATTTTTTA GTAGAGACAG 1860
 AGTTTACCA TGTGGGCCAG GCTGGTTTCA AACTCCTGAC CTCAGTGAC CCACCTTGGC 1920
 CTCACCAAGT TTTGGGATTA CAAGTGTGGG CCACCGCGGC CAGCCTATGA TCCATTTTGA 1980
 ATGAATTTT TATATGGTGC AAGGTGTCAA TCCACCTTCA CTTTTTCTTG GGAATATAGA 2040
 TATCCAGCTG TTCTACTACC ATTTTTTGAA AGGACTGCCC TTTGCTCTAT CACCTTGTGA 2100
 TTTTGTGTTA AAAGTAGTTC TCAATGTATA TGTGGGTTTA TTTCAAGACT CTGTTTGTGT 2160
 CCATTGACCT GTTTTCTCT CTGAAATGCC AATACCATAT TTGTATGTAG TGTATGTAAT 2220
 TTTCTAATAA TTCTTGAAAC AGATAGTATT AATGTGTAT ATTTTGTCTG TTGTTGTAT 2280
 TTTTGTGTA GATGGGTTT CACCGTGTG GCCAGGCTGT GTTGAACCTC TGAGCTAAAG 2340
 CAATACACTT GCCTGCTCT CCCCATGTGC TGGGATTACA GCGGTGAGCC TTGGTGTCTG 2400
 CCCAGTGTAC CACATTTCTT TTTGAGATT GTTTTGGCTA TGTAAAGTCC TTTGCTTTTG 2460
 ATGTGAAATT TGGGAACAGG CAGGGTGTGG TGGCTATGC CTGTAATCCT AGAAGCTTTG 2520
 GAGGCTAGA TGGGTGATC ACTTGAGCTC AGGAGTTCCA GACCAGCCCG GGCCTATGGC 2580
 AAACTCCGT CTCTACAAAA AATAGAAAAA ATTAGCCAGG TGTGGTGGTG CATGCCTGTA 2640
 GTCACAGTTA CACGGCAGGC TGAGGTGGGA GGTACACTTG AACCCAGAG GTCAAGACTG 2700
 CAGTGAGCTG AGATCACACC ACTGTACTCC AGCCTGGGTG ACRAAGTGAG ACTCTATCTC 2760
 AAAAAAGAAAT TAGGATCAAT TTGTCAATTT CTACAACAAC AACCAACAAA ACCCTGTTG 2820
 GGCACCTTGA TTGAGATTGC ATTGAATTTA TATAAACTG TTGGGAGAAAT TGACATCTTA 2880
 ATAATATTGA GTCTCTGGC CTATAACAA GGTCTGTCTT CCTAGGTATT AATGTTTTGT 2940
 CTCTATTTC TCTTAATAAT CTTTTGTAGT TTTCAGTGTG CAGTCTACCT ATGTGAGCAT 3000
 TTCATAGTTT TGATGCTAAA TGGTATTTTA AAATTTCAA TTCTAACCA CTGTGAGTTC 3060
 TAAATAGAAA TACAATTGAT GTTGAACCTG TATCCTTCAG CCTGTCTAAA CTGTGAGTTC 3120
 TCATGGTGT TTTGTAAATT ACATCAACAG TCATGTGTTC TATGAATAAA GAGTTTACT 3180
 CCTTC

Seq ID NO: 158 Protein sequence:
Protein Accession #: Bos sequence

1 11 21 31 41 51
 | | | | |

MFCEKAMELI RELHRAPEGQ LPAPNEDGLR QVLEEMKALY EQNQSDVNEA KSGGRSDLIP 60
TIKPRHCSLL RNRRTVAYL YDRLLRIRAL RWEYGSVLPN ALRFHMAAEE VRCLKDYGEF 120
EVDDGTSVLL KNSQHFLLPR WKCEQLIRQG VLEHILS

5

Seq ID NO: 159 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 149-229

10 1 11 21 31 41 51
GTTCCGCGCC AAAGCGCGGA GCGGAGGCCG AGGCGAGAGC CTGGCGCTGT AGGACTAGAA 60
CGAAAGGAGT GAGGCGCCGA GAGCCAGAT ACCATTTTGG CGTGAGAGCT GGTGGTTGGC 120
AAGGCCGCGG GAGTGGGAAG CGTCCGCCAT GTTCTGCGAA AAAGCCATGG AACTGATCCG 180
CGAGCTGCAT CGCGCGCCCG AAGGGCAACT GCCTGCCTTC AACAATTAGC TGGGTGTGGT 240
15 GGCACACACC TGTAAGTCCA GCAACTTAGG AGGCTGAAGT GAGAGGATTG CATGGCTCCA 300
GGAAGTTGAA ACTGCAGTGA ACTGTGGTCA CGCTATTACA CTCCAGCCTG GGTGACAGAC 360
TGAATCCCTG TCTCAAAAAG GAAAAGGAGG ATGGACTCAG ACAAGTCTCT GAGGAGATGA 420
AAGCTTTGTA TGAACAAAAC CAGTCTGATG TGTTCTCTGT TAAGAAATCG ACGCTGCAC 480
GTAGCATACC TGATATGACC CTGTCTCGG ATCAGAGCAC TCAGATGG

20

Seq ID NO: 160 Protein sequence:
Protein Accession #: Eos sequence

25 1 11 21 31 41 51
ATGTTCTGCG AAAAAGCCAT GGAAGTATC CGCGAGCTGC ATCGCGCGCC CGAAGGGCAA 60
CTGCCTGCCT TCAACAATTA G

30

Seq ID NO: 161 DNA sequence
Nucleic Acid Accession #: U10694
Coding sequence: 1333-2280

35 1 11 21 31 41 51
GGATCCGGCC GGATCTCAGG GAGGTGAGGA CTTTGTCTC AGAGGGTGTG TGTGGACAAA 60
ACAGGGAGGC CTTGTGTTCC ACAGACACAG TGGTCCCAGG ATTGGAGAGC AGTCCAGGTG 120
AGGAACCTAA GGGAGGATCG AGGGTACCTC CAGGCCAGAG AAATCTCTAG ATCAAGAGAG 180
TTTGCCCTGC CCTACTGTG ACCCCAGAGA GCCCGGGCAG GGCTGTCTGC TGAGGTCCCT 240
40 CTTTATCCCT GGGATCACTG GTGTGCGGGA GGGCTGGCCT TGGTCTGAGG GGGCTGCAC 300
CAGCTCAGCA GAGGAGGGGT CCCAGGCCCT GCCAGGAGTC CAGGTGAGAG CTGAGGGGAC 360
CCCACTCAC AAACACAGAG GACCTAGCCC CACCCTGCC CTGTGTCTAG CTGAGGGGAA 420
CCGCTGGGTG GATGGACTCC CTTCACTTCC TCTTCAGGTG TCTCCTGGAG ATAGGGCCTC 480
AGGTCAACAG AGGAGGGGTT CCAGACCCTG CAGGCATCAA GATCAGGACC AGGCAGTATC 540
CTCACCCAG GACACATGGA CCCCATGTA TTTAGACATC TCTTACTGTA CTTCCGAGGA 600
45 AACCTCTGGC AGGTGTGGGC AGATGTTGGT TGGGGCATGT CCTTCTGTTC CATATCAGGG 660
ATGTGAGCTC CTGATCTGAG AGACTCTCAG GCAAGTAGAG GAGTAGAGTC CAGTCCCTGC 720
CAGGAGAAAG GTCAGGGCCC TGAGTGAGCG CAGAGGGGAC CATCCACCCC AAAAGTGTGT 780
AGAACTCAAG AGTGTCCAGC CCGCCCTCTT GACAGCACTG AGGAGCCGGG GCTCTGCCTG 840
CAGTCTGAG CCAAGGGGCC CCTCGATTCC TCTTCCAGGA GCTCCAGGAA GCAGGCAGGC 900
50 CTTGTCTGTA GACAGTGTCC TCAGGTGCGA GAGCAGAGGA GACCCAGGCA GTGTGAGCAG 960
TGAAGGTGAA GTGTCTACCC TGAATGTGCA CCAAGGGGCC CACCTGCCCC AGCACACATG 1020
GGACCCATA GCACCTGGCC CCATTCCCC TACTGTCACT CATAGAGCCT TGATCTCTGC 1080
AGGCTAGCTG CAGCTGAGT GGGCCTGATG GGTGCAAGG AACCCACAGG CGAGGAGGAG 1140
55 ACCAGGAGGA CAGGAGCCCC AAGAGGCCCC AGAGCAGCAC TGACGAAGAC CTGTAAGTCA 1200
GCCTTTGTTA GAACCTCCAA GGTTCGGTTC TCAGCTGAAG TCTCTACAC ACTCCCTCTC 1260
TCCCAGGCC TGTGGGTCTC CATCGCCAG CTTCTGCCCA CGTCTCTGTC TGCTGCCCTG 1320
ACCAAGTCA TCATGTCTCT CGAGCAGAGG AGTCCGCACT GCAAGCCTGA TGAAGACCTT 1380
GAAGCCCAAG GAGAGGACTT GGGCCTGATG GGTGCAAGG AACCCACAGG CGAGGAGGAG 1440
60 GAGACTACCT CCTCTCTGTA CAGCAAGGAG GAGGAGGTGT CTGCTGCTGG GTCATCAAGT 1500
CCTCCCCAG GTCTCTAGG AGGCGCTTCC TCCTCCATTT CCGTCTACTA CACTTTATGG 1560
AGCCAAATCG ATGAGGGCTC CAGCAGTCAA GAAGAGGAAG AGCCAAGCTC CTCGGTCCAG 1620
CCAGCTCAGC TGGAGTTCAT GTTCCAAGAA GCACTGAAAT TGAAGGTGGC TGAGTTGGTT 1680
CATTTCCCTG TCCACAAATA TCGAGTCAAG GAGCCGTTCA CAAAGGCAGA AATGCTGGAG 1740
65 AGCGTCATCA AAAATTACAA GCGCTACTTT CTTGTGATCT TCGGCAAGC CTCGAGTTC 1800
ATGCAGGTGA TCTTTGGCAC TGATGTGAAG GAGGTGGACC CCGCCGGCCA CTCCTACATC 1860
CTTGTCACTG CTCTTGCCCT CTCGTGCGAT AGCATGCTGG GTGATGGTCA TAGCATGCC 1920
AAGGCCGCCC TCCTGATCAT GTCTCTGGGT GTGATCCTAA CCAAGACAA CTGCGCCCT 1980
GAAGAGTTA TCTGGGAAGC GTTGAAGTGT ATGGGGTGT ATGTTGGGAA GGAGCACATG 2040
70 TTCTACGGGG AGCCAGGAA GCTGCTCACC CAAGATTGGG TGCAAGAAA CTACCTGGAG 2100
TACCGGCAGG TGCCCGGCG TGATCTGCG CACTACGAGT TCCTGTGGGG TTCCAAGGCC 2160
CACGCTGAAA CCAGCTATGA GAAGGTCATA AATTATTTGG TCATGCTCAA TGCAAGAGAG 2220
CCCATCTGCT ACCCATCCCT TTATGAAGAG GTTTTGGGAG AGGAGCAAGA GGGAGTCTGA 2280
GCACAGCCG CAGCCGGGAG CAAAGTTGT GGGGTGAGG CCCATCCAG CAGCTGCCCT 2340
75 GCCCATGTG ACATGAGGCC CATTCCTGCG TCTGTGTTTG AAGAGGCAA TCAGTGTCT 2400
CAGTGGCAGT GGGTGAAGT GAGCACACTG TATGTCATCT CTGGGTCTCT TGTCTATTGG 2460
GTGATTTGGA GTTATATCCT TGCTCCCTTT TGAATTTGT CAAATGTTCT TTTAATGGTC 2520
AGTTTAATGA ACTTCACCAT CGAAGTTAAT GAATGACAGT AGTCACACAT ATGTCTGTTT 2580
ATGTTATTTA GGATGAAGT TCTTGCTTTT GAGTCACATG GGGAAATCCC TGTATTATTG 2640
TGAATTGGGA CAAGATAACA TAGCAGAGGA ATTAATAATT TTTTGAAC TTGAACCTTAG 2700
80 CAGCAAAATA GAGCTCATAA AGAATAGTG AAATGAAAT GTAGTTAATT CTGCCTTAT 2760
ACCTCTTTCT CTCTCTGTA AAATTAAAC ATATACATGT ATACCTGGAT TTGCTTGGCT 2820
TCTTTGAGCA TGTAAAGAA ATAAAAATTG AAAGAATAAT TTTTCTGTT CACTGGCTCA 2880
TTTTTCTTC AGACACGCAC TGAACATCTG TTATTCGGAA CACCTGGGT T

85

Seq ID NO: 162 Protein sequence:
Protein Accession #: AAA68877.1

1 11 21 31 41 51
 5 MSLEQRSPHC KPDEDLEAQQ EDLGLMGAQE PTGEEEEETS SSDSKEEVS AAGSSSPFQS 60
 POGGASSSIS VYVTLWSQFD EGSSSQESEE PSSSVDPQAL EFMFQALKL KVAELVHFL 120
 HKYRVKEPVT KAEMLESVIK NYKRYFPVIF GKSEFMQVI FGDVKEVDF AGHSYILVTA 180
 LGLSCDSMLG DGHSMKPAAL LIIVLGVILT KDNCAPEEVI WEALSVMGVY VGKEHMFYGE 240
 PRKLLTDQWV QENYLEYRQV PGSDPAHYEF LWGSKAHAET SYEKVINYL V MLNAREPICY 300
 PSLYEEVLGE EQBQV

Seq ID NO: 163 DNA sequence
 Nucleic Acid Accession #: AF292100
 Coding sequence: 30-809

1 11 21 31 41 51
 15 GGGGGGGGAG AGGCCTGGAG GACACCAACA TGAACAAGTT GAAATCATCG CAGAAGGATA 60
 AAGTTCGTC A GTTTATGATC TTCACACAAAT CTAGTGAAAA AACAGCAGTA AGTTGTCTTT 120
 20 CTCAAAAATGA CTGGAAGTTA GATGTTGCAA CAGATAATTT TTTCCAAAAT CCTGAACTTT 180
 ATATACGAGA GAGTGTAAAA GGATCATTGG ACAGGAAGAA GTTAGAACAG CTGTACATA 240
 GATACAAAGA CCTCAAGAT GAGAATAAAA TTGGAATAGA TGGCATACAG CAGTTCTGTG 300
 ATGACCTGGC ACTCGATCCA GCCAGCATT A GTGTGTTGAT TATTGCGTGG AAGTTCAGAG 360
 CAGCAACACA GTGCGAGTTC TCCAAACAGG AGTTTCATGGA TGGCATGACA GAATTAGGAT 420
 25 GTGACAGCAT AGAACCACTA AAGGCCAGTA TACCCAAGAT GGAACAAGAA TTGAAAGAAC 480
 CAGGACGAT TAAGGATTTT TACCAGTTTA CTTTAAATTT TGCAAGAAT CCAGGACAAA 540
 AAGGATTAGA TCTAGAAATG GCCATTGCCT ACTGGAACCT AGTGCTTAAT GGAAGATTTA 600
 AATTCTTAGA CTTATGGAAT AAATTTTGTG TGGAAACATCA TAAACGATCA ATACCAAAAG 660
 ACATTGGA A TCTTCTTTTA GACTTCAGTA CGATGATTGC AGATGACATG TCTAATTATG 720
 30 ATGAAGAAG AGGATCGGCT GTTCTTATTG ATGACTTTGT GGAATTGCA CGCCCTCAA 780
 TTGCTGGGAC AAAAAGTACA ACAGTGTAGC ACTAAAGGAA CCTTTTAGAA TGTACATAGT 840
 CTGTACAATA AATACAACAG AAAATTGCAC AGTCAATTC TGCTGGCTGG ACTGAACTGA 900
 AGATCAATCC TCACAATTC A GACTGAGGTG TGAGACAAA CTTTAAGGAT ACATCTTGA 960
 CCATATCGTA TTTTCATCTT CTAATGGTGG TTTGGGCTTG TCTTCTAGTC TGGGCGCTC 1020
 35 TAAACATTTA ATTTGGAAT TCACTTTATA TCTGTGGACC ATCCTAGTTT 1080
 ATTCCTCCAT AAGTCTTAGA AGCTTTATGG TGATTATTT GAGGTTTCA TTCTCGCATA 1140
 AAGCACAATG CTGTCTTCAT CAGAAAACAG TTGGCATAAG AATTAAACAT ATGAACATCA 1200
 CAAAACAATT TATAAAACT TCTTAAATAT ACGCTTTGGG CTAGTTGCAA AGACTATGCT 1260
 AATAGCACTT CCAGTGAGAG TGATATATTT AAGTGTACTG GATCTGGAAT GGTGTTTGG 1320
 40 TTTGGGGGGA ATTTTTTTT TTTCTGGCA AATCACATAT GTTGTGATG TGAGTATCTG 1380
 ATGAAAAAAC AATGTGAGAA TAACCGACAT GAAAATTTT TAGGATAACT TGGTGCCTAC 1440
 CTGAAAAATG TATTGTGTTT TAGACTCTTG ATTTCAAAAG GTTCCACAGA ACTAGTCTCG 1500
 GCTTACCTTA CCCATGTTTA TATATAGCTG TCCTACAGGG AGCTTTTATT TAGAAAAATG 1560
 CTGCATAATG TTAGATTCTT CTCCTGTCTA CATTATGCAC TACATAATTG GACTTCATTA 1620
 45 TGCTTTTGA AATCTTATCT GCCTGTCA TAAGTTAAAC TATTTAATTT GTTTTGAATG 1680
 TTTTGGATTG CTACACAATA CAATATTCTA AATTTAGGCA TGAGGGTTT TTTGTTTAT 1740
 TTTTACTTTT TTTTGTGCT TGCATATGG AACACAATG AAATCTCTT AATTATAAG 1800
 AAGATAGTAG GAGTTAAATT TTGAAATGG TTGTGATGAG CCACGAAAT CAATCTTAT 1860
 AATATAGGTA CTGCTCTTTC AGACAAACAG TCCATTTTTA ATGACTTCTT ATTTGTGTA 1920
 50 AATTACTTTA ACTGTCTAATC ACTGTGGTTG CCAAAATTTT ACTTCAGAA CAAAGATTTT 1980
 CAAACAAGCA TACACGATGC AAAATACCA G TCTGGCTTCT AGTCTATTTA CTGTTTGTG 2040
 TCACCTAGAT TAGCTCAGT TTCTCATCAA AGCAGAAATG TATCTTGCCT GTGTGTGTGT 2100
 GTGTGTGTGT GTGTGTGTGT GTATGTGTGT ATATATATAT ATATATATAT ATATATATTT 2160
 TTTTCTTATG TTTTCTTAA ATTACAAAG CCATGAGCTG CTTTATGCT GAAAATGGTC 2220
 55 ATTTCCCTGT TCACCTACTG ACATGTGAAG AAGGGTTTCT TGCTTCTTA AACATTTCCG 2280
 TAAGGCAGCG TAGAAATGTA ATACTTCAA TGTTTGATGA TTAGTGTCTT TTGATAGGAA 2340
 TAGATTCTGC TGTCTTCAATA TATCCAGGCA CTCTCAAGG TCTAGGTTG ATATTAACAA 2400
 AGGAATGTAC TTAGAATAGC AGTACATTT ATGCAAAAT GGAATATAT TTAAGAAACA 2460
 ATGACATATC AAAACTGCTT TTTACATGAT TTTGAAATAG ACTAGAAAGC TTTCCCTATA 2520
 60 GACATATTAA TATTCCAATC ATAACTTTAA TTCAAGAAAT CAGTTTACC AAAAGAAAA 2580
 TTTGAAATTT TCTATTCAAG CTACTGGAAT TGGTTATTAA AAGAAAAAGG AAAAAGAA 2640
 ATCTTGCTGC TTTCTGATT TTTGTAATA TAAAGAGGAA CTTCAATTAT 2700
 GAAAAATTTT TAAAGATAT ATATATCTAT ATATCTATAT ATATGACTG TTTTGTTC 2760
 65 TGCTTGAAG ATTTTGAGTT ATGGTTATTG GTTTCAGATT GATTAATTCA CATATGCTGT 2820
 GTTTCTTTA AAAGTCATAT GGGTTCGTGG CCTAATGCCT TGGATTTTAC ATATTTTCT 2880
 TTTTAAATGC AAAACCTTTT CAACAAAATA GTGTTTGTCA TCAGGTTGGT ACTAAACATT 2940
 TATAATTACT GTGTAATTAT AAACAAAAT ACATAAAGCT TTGAATATAA TTATGTAGCA 3000
 TAAAGTTAA GGTGTTTAC TATGATGGCA TCTTAGAATT AAACAAAAT TTTACTAGGG 3060
 70 CTGAAAAGAG AAGACTGATT TAATGTGGTG TGATTATTCT GAAGATAAAT GTCTGGCTAC 3120
 AGGGAATATT TTGTAATAA AAATGATTAC ACATATGGCT GTGTGTGTTT GAGTCTGTGT 3180
 CTGTGAGAGA GCCAGAGAGA GTGAGAGAGA TTGACAGAGA AAGGGAGAGA CACACACAG 3240
 CCCCTTGAAT TGTCTTAACT CCTAAGTGTG TCAGTCTCTA TTCCGGTAAA CTCCCATGC 3300
 TGATTCTTGT TTTTAACTG AACCATAGGT ACAGTTTCTT TTTTGCCTAA TGTCAAACA 3360
 75 GGTACAAAT TTAAGATGTA ATGCTTTTAA AATAGAAAAA TGTATAAAAT TAGAAGTGCC 3420
 CACATATAAA AAATACTTGA GATGAAGATT ATCTTTAGTG AATATCATCT GCATATCTCT 3480
 GTAAGTTCAA TTGTGTTTCT TACAGTCCCT GTCATATTAC CAACAGAGGC AATAAAAGCT 3540
 GCAGTGAAT TG

Seq ID NO: 164 Protein sequence:
 Protein Accession #: AAG00606

1 11 21 31 41 51
 80 MNKLLKSSQKD KVRQFMIFTQ SSEKTAVSCL SQNDWKLDVA TDNFFQNPFL YIRESVKGSL 60
 DRKKLEQLYN RYKDPQDENK IGIDGIQQFC DDLALDPASI SVLLIAWKFR AATQCEFSKQ 120
 85 EFMDDGMEELG CDSIEQLKQ IKPMEQELKE PGRFKDFYQF TFNFAKNPGQ KGLDLEMAIA 180
 YWNLVLNGRF KFLDLWNKFL LEHKKRSIPK DTWNLLDFFS TMIADDMSNY DEEGAWPVLI 240
 DDFVEFARPO IAGTKSTTV

Seq ID NO: 165 DNA sequence
Nucleic Acid Accession #: AF256215
Coding sequence: 220-2028

5	1	11	21	31	41	51	
	CTCCAGTCCG	CATGCTCAGT	AGCTGCTGCC	GGCCGGGCTG	CGGGGCGGCG	TCCGCTGCCG	60
10	GCCACGCGGC	TGCGGTGGCG	GCCGCCGCGG	CACCCGGCAG	GGCCCGCCAG	TCCCCGCTTC	120
	CCTGTCTCCAG	AGCCGCGCGC	TGGGCCGCGG	CAGGGCGGGC	CCGGGGCTCC	TCCATGCTGC	180
	CAGCCGCGCG	GCTGCGGAGC	CGACCAAGTG	GCTCCTGCGA	TGGCGGCGGA	AGAGGAGGCT	240
	GCGGCGGGAG	GTAAGTGTT	GAGAGAGGAG	AACCAAGTCA	TGCTCCTGT	GGTTTCCAGC	300
	CGCGTGAGTC	CAGGGACAAG	ACCAACAGCT	ATCGGGTCTT	TCAGCTCACA	CATGACAGAG	360
15	TTTCCACGAA	AACGCAAAAG	AAGTGATTCA	GACCCATCCC	AAGTGGGAAG	TGGTGAACAC	420
	CAAGTTAAAA	TGAAGGCCTT	CAGAGAAGCT	CATAGCCAAA	CTGAAAAGCG	GAGGAGAGAT	480
	AAAATGAATT	ACCTGATTGA	AGAACTGTCT	GCAATGATCC	CTCAGTGCAA	CCCCATGGCG	540
	CGTAAACTGG	ACAACTTAC	AGTTTTAAGA	ATGGCTGTTC	AACACTTGAG	ATCTTTAAAA	600
	GGCTTGACAA	ATTCTTATGT	GGGAAGTAAT	TATAGACCAT	CATTCTTCA	GGATAATGAG	660
20	CTCAGACATT	TAATCCTTAA	GACTGCAGAA	GGCTTCTTAT	TGTGGTGG	ATGTGAAGA	720
	GGAAAAATTC	TCTTGGTTTC	TAAGTCAGTC	TCCAAAATAC	TTAATTATGA	TCAGGCTAGT	780
	TGACTGGAC	AAAGTCTTAA	TGACTTCTTA	CATCCAAAAG	ATGTTGCCAA	AGTAAAGGAA	840
	CAACTTTCTT	CTTTTGATAT	TTCAACCAAG	GAAAAGCTAA	TAGATGCCAA	AACCTGGTTG	900
	CAAGTTTACA	GTAATCTCCA	CGCTGGAAGG	ACACGTGTGT	ATTCTGGCTC	AAGACGATCT	960
25	TTTTTCTGTC	GGATAAAGAG	TTGTAAAATC	TCTGTCAAAG	AAGAGCATGG	ATGCTTACCC	1020
	AACCTCAAGA	AGAAAAGACA	CAGAAAATTC	TATACATATC	ATTGCATGG	TTACTTGAGA	1080
	AGCTGGCCTC	AAAGTATTGT	TGGAATGGAA	GAAGAAAGGA	ACAGTAAGAA	AGACAACAGT	1140
	AATTTTACCT	GCCTTGTGGC	CATTGGAAGA	TTACAGCCAT	ATATTGTTC	ACAGAACAGT	1200
	GGAGAGATTA	ATGTGAACCC	AACCTGAATT	ATAACCCGGT	TTGCAGTGAA	TGGAAAATTT	1260
30	GTCTATGTAG	ATCAAAGGGC	AACAGCGATT	TTAGGATATC	TGCCTCAGGA	ACTTTTGGGA	1320
	ACTTCTTGTT	ATGAATATTT	TCATCAAGAT	GACCAACAATA	ATTTGACTGA	CAAGCACAAA	1380
	GCAGTTCTAC	AGAGTAAAGG	GAATAACTCT	ACAGATTCCCT	ACAAATTTCAG	AGCAAAAGAT	1440
	GGCTCTTTTG	TAACTTTAAA	AAGCCAATGG	TTTAGTTTCA	CAAACTCCTG	GACAAAAGAA	1500
	CTGGAATATA	TGTATCTGT	CAACACTTTA	GTTTGGGAC	ATAGTGAGCC	TGGAGAAGCA	1560
35	TCATTTTAC	CTTGTAGCTC	TCAATCATCA	GAAGAATCCT	CTAGACAGTC	CTGTATGAGT	1620
	GTACCTGGAA	TGCTACTTGG	AACAGTACTT	GGTGCTGGTA	GTATTGGAAC	AGATATTGCA	1680
	AATGAAATTC	TGGATTTTCA	GAGGTTACAG	TCTTCTTCAT	ACCTTGATGA	TTGAGTCCA	1740
	ACAGGTTTAA	TGAAAGATAT	TCATACTGTA	AACCTGCAGG	GTATGTCAA	TAAGGAGTTG	1800
40	TTTCCACCAA	GTCTTCTGTA	AATGGGGGAG	CTAGAGGCTA	CCAGGCAAAA	CCAGAGTACT	1860
	GTGTGCTGCC	ACAGCCATGA	GCCACTCTCT	AGTGATGGTG	CACAGTTGGA	TTTCGATGCC	1920
	CTATGTGACA	ATGATGACAC	AGCCATGGCT	GCAATTTATGA	ATTACTTAGA	AGCAGAGGGG	1980
	GGCCTGGGAG	ACCCTGGGGA	CTTCAGTGAC	ATCCAGTGGA	CCCTCTAGCC	TTTGATTTTT	2040
	AACCTCAAAA	ATGAGAAACA	TTTTAAAGCA	TTATTTACGA	AAAAACTGTC	TCAACTATTC	2100
	TTAAGTACTG	TATTGATATT	TTTGTATCT	TTTATTAATG	TTCTACCACT	TTTTATAGAT	2160
45	TTGCATCTTC	CTGTACAGG	GATGTGGGGA	AATACGTTTT	CCTCCCAAGA	GAACCAAGTT	2220
	TATTATAGAC	TCCTTTATTC	AGTGAATATG	CTTATAATCC	ACTAGTTGCC	ATATTTTTGC	2280
	TAAAAATATT	CTAAGCAAGA	ATACTACTTA	CATATTGTTT	TGGCTTTGTT	TTATTTTTGA	2340
	TGCAGTTTTT	TTAGTTGAG	GTAATGTAAT	ATATTGATGT	TTTCTTTGTT	GTCTAAGATT	2400
	GATTTATAAT	AGTAGGTTTG	TATAATTTGG	AACATTTTCC	ATGCTTTGCG	AATTTCTCTA	2460
50	ATTGAGGATA	GGGCTTACAC	ACTTTAAGAA	AACAGTGAGT	ACTTGAACAT	TTAAAGGGAC	2520
	AGTGCAATTT	ATAGTCATA	TCACATTGAA	TACTGTATTT	GATCTTTTGA	GACTTAGGCA	2580
	GGACAGAGC	TGGATATTTT	ATGCTCAGTT	GAGCACTTTA	AGATGAATTT	TAAGTGAGAT	2640
	GATTTCTTGC	TAAAACCTCA	GAAAGTCAAA	AGAGTTTCAG	CTTTCCTTAC	AGAAAAGGAA	2700
	GGATCTTGGG	CCCTAGATCT	TGGGGATTAA	CCTCTGCATA	TAAGATTATC	TCTTAATAGG	2760
	CCAGAGGTGG	TGCTCACGCC	TGTAATCCCA	GTACTTTGGG	AGGCTGAGAC	GGGCAGATCA	2820
55	CTTGAGGTCA	GGAGTTCAA	ACCAGCCTGG	CCAATATGGT	GAAACCCCGT	TTCTACTAAA	2880
	AATACAAAAA	AAATTACCCA	GGCACTCACT	CTTGAGGTAA	CTAACCAACT	CCCACGATAA	2940
	TGACAGTCCA	TCATGAGCG	CAAAGGCCTC	ATGACCTAAT	GGCACACACC	TGTAATCCCA	3000
	ACTGCTTGGG	AGGCTTGAGC	GAGAGGATTG	CTTGAACTTG	GGAGGCAGAG	GTGTCAGTGA	3060
	CGCGAGATCG	CACCACTGCA	CTCCAGTCTG	GGCAACAGAG	TGAGACTTCA	TCTCAAAAAA	3120
60	AGTAAAAAAA	AAGATTTAAT	ATAATCACTG	AAGATCTCTA	TTATAGATAG	ATTAGGTTTT	3180
	TGACATTGGA	AACATACTTA	GGGATAGATT	TGTCCTAAAG	GAAAAAAGTA	GGCCCGGCA	3240
	GATTAATATG	CTTGTGTAAA	GTACACACAT	AAATTCACTG	ACACATTAAA	TTCATAGAGT	3300
	TTTAAATGTT	TAATGTATAT	AAACCAAGTT	CTTTATACAC	ATTTGGGAAA	ACATTGGTCT	3360
	CACAGATTAA	ATGATTAACT	AACGTACCCA	GGAACTAGTT	GTAGCTTTCT	AAGTAATTAG	3420
65	GCAATTACAG	TTATTGCCGT	TAACCAAAGG	TAATAAAACA	AAATGACAAG	TACATGTTTA	3480
	AAATTATGAG	GCAATGAGAA	ATAATTTAAA	AACCAATTTT	CTAGTTATAA	TTTAAATTTT	3540
	GGAGAGCATT	TTTACAGTA	ATTAATCCAG	AGGTGGCTCA	AATTGAGTAT	AAGAAATTAAG	3600
	ATTATTAAAA	ATACTGCATG	TCTACCTTCT	CGGGGATCAT	ACTTTATAAC	ACTTTCTGCT	3660
70	TCAGTAGCTC	TTCTAGCTTT	GCCAAAGTAT	CTCCCATATT	TTCTCTCTCG	TGCTTCGCAA	3720
	ATGAAAGTCA	GATAGGCTGG	GAACCTCATG	GGCAGCCCTC	AGACTTCAAT	GTGGGCTTCA	3780
	AATCCAGTTT	CCTGTTCTAT	ATGGTGCTAC	ATCTTTCCAG	AAAATTTCCC	TCAGAGCCCC	3840
	TCGCCAAAAA	AAAGCATTAT	TTTGACCTTG	CATGCTATTT	CTTTAGCTGT	AGGTGATAGA	3900
	TTAGAACTTC	TGTCAGACAT	GTTAATGACA	AACATACCAA	CAGACAATAA	CCAAAGCAAA	3960
	TGTTTCTTTC	AAGTGTGAAA	TGTGCAGGGG	CTCGTGGGCA	AGGATGTATT	GGCAGACTGT	4020
75	CCTCTTGAAC	TGATAGTGTC	CCAGCAATGT	TGGAGGTTGG	CACCAATCCT	GGTCCGACAC	4080
	TTGAGGACCT	GAGAGACATC	AGGTTTAGAA	TGAGCCAAAG	AAATCCTACA	AGATGGGGAG	4140
	AATTGGTGTG	CAGCAGCCTA	AGTGTATAG	TTAAGTCTAA	AGAAGTATGA	AAGATCCCCC	4200
	GTGTTCTCTA	AATTGAGCAG	AGGGGCTGCT	CTACCAATAT	CATTTTATGA	GGGACTGAAC	4260
	CATTGCAAGT	TAGACTTGGC	TTCCAAAGAG	TCTGCTTAAG	CCAGGGGTGG	CAGGGTAGGC	4320
80	CATCATAGCT	GGATGGCTCT	AAAGCAGAT	GGGGGCAGAC	TTGCCCTCGT	GATGCCAGGA	4380
	TTTGAGAGGC	AGAGTTTCTA	GAGGGAGACC	AGTGCTGCCT	CTCAGCTGG	CAGTTTCTTC	4440
	CTTTTGCAAG	AGGAGGGGCT	GTTCAATTCC	ATAGACCACT	GGGCAGATAG	CCAGTTGAAT	4500
	ACTCTGTGCA	TGTTTGTATC	CTTTTATAGT	TCGCTCTAAT	ATTTTCTGCT	AGATCCTTTT	4560
	GTCTGTGAGT	CAAAATCTAA	TCCATGCATT	GTATGATACC	GTAGCTCTCC	TAAGGTTTGT	4620
85	GTTTCTCTCA	AAATGTTTAA	GTTTCTTCA	ACTAAATTTG	ATTTTGTGCT	TTAGAAAGTG	4680
	CATATTTTAA	TGGTATACAC	TATGTTCTCT	TTTTCTACTG	CGAGTCAATT	TTTTGAATTT	4740
	TCGTGAGAAA	GAATATATCT	ACAAATTGCA	CGAAAGTATC	ATAAAACAG	TACTCTAGAG	4800

CAGCGCTGTC CAATAGAAAT ATAATCTGAG CCACATGTAT AATTTTATTT TCTTCTAGCC 4860
 ACATTAAAGA AGTAAAAAGA TACAAGTAGA ACTAATTTTA ATGTTTAAAT TCAGTATATC 4920
 CAAAATATCA TTTGAACATG TAATTAATAT AAAATTATTA ATGTGATATT TTACATTCTT 4980
 TTGGTAATAC TAGTCTTCAA AATCTGGTAT GTATCTTACA TTGATAGCAC ATCTCACTTT 5040
 GTACTAGCCA CATGTCAAGT GCTCAGTAGC CACATGTGGC TAGTGGCTAC TGCCTGGAC 5100
 AGCACAGTTC TAGGTTCCAC CCTAACACCC AAGTCTCTGT GATTAGAATC CCAGATCAG 5160
 AGCTGGAAGT AAACATAGAG ATCAAACCTC CTTTTAAAAA TGAGGACGCT GAGGCACAGA 5220
 GTTTAAATGG CTTCATAGAG GTCATACAGC TAAATTCAGC CTCAACAGGG TCTTCTGATT 5280
 CCAGGCACCT TGTCCACTCC ACTACATTAC TGTAGTGGTA ATTCTTAGGG TTAATAAAG 5340
 TGTAGAGTAG GCCGGGCGCA GTGGCTCATG CCTGTAATCC CAGCACTTGG GGAGGCCGAA 5400
 GTGGGCGGAT CACGAGGTCA GGAGATCGAG ACCATCCTGG CCAACATGGT GAAACCCCGT 5460
 CTCTACTGAA AATACAAAGC AAAATTAGCC AGGTGTGGTG GCGGGCGCCT GTGGTCCCAG 5520
 CTGCTCTGGA GGCTGAGGCA GAATGGCGTG AACCAGGAG GCAGAGATGC CAGTGAGCCA 5580
 AGATCGCGCC AGTCGACCCC AGCCTGGGCG ACAGAGCGAG ACTCCATCTC AAAAAAAG 5640
 AAAAAAAGAA AAGAAAAGAA AAGAAAAGTC TAGAGAACAT TATATTAAAT GGTATTATT 5700
 GAAGTAGACC AAGTTTATA CCATAAGGAT ATTTTCTCTT AAATACCATG TTTGAAGAAC 5760
 AATTATTATAT TGATCCTTGA ATCTGTAAGA TCAATAACA AGTCTCTATC CATGTTACCA 5820
 AATTAAACCT TTTGAAAATA ATAACTTTTA AAATATCAGA TGTGTTATTA CAGGATGATA 5880
 CTTGGAATCA AGTGAATGA GTTATATGGT CATCTACTAA TTTAGAAATC TATTGTGAAA 5940
 CAAAGACAAA CAGGAAGTCA CAGAATAGAG ACTTTTAGTA AATAAATGGA ATTTAAAGA 6000
 AAGTGTTTAT TTACAGTGTG ACACAGAAA AGGATGTCTT TGTGTGATA GTCTTTGAGG 6060
 GATCTCCGTA AAATCTGGGG CACAGGTACA AGAAATAGCC AATATTAGT TCCAGACCA 6120
 TGTTTAGTAG TGTCAGTTT CAGATCATGC TGCCAGAGG TATCTCCCC TCAGGTGGGT 6180
 CATCTAGTAG CCCTGGAATT GGAGACTCAT ACTTGCCAG CACAATGTTA CGGGCAGACA 6240
 GGCCGACATC TATGATTAGC TAGAAGCCAT AAGAAAAGC TGCTAAGTGG CCACTAGGTG 6300
 CCACITTTCT GTTTTGTGAT TGTCTTCATT AGCAGATCTT TTTTTCCTCA GCTCCATGGG 6360
 GCCTATGAGA GGCATTATG ATTTTGTGTC CTACAATAAG TCAGCCTGTC TGGTGTGAGT 6420
 TGTTTATGTA GAAATGCTTT CCAAGGAGG TCTAGGAAGA TCCTGACACA TAAGAACTTT 6480
 GGCTTAGAGA GCTTTCCAGG GTAGTGCCA ATAAAACTG ACCTGGAAAG AAAACCTGCC 6540
 CAGCACGGA CATGCTTTCT GAACTCACTT GAGAGTGAT GGTGTATGTC ACTTCTCATA 6600
 TATTCTTGAG TTTAGATTGT TCTTTTATAC AATTTTATAG TCTTTTCCAG TTCCTTGTG 6660
 CTCGTCTGTA TATTGTGATT TTTAAATTTT TGTGGTAAAT AATGAAAAGA GTGAAATTAT 6720
 ATTTTATAAT TACTCATTTG TAGTTTTTT TTTTAAATTA ATAACTTCC TCCAAAAAGT 6780
 GCTCCCTTAA AA

Seq ID NO: 166 Protein sequence:
 Protein Accession #: AAG34652

1 11 21 31 41 51
 MAEEBAAAAG GKVLREENQC IAPVVSSRVS PGTRPTAMGS FSSHMTFFPR KRKGSDDSPS 60
 QVEDGEHQVK MKAPREAHQK TEKRRRDKMN NLIEELSAMI PQCNPMARKL DKLTVLRMAV 120
 QHLRSLKGLT NSYVGSNYRP SFLQDNELRH LILKTAEGFL FVVGCEPGRKI LFVSKSVSKI 180
 LNYDQASLFG QSLDFLHPK DVAKVKEQLS SFDISPREKL IDAKTGLQVH SNLHAGTRTV 240
 YSGRRSFFTC RIKSKCIKVK EEHGCLENSK KKEHRKFYTI HCTGYLRSWP PNIVGMEER 300
 NSKKDMSNPT CLVATGRLOP YIVPQNSGEI NVKPTFEITR FAVNGKPYVY DQRATAILGY 360
 LPQELGTS YEPHQDDHN NLTDKHKAVL QSKEKILTDS YKFRKDGSGF VTLKSQWFSF 420
 TNFWTKLEY IVSVNTLVLG HSEFGEASFL PCSQSSEES SRQSCMSVPG MSTGTVLGAG 480
 STGTDIANEI LDQLRLQSS YLDDSSPTGL MKDTHTVNCR SMSNKLFPFP SPSEMGELEA 540
 TRQNQSTVAV HSHBELLSDG AQLDFDALCD NDDTAMAAFM NYLEAEGGLG DFGDFSDIQW 600
 TL

Seq ID NO: 167 DNA sequence
 Nucleic Acid Accession #: NM_014400
 Coding sequence: 86-1126

1 11 21 31 41 51
 60 GGTACTCAT CCTGGGCTCA GGTAAGAGGG CCCGAGCTCG GAGGCGGCAC ACCCAGGGGG 60
 GACGCCAAGG GAGCAGGACG GAGCCATGGA CCCGCCAGG AAAGCAGGTG CCCAGGCCAT 120
 GATCTGGACT GCAGGCTGGC TGTGCTGCT GCTGCTTCGC GGAGGAGCGC AGGCCCTGGA 180
 GTGCTACAGC TGCGTGACAG AAGCAGATGA CGGATGCTCC CCGAACAAAG TGAAGACAGT 240
 GAAAGTCGCG CCGGGCGTGG ACGTCTGCAC CGAGGCGGTG GGGGCGGTGG AGACCATCCA 300
 65 CGGACAATTC TCGCTGGCAG TGCSSGGTGG CGGTTCGGGA CTCGCCGGA AGAATGACCG 360
 CGGCCCTGGAT CTTACGCGGC TCTGCGCTT CATCCAGCTG CAGCAATGCG CTCAGGATCG 420
 CTGCAACGCC AAGCTCAACC TCACCTCGCG GCGCTCGAC CCGGCAGGTA ATGAGAGTGC 480
 ATACCCGCCC AACGCGTGG AGTGCTACAG CTGTGTGGGC CTGAGCCGGG AGGCGTGCCA 540
 GGGTACATCG CCGCGGTGCG TGAGCTGCTA CAACGCCAGC GATCATGTCT ACAAGGGCTG 600
 70 CTTCGACGCG AACGTCACTT TGACGGCAGC TAATGTGACT GTGTCTTTCG CTGTCCGGGG 660
 CTGTGTCCAG GATGAATTTT GCACCTCGGA TGGAGTAACA GGCCAGGGT TCACGCTCAG 720
 TGGCTCCTGT TGCCAGGGGT CCGCTGTAA CTCTGACCTC CGCAACAAGA CCTACTTCTC 780
 CCTCTGAATC CCACCCCTTG TCCGGCTGCC CCTCCAGAG CCCACGACTG TGGCCTCAAC 840
 75 CACATCTGTC ACCACTTCTA CTTGGGCCCC AGTGAGACCC ACATCCACCA CCAAAACCAT 900
 GCCAGCGCCA ACCAGTCAGA CTCGAGACCA GGGAGTAGAA CACGAGGCT CCGGGATGA 960
 GGAGCCGAGG TTGACTGGAG GCGCCGCTGG CCACCAGGAC CGCAGCAATT CAGGGCAGTA 1020
 TCCTGCAAAA GGGGGGCCCC AGCAGCCCCA TAATAAAGGC TGTGTGGCTC CCACAGCTGG 1080
 ATTGGCAGCC CTCTGTGTGG CCGTGGCTGC TGGTGTCTTA CTGTGAGCTT CTCACCTGG 1140
 AAATTTCCCT CTCACCTACT TCTCTGGCCC TGGGTACCCC TCTTCTCATC ACTTCTCTGT 1200
 80 CCCACCACCT GACTGGGCTG GCCAGCCCC TGTTTTCCA ACATTCCCCA GTATCCCCAG 1260
 CTTCTGTGCG GCTGGTTTGC GGCCTTGGGA AATAAAATAC CGTGTATAT ATTCTGGCAG 1320
 GGGTGTCTGA GCTTTTGTAG GACAGCTCCT GTATCCTTCT CATCTTGTG TCTCCGCTTG 1380
 TCCTCTTGTG ATGTTAGAGC AGAGTGAGAG AAGTCAGCTG TCACGGGGAA GGTGAGAGAG 1440
 AGGATGCTAA GCTTCTACT CACTTCTCC TAGCCAGCCT GGACTTTGGA GCGTGGGGTG 1500
 85 GGTGGGACAA TGGCTCCCCA CTTAAGCAC TGCTCTCCCT ACTCCCGCA TCTTTGGGGA 1560
 ATCGGTTCCC CATATGTCTT CCTTACTAGA CTGTGAGCTC CTCGAGGGCA GGGACCGTGC 1620
 CTTATGTCTG TGTGTATCA GTTCTGGCA CATAAATGCC TCAATAAAGA TTTAATTACT 1680

TTGTATAGTG AAAAAAA

Seq ID NO: 168 Protein sequence:
Protein Accession #: NP_055215

5
10
15

1	11	21	31	41	51	
MDPARKAGAQ	AMIWTAGWLL	LLLLRGGAQA	LECYSCVQKA	DDGCSPNKMK	TVKCAPGVVDV	60
CTEAVGAVET	IHQGFSLAVX	GCGSGLPGKN	DRGLDLHGLL	AFIQLQQCAQ	DRCNKLNLIT	120
SRALDPAGNE	SAYPPNGVEC	YSCVGLSREA	CQGTSPFVVS	CYNASDHVYK	GCFDGNVTIT	180
AANVTVSLPV	RGCVDDEFCT	RDGVTGPGFT	LSGSCCQGSR	CNSDLRNKTY	FSPRIPLVLR	240
LPPPEPTTVA	STTSVTTSTS	APVRPTSTTK	PMPAPTSTPT	RQGVHEEASR	DEEPRLTGGA	300
AGHQDRSNSG	QYPAKGGPQQ	PHNKGCVAPT	AGLAALLLAV	AAGVLL		

Seq ID NO: 169 DNA sequence
Nucleic Acid Accession #: NM_006875
Coding sequence: 186-1190

20
25
30
35
40
45
50
55

1	11	21	31	41	51	
GAATTCGGCA	CGAGCGCGCG	GCGAATCTCA	ACGCTGCGCC	GTCTGCGGGC	GCTTCGCGGC	60
CACCAAGTTC	TCTGCTTTCC	ACCTGCGGCG	CCCCAGCGCC	TGGCTCCCCA	GCTGCGCTGC	120
CCCGGGCGTC	CACGCCCTGC	GGGCTTAGCG	GGTTCACTGG	GCTCAATCTG	CGCAGCGCCA	180
CCTCCATGTT	GACCAAGCCT	CTACAGGGGC	CTCCGCGCGC	CCCCGGGACC	CCCACGCCGC	240
CGCCAGGAGG	CAAGGATCGG	GAAGCGTTCG	AGGCCGAGTA	TGCACTCGCG	CCCCTCCTGG	300
GTAAGGGGGG	CTTTGGCACG	GTCTTCGCAG	GACACCGCCT	CACAGATCGA	CTCCAGGTGG	360
CCATCAAAAT	GATCCCCCGG	AATCGTGTGC	TGGGCTGGTC	CCCCCTGTCA	GACTCAGTCA	420
CATGCCCACT	CGAAGTCGCA	CTGCTATGGA	AAGTGGGTGC	AGGTGGTGGG	CACCCCTGGG	480
TGATCCGCGT	GCTTGACTGG	TTTGAGACAC	AGGAAGGCTT	CATGCTGGTC	CTCGAGCGGC	540
CTTTGCCCGC	CCAGGATCTC	TTTGACTATA	TCACAGAGAA	GGGCCCACTG	GGTGAAGGCC	600
CAAGCCGCTG	CTTCTTTGGC	CAAGTAGTGG	CAGCCATCCA	GCACTGCCAT	TCCCGTGGAG	660
TTGTCCATCG	TGACATCAAG	GATGAGAAAC	TCCTGATAGA	CCTACGCCGT	GGCTGTGCCA	720
AACTCATGGA	TTTTGGTTCT	GGTGCCCTGC	TTTATGATGA	ACCCTACACT	GACTTTGATG	780
GGACAAGGGT	GTACAGCCCC	CCAGAGTGGG	TCTCTCGACA	CCAGTACCAT	GCACTCCCGG	840
CCACTGTCTG	GTCAGTGGGC	ATCCTCCTCT	ATGACATGGT	GTGTGGGGAC	ATTCCCTTTG	900
AGAGGGACCA	GAGGATTCCTG	GAAGCTGAGC	TCCACTTCCC	AGCCCATGTC	TCCCCAGACT	960
GCTGTGCCCT	AATCGCGCGG	TGCCCTGGCC	CCAAACCTTC	TTCCCGACCC	TCACTGGAAG	1020
AGATCCTGCT	GGACCCCTGG	ATGCAAAAC	CAGCCGAGGA	TGTTACCCCT	CAACCCCTCC	1080
AAAGGAGGCC	CTGCCCTTTT	GGCCTGGTCC	TTGCTACCCT	AAGCCTGGCC	TGGCCTGGCC	1140
TGCCCCCAAC	TGGTCAGAAG	AGCCATCCCA	TGGCCATGTC	ACAGGGATAG	ATGGACATTT	1200
GTTGACTTGG	TTTACAGGAT	CATTACCAAT	CATTAAAGTC	CAGTATTACT	AAGGTAAGGG	1260
ATTGAGGATC	AGGGGTTAGA	AGACATAAAC	CAAGTTTGCC	CAGTTCCTTT	CCCAATCCTA	1320
CAAGGAGGCC	TTCTCTCCAG	AACCTGTGGT	CCCTGATTTT	GGAGGGGGAA	CTTCTTGCTT	1380
CTCATTTTGC	TAAGGAAGTT	TATTTTGGTG	AAGTGTGTC	CATTTTGAGC	CCCGGGACTC	1440
TTATTTTGAT	GATGTGTGAC	CCCACATGG	CACCTCCTAC	TACCACCACA	CAAACCTTAGT	1500
TCATATGCTT	TACTTTGGGC	AAGGGTGCTT	TCCTTCCAAT	ACCCAGTAG	CTTTTATTTT	1560
AGTAAAGGGA	CCCTTTCCCC	TAGCCTAGGG	TCCTATATTG	GGTCAAGCTG	CTTACCTGCC	1620
TCAGCCCAAG	ATTTTATTAT	TTGGGGGAGG	TAATGCCCTG	TGTTTACCCC	AAGGCTTCTT	1680
TTTTTTTTTT	TTTTTTTTTG	GGTGAGGGGA	CCCTACTTTG	TTATCCCAAG	TGCTCTTATT	1740
CTGGTGAGAA	GAACCTTAAT	TCCATAATTT	GGGAAGGAAT	GGAGATGGA	CACCACCGGA	1800
CACCAACAGA	CAATAGGATG	GGATGGATGG	TTTTTTGGGG	GATGGGCTAG	GGGAAATAAG	1860
GCTTGCTGTT	TGTTTCTCTG	GGGCGCTCCC	TCCAATTTTG	CAGATTTTGG	CAACCTCCTC	1920
CTGAGCCGGG	ATTGTCCAAT	TACTAAATG	TAAATAATCA	CGTATTGTGG	GGAGGGGAGT	1980
TCCAAGTGTG	CCCTCCTTTT	TTTTCTTGCC	TGGATTATTT	AAAAAGCCAT	GTGTGGAAC	2040
CCACTATTTA	ATAAAGTAA	TAGAATCAGA	AAAAAATAAA	AAAAAATAAA		

Seq ID NO: 170 Protein sequence:
Protein Accession #: NP_006866

60
65
70

1	11	21	31	41	51	
MLTKPLQGP	APPGTPTPPP	GGKDREAFEA	EYRLGPLLKG	GGFGTVFAGH	RLTDLRLQVAI	60
KVIPRNRVLG	WSPLSDSVTC	PLEVALLWKV	GAGGGHPGVI	RLLDWPFETQ	GFMLVLERPL	120
PAQDLDPDIT	EKGPLGEGPS	RCFFGQVVAA	IQHCHSRGVV	HRDIKIDENIL	IDLRRGCAKL	180
IDFGSGALLH	DEPYTDFDGT	RVYSPPPEWIS	RHQYHALPAT	VWSLGILLYD	MVCGDIPFER	240
DQILEAEALH	FPAHVSPDCC	ALIRRCCLAPK	PSSRPSLEEI	LIDPWWQTPA	EDVTPQLQQR	300
RPCPFGLVLA	TLSLAWPLGA	PNGQKSHFMA	MSQG			

Seq ID NO: 171 DNA sequence
Nucleic Acid Accession #: NM_003646
Coding sequence: 89..2875

75
80
85

1	11	21	31	41	51	
GCGGCGCGGA	GCGGCGGTGC	TGAGCCCCCG	CCGCGGCGCC	GGCATGGGCG	TCTCCGCGCG	60
GCCTCCGCGC	GGCCGGGGCT	AGGGCCCGAT	GGAGCCGCGG	GACGGTAGCC	CCGAGGCGCG	120
GAGCAGCGAC	TCCAGTCTGG	CTTCGCGCTC	GTCCAGCGCG	TCCGAGCGCG	ACGCGGCTCC	180
CGAGCCGGAC	AAGGCGCGCG	GGCGACTCAA	CAAGCGGCGC	TTCCCGGGCG	TGCGGCTCTT	240
CGGCGACAGG	CAAGCCATCA	CCAAGTCGGG	CCTCCAGCAC	CTGGCCCCCG	CTCCGCGCAC	300
CCCTGGGGCC	CGGTGCAGCG	AGTCAGAGCG	GCAGATCCGG	AGTACAGTGG	ACTGGAGCGA	360
CTCAGCGACA	TATGGGGAGC	ACATCTGGTT	CGAGACCAAC	GTGTCCGGGG	ACTTCTGCTA	420
CGTTGGGGAG	CAGTACTGTG	TAGCCAGGAT	GCTGAAGTCA	GTGTCTCGAA	GAAAGTCGCG	480
AGCCTGCAAG	ATTGTGGTGC	ACAGCCCTCG	CATCGAGCAG	CTGGAGAAGA	TAAATTTCCG	540
CCGTAAAGCG	TCTTTCCTGT	AATCAGGCTC	CAGGAATGTC	CGCGAGCCAA	CCTTTGTACG	600
GCACCACTGG	GTACACAGAC	GACGCCAGGA	CGCAAGTGT	CGGCAGTGTG	GGAGGGGATT	660
CCAGCAGAAG	TTCACCTTCC	ACAGCAAGGA	GATTGTGGCC	ATCAGCTGCT	CGTGGTGCAA	720

	GCAGGCATAC	CACAGCAAGG	TGCTCTGCTT	CATGCTGACG	CAGATCGAGG	AGCCGTGCTC	780
	GCTGGGGGTC	CACGACGCGG	TGCTCATCCC	GCCACCTGGG	ATCCTCCGCG	CCCGGAGGCC	840
	CCAGAATACT	CTGAAGACAA	GCAAGAAGAA	GAAGAGGGCA	TCCTTCAAGA	GGAAGTCCAG	900
5	CAAGAAAGGG	CCTGAGGAGG	GCGGCTGGAG	ACCCCTTCATC	ATCAGGCCCA	CCCCCTCCCC	960
	GCTCATGAAG	CCCTGTCTGG	TGTTTGTGAA	CCCCAAGAGT	GGGGGCAACC	AGGGTGCAAA	1020
	GATCATCCAG	TCCTTCTCTT	GGTATCTCAA	TCCCGACAA	GTCTTCGACC	TGAGCCAGGG	1080
	AGGGCCCAAG	GAGGCGCTGG	AGATGTACCG	CAAAGTGCA	AACCTGCGGA	TCCTGGCGTG	1140
	CGGGGGCGAC	GGCAGCGTGG	GCTGGATCCT	CTCCACCCTG	GACCAGCTAC	GCCTGAAGCC	1200
10	GCCACCCCTT	GTTGCCATCC	TGCCCCGGG	TACTGGCAAC	GACTTGGCCC	GAACCTCAA	1260
	CTGGGGTGGG	GGCTACACAG	ATGAGCCTGT	GTCCAAGATC	CTCTCCACG	TGGAGGAGGG	1320
	GAAOCTGGTA	CAGCTGGACC	GCTGGGACCT	CCACGCTGAG	CCCAACCCCG	AGGCAGGGCC	1380
	TGAGGACCGA	GATGAAGGCG	CCACCGACCG	GTTGCCCTGT	GATGTCTTCA	ACAACACTT	1440
	CAGCCTGGGC	TTTGACGCCC	ACGTCACCTT	GGAGTTCAC	GAGTCTCGAG	AGGCCAACCC	1500
15	AGAGAAATTC	AACAGCGGCT	TTCCGAATAA	GATGTTCTAC	GCCGGGACAG	CTTCTCTGA	1560
	CTTCTGATG	GGCAGCTCCA	AGGACCTGGC	CAAGCACATC	CGAGTGGTGT	GTGATGGAAT	1620
	GGACTTGACT	CCCAGATCC	AGGACCTGAA	ACCCAGTGT	GTTGTTTTCC	TGAACATCCC	1680
	CAGGTACTGT	GCGGGCACA	TGCCCTGGGG	CCACCTGGG	GAGCACCACG	ACTTTGAGCC	1740
	CCAGCGGCAT	GACGACGGCT	ACCTCGAGGT	CATTGGCTTC	ACCATGACGT	CGTTGGCCGC	1800
20	GCTGACAGTG	GGCGACGAG	GCGAGCGGCT	GACGCAAGTG	GCGAGGTGG	TGCTCAACCA	1860
	ATCCAAGGCC	ATCCCGGTGC	AGGTGGATGG	CGAGCCCTGC	AAGCTTGACG	CCTCACGCAT	1920
	CCGCATCGCC	CTGCGCAATC	AGGCCACCAT	GGTGCAAGAG	GCCAAGCGGC	GGAGCGCGGC	1980
	CCCCCTGCAC	AGCGACACGC	AGCCGCTGCC	AGAGCAGTTG	CGCATCCAGG	TGAGTCGCGT	2040
	CAGCATGCAC	GACTATGAGG	CCCTGCACTA	CGACAAGGAG	CAGCTCAAGG	AGGCCCTCTGT	2100
25	GCOGCTGGGC	ACTGTGGTGG	TCCAGGAGA	CAGTGACCTA	GAGCTCTGCC	GTGCCACAT	2160
	TGAGAGACTC	CAGCAGGAGC	CCGATGGTGC	TGGAGCCAA	TCCCGACAT	GCCAGAAACT	2220
	GTCCCCAAG	TGGTCTTCC	TGACGCCAC	CAGTCCAGC	CGCTTCTACA	GGATCGACCG	2280
	AGCCGAGGAG	CACCTCAACT	ATGTGACTGA	GATCGCACAG	GATGAGATT	ATATCTTGA	2340
	CCCTGAGCTG	CTGGGGGCT	CGGCCCGGCC	TGACCTCCCA	ACCCCACTT	CCCCCTCTCC	2400
30	CACCTCACCC	TGCTACCCCA	CGCCCGGTC	ACTGCAAGGG	GATGCTGAC	CCCCCAAGG	2460
	TGAAGAGCTG	ATTGAGGCTG	CCAAGAGGAA	CGACTTCTGT	AAGCTCCAGG	AGCTGCACCG	2520
	AGCTGGGGGC	GACCTCATGC	ACGAGACGGA	GCAGAGTCGC	ACGCTCTGTC	ACCACGCACT	2580
	CAGCACTGGC	AGCAAGGATG	TGGTCCGCTA	CCTGCTGGAC	CACGCCCTCC	CAGAGATCCT	2640
	TGATGCGGTG	GAGGAAAACG	GGGAGACCTG	TTTGACCAAA	GCAGCGGCCC	TGGGCCAGCG	2700
35	CACCATCTGC	CAGTACATCG	TGGAGGCGCG	GGCCTCGCTC	ATGAAGACAG	ACCAGCAGGG	2760
	CGACACTCCC	CGGCAGCGGG	CTGAGAAGGC	TCAGGACACC	GAGCTGGCCG	CCTACTCTGA	2820
	GAACCGGCAG	CAGTACCAGA	TGATCCAGCG	GGAGGACCAG	GAGACGGCTG	TGTAGCGGGC	2880

Seq ID NO: 172 Protein sequence:
Protein Accession #: NP_003637

40	1	11	21	31	41	51	
	MEPRDGSPEA	RSSDSSESASA	SSSGSERDAG	PEPDKAPRRL	NKRRFPGLRL	FGHRKAITKS	60
45	GLQHLAPPPP	TPGAPCSESE	RQIRSTVDWS	ESATYGEHIW	FETNVSGDFC	YVGEQYCVAR	120
	MLKSVSRKRC	AACKIVVHTP	CIEQLEKINF	RCKPSFRESG	SRNVREPTFV	RHHVHRRRQ	180
	DGKCRHCKGK	FQKFTPHSK	EIVAISSWC	KQAYHSKVC	FMLQIEBPC	SLGVHAAVVI	240
	PPTWILRARR	PONTLKASKK	KKRASFKRKS	SKKGPEBGRW	RPFIIRPTPS	PLMKPLLVFV	300
	NPKSGGNQGA	KIIQSFLWYL	NPRQVFDLSQ	GGPKALEMY	RKVHNLILA	CGDGTGVGI	360
50	LSTLDQLRLK	PPFPVAILPL	GTGNDLARTL	NWGGGYTDEP	VSKILSHVEE	GNVVQLDRWD	420
	LHAEPNPEAG	PEDRDEGATD	RLPLDVFNNY	FSLGFDHVT	LEFHESREAN	PEKFNRSFRN	480
	KMFYAGTAFS	DFLMGSSKDL	AKHIRVVDG	MDLTPKIQDL	KPQCVVFLNI	PRYCAGTMEW	540
	GHPGHEHDFE	PQRHDDGYLE	VIGFTMTSLA	ALQVGGHGER	LTQCREVVL	TSKAIPVQVD	600
	GEPCKLAAAR	RIALRNQAT	MVQKAKRRA	APLHSDQPFV	PEQLRIQVSR	VSMHDEYALH	660
55	YDKEQLKEAS	VPLGTVVVPG	DSLELCRAH	IERLQQEPDG	AGAKSPTCQK	LSPKWCFLEA	720
	TTASRFYPIQ	RAQSHLNYVT	EIAQDEIYIL	DEPLLGAASR	PDLPPTSPFL	PTSPCSPTPR	780
	SLQGDAAFPD	QEGDIEAAR	NDPCKLQELH	RAGGDLMHDR	EQSRTLHLHA	VSTGSKDVVR	840
	YLLDHAPPEI	LDVEENGET	CLHQAAALGQ	RTICHYIVEA	GASLMKTDQ	GDTPRQRAEK	900
	AQDTLAAAYL	ENRQHYQMIQ	REDQETAV				

Seq ID NO: 173 DNA sequence
Nucleic Acid Accession #: AF232772
Coding sequence: 1-1662

65	1	11	21	31	41	51	
	ATGCCCGTGC	AGCTGACGAC	AGCCCTGCGT	GTGGTGGGCA	CCAGCCTGTT	TGCCCTGGCA	60
	GTGCTGGGTG	GCATCCTGGC	AGCCTATGTG	ACGGGCTACC	AGTTCATCCA	CACGGAAAG	120
	CAGTACCTGT	CCTTCGGCCT	GTACGGCGCC	ATCCTGGGCC	TGCACCTGCT	CATTGAGAGC	180
70	CTTTTTCGCT	TCCTGGAGCA	CGGGCGCATG	CGACGTGCGG	GCCAGGCCCT	GAAGCTGCCC	240
	TCCCCGCGGC	GGGGCTCGGT	GGCACTGTGC	ATTGCGGCAT	ACCAGGAGGA	CCCTGACTAC	300
	TTGCGCAAGT	GCCTGCGCTC	GGCCAGCGC	ATCTCCTTCC	CTGACCTCAA	GGTGGTCATG	360
	GTGGTGGATG	GCAACCGCCA	GGAGGACGCC	TACATGTCTG	ACATCTTCCA	CGAGGTGCTG	420
	GGCGGCACCG	AGCAGGCGCG	CTTCTTTGTG	TGGCGCAGCA	ACTTCCATGA	GGCAGGCGAG	480
75	GGTGAGACGG	AGGCCAGCCT	GCAGGAGGGC	ATGGACCGTG	TGCGGGATGT	GGTGGCGGCC	540
	AGCACCTTCT	CGTGATCAT	GCAGAAGTGG	GGAGGCAAGC	GCGAGGTGAT	GTACACGGCC	600
	TTCAAGGCC	TCGGCGATT	GGTGGACTAC	ATCCAGGTGT	GCGACTCTGA	CAGTGTGCTG	660
	GATCCAGCCT	GCACCATCGA	GATGCTTCGA	GTCTGGGAGG	AGGATCCCCA	AGTAGGGGGA	720
	GTCCGGGGAG	ATGTCTAAGT	CTCAACAAG	TACGACTCAT	GGATTTCTCT	CCTGAGCAGC	780
80	GTGCGGTACT	GGATGGCCTT	CAACGTGGAG	CGGGCCTGCC	AGTCTTACTT	TGGCTGTGTG	840
	CAGTGATATTA	GTGGGCCCTT	GGGCATGTAC	CGCAACAGCC	TCCTCCAGCA	GTTCTTGAG	900
	GACTGGTACC	ATCAGAAAGT	CCTAGGCAGC	AAGTGCAGCT	TCGGGATGA	CCGGCACCTC	960
	ACCAACCGAG	TCCTGAGCCT	TGGCTACCGA	ACTAAGTATA	CCGCGCGCTC	CAAGTGCCCTC	1020
	ACAGAGACCC	CCACTTAAGT	CTCCCGGTGG	CTCAACCGAG	AAACCCGCTG	GAGCAAGTCT	1080
	TACTTCCGGG	AGTGGCTCTA	CAACTCTCTG	TGGTTCCATA	AGCACCACTT	CTGGATGACC	1140
85	TACGAGTCAG	TGGTCACGGG	TTTCTTCCCC	TTCTTCTCTA	TTGCCACGGT	TATACAGCTT	1200
	TTCTACCGGG	GCCGCACTCG	GAACATTCTC	CTCTTCTCTG	TGACCGGTGCA	GCTGGTGGGC	1260
	ATTATCAAGG	CCACCTACGC	CTGCTTCTCT	CGGGGCAATG	CAGAGATGAT	CTTCTATGTC	1320

	CTCTACTCCC	TCCTCTATAT	GTCCAGCCTT	CTGCCGGCCA	AGATCTTTGC	CATTGCTACC	1380
	ATCAACAAAT	CTGGCTGGGG	CACCTCTGGC	CGAAAAACCA	TTGTGGTGAA	CTTCATTGGC	1440
	CTCATTCCTG	TGTCATCTCG	GGTGGCAGTT	CTCCTGGAGG	GGCTGGCCTA	CACAGCTTAT	1500
5	TGCCAGGACC	TGTTCACTGA	GACAGAGCTA	GCCTTCCTTG	TCTCTGGGGC	TATACTGTAT	1560
	GGCTGCTACT	GGGTGGCCCT	CCTCATGCTA	TATCTGGCCA	TCATCGCCCG	GCGATGTGGG	1620
	AAGAAGCCCG	AGCAGTACAG	CTTGGCTTTT	GCTGAGGTGT	GACATGGCCC	CCAAGCAGAG	1680
	CGGGTAAAGT	GCAATGGGTA	AGGGAGGGAA	GGGGAATGGA	AGAGAAAAGA	CAGGGTGGGA	1740
	GGGAGGAGGG	AGTGCTGTGT	TTTAGTCTCT	TAATGGTCCA	AAGGACAAAT	CTAAATGCA	1800
10	AAGAACGGTG	ATGTAGTAGG	GCCTGCACAG	TCTGTTTGA	GGAGGCAACA	CTGATCCCCC	1860
	AGATGCAGGG	CTGCAGGGGA	TTCTGTGTTT	TCAGACTGCC	TGTCTGCTTG	CATCTGCACA	1920
	TAGGCAGTAG	CCTCCTCCTG	GGCTCCAGAG	GGCACTCAGA	AGTTGTGCTA	AACCAAGTTA	1980
	AGTCCCATTC	AGTGGCAACT	TGTGATAGGT	ACCTGAGTGA	CGGCAACCTG	CGGAAGGAGG	2040
	TTCTCCACAG	CCATCTGAAC	ACAACCAGAG	GTGGCAGGAG	AAATTTCTACT	GAGCGAGGTG	2100
	GGCGGGTTAG	TGATGTGTAC	CCCCACCCCA	CCCATAAGTA	GTCACTCAATG	CAATAAGATT	2160
15	GGCGGTGAGA	TACAAGGCCCC	AGAAGCCCTGA	TCTTTGGGCA	TCAGAAAACA	GGGTCCAGGA	2220
	ATGGTGCTTT	ATGTGAGATA	CCCCACTCCA	CATCAACATT	CCAGGGATGA	GCCAAACCAG	2280
	CAGGGAGTTA	GCACTGAACT	GCTTTTAAAA	GTGCACATTA	AAAAGGAAAG	TTTGCCAGGA	2340
	GGAAACAAAG	GATTGTGGTG	GTGCTAAAGG	AGGCCATAAG	CTACACAGAG	GCCTTGGGTG	2400
20	TTCCACCTGG	AAACTGCTGA	GACGTCTAGA	TGGGTTCTTA	GCTTGTCTGT	GATCTCTGCT	2460
	GGGGAGATAA	AAAGATTAAAG	CCCCAACATG	TTCAAGAAAG	AAGTGAAGTC	TTGGGTATT	2520
	TAACCTGTAT	ACTCTTGAAT	TCTCTCAAA	TTCAAGCTCTG	ATCTGAGGCT	AAGACACACT	2580
	CCCCACTTCA	CTTTCTTCAA	AGCCACATTT	TTTGAGGTAT	CACTGCACTG	ACCTCTTCTA	2640
	CCCTCATCAT	CATAGGTAAG	GTTTTTCAAGG	TGGCAATTGG	GGCGGAGCCC	CGGCTTCTTA	2700
25	TAGAAGCTTC	AGCAGGAGGC	AAGCGTGTTC	TCAGCACATA	TGGGAACTAT	GAGGAGCCTC	2760
	TGATCAAAAT	GGCTCAAACT	TGTGAGCTGC	TTGGACGGAT	TCCTTGGCAG	CCGGGTAGC	2820
	ATGTGTGACT	TTGAGGCTAC	TGTTCTTGAC	AATCATCTCC	AATGGAAGC	TTTTCAGTGT	2880
	TCCCAAAGTG	AACTCTCAAA	TCCAAATGSG	TTATCTTTGA	GACCATCCAT	TCTCCTCAGT	2940
	GGCTTCTCCA	GGGAATTCCT	ACAGCCAAAGT	TGTGACAGTC	ACTGCATTGG	CCTGCTTCTT	3000
30	TCAGAAAACG	AGCTAGGAGT	ATGAAACTGG	TTCTTACATC	CTAAGGTTCT	TGCTTTCTCT	3060
	CTCATGCCCT	CTGAGGCTGT	TTTTGGCTGT	TTTCCCTCTG	CTGCTTTTGG	GGAAATGAGG	3120
	GAAGCCATT	TCCAAGTGAC	TGCAATCCA	GGCTGTTCTC	AGCGTTTGA	GTTTAAACCC	3180
	TGGGATCCTG	ACTAAGCCTT	TGACTTAAGG	GTTGCTTGCT	TGCCCTCCAA	ATGCTCTTTC	3240
	TCAAAGGGGC	CAACTAAACC	GTGCAGAAC	AGCACTAAGG	TGGACAGCAG	ACAAGAGGGC	3300
35	AAGCCTCTAA	TGTACCAAGT	GCTTCCTACA	AAGACGCAAG	GTGTGCTCCG	AACCCAGAGT	3360
	GGGCAAAACC	TGGTGCTTTC	CTTCATCTCC	CACGAACTCA	AGGGTTTTC	AAGTGTAGCT	3420
	AACAGTTGCC	ACATCACACA	GACCTCCAGT	TTCTGGTAAG	ACTGCTGGTT	GACATCAGAG	3480
	CCAACCCATT	GAAGGCTGGA	AGGCAGCAGG	CATTGCTAA	GGCAGCTGAT	CCAGGCAATC	3540
	GTCTGCTGG	CCAAGAAAGT	AACTATTTT	GAGCATTAGA	ATGGAGGAAA	TCCGGTCAGC	3600
40	CAAGTGACAG	GTTCAGACTT	CGCTAAGGGC	TTGTTTTTCT	TCAGCATTTA	CTTGAAGATT	3660
	AATGTAGGAT	GACAGGCTCT	CCTGGCTGTC	CTACCATCAG	CTCTGCCTTG	CAGTGTGGTC	3720
	GTCAACTTTC	CTCAAACTCA	AAACAGGCAG	GTACAGGTAG	TGGGCTCACA	ACGTTTGACC	3780
	TCGACTGGTT	TTTCTAAGTT	ATTTTGTACA	TTTTTCAGCA	GCAAAACCAA	ACTGGGTCTT	3840
	CAGCTTTATC	CCCGTTTCTT	GCAAGGGAAG	AGCCTTTATA	CAATTGGACG	CATTTTGGTT	3900
45	TTTCTCATTT	GAGAATTCAA	ATCCTCTTTT	GTATTGTTTC	TACAATAATT	TGTAACATA	3960
	TTTATTTTAA	CCTGCTTTT	TTTTTTTTTT	TAATTTTCAG	GTCAGTTTT	TTTACTGCA	4020
	CTTATTTGTC	AAAAATAAGA	TTCTCACAT				

Seq ID NO: 174 Protein sequence:
Protein Accession #: AAF36984

50	1	11	21	31	41	51	
	MPVQLTTLAL	VVGTSFLPALA	VLGGILAAVY	TGYQFIHTEK	HYLSFGLYGA	ILGLHLIIQS	60
55	LFAPLEHRRM	RRAGQALKLP	SPRRGSVALC	IAAYQEDPDY	LRKCLRSAGR	ISFPDLKVVM	120
	VDVGNQBEDA	YMLDIFHEVL	GGTEQAGFFV	WRSNFHEAGE	GETEASLQEG	MDRVDRVVRA	180
	STFSCIMQK	KGKREVMYTA	FKALGDSVDY	IQVCDSDTVL	DPACTIEMLR	VLEEDPQVGG	240
	VGGDVQLLNK	YDSWISFLSS	VRYWMAFNVE	RACQSYFGCV	QCISGFLPMY	RNSLLQQFLE	300
	DNVHKQFLGS	KCSFPGDDRL	TNRVLSLGYR	TKYTARSKCL	TETPTKYLWR	LNQOTRWSKS	360
60	YFREWLYNSL	WFHKKHLWMT	YESVVTGFFP	FPLIATVIQL	FYRGRIWNIL	LFLLTVLQLVG	420
	IIKATYACPL	RGNAMIFMS	LYSLLYMSSL	LPKIFAIAT	INKSGWGTSG	RKTIVVNFIG	480
	LIPVSIWVAV	LLEGLAYTAY	QDLFSETEL	APLVSGAILY	GCVWVALML	YLAIARRCG	540
	KKPEQYSLAF	AEV					

Seq ID NO: 175 DNA sequence
Nucleic Acid Accession #: NM_000691
Coding sequence: 43..1404

65	1	11	21	31	41	51	
70	CCAGGAGCCC	CAGTTACCGG	GAGAGGCTGT	GTCAAAGGCG	CCATGAGCAA	GATCAGCGAG	60
	GCCGTGAAGC	GGCCCGCGC	CGCCTTCAGC	TCGGGCAGGA	CCCGTCCGCT	GCAGTTCGGA	120
75	TTCCAGCAGC	TGGAGGCGCT	GCAGCGCCTG	ATCCAGGAGC	AGGAGCAGGA	GCTGGTGGGC	180
	GGCTGGCCG	CAGACCTGCA	CAAGAATGAA	TGGAACGCCT	ACTATGAGGA	GGTGGTGTAC	240
	GTCTAGAGG	AGATCGAGTA	CATGATCCAG	AAGCTCCCTG	AGTGGGCCGC	GGATGAGCCC	300
	GTGGAGAAGA	CGCCCCAGAC	TCAGCAGGAC	GAGCTCTACA	TCCACTCGGA	GCCACTGGGC	360
	TGGTCTCTCG	TCATTGGCAC	CTGGAACATC	CCCTTCAACC	TCACCATCCA	GCCCATGGTG	420
	GGCGCCATCG	CGACGAGGAA	CGCAGTGGTC	CTCAAGCCCT	CGGAGCTGAG	TGAGAACATG	480
80	GCAGCCTCG	TGGTACCAT	CATCCCCCAG	TACCTGGACA	AGGATCTGTA	CCCAAGTAATC	540
	AATGGGGGTG	TCCCTGAGAG	CACGGAGCTG	CTCAAGGAGA	GGTTCGACCA	TATCCTGTAC	600
	ACGGGCAGCA	CGGGGGTGGG	GAAGATCATC	ATGACGGCTG	CTGCCAAGCA	CCTGACCCCT	660
	GTCAACGCTG	AGCTGGGAGG	GAAGAGTCCC	TGCTACGTGG	ACAAGAACTG	TGACCTGGAG	720
	GTGGCCTGCC	GACGCATCGC	CTGGGGGAAA	TTCAATGAACA	GTGGCCAGAC	CTGGTGGGCC	780
85	CCAGACTACA	TCTCTGTGTA	CCCCTCGATC	CAGAACCAAA	TTGTGGAGAA	GCTCAAGAAAG	840
	TCACTGAAAG	AGTTCTACCG	GGAAGATGAG	AGGAAATCCC	GGGACTATGG	AAGAATCATT	900
	AGTGCCCGGC	ACTTCCAGAG	GGTGTGGGTC	CTGATTGAGG	GCCAGAAGGT	GGCTTATGGG	960
	GGCACCGGGG	ATGCCCGCAC	TCGCTACATA	GCCCCACCA	TCTTCACGGA	CGTGAGACCC	1020

CAGTCCCCGG TGATGCAAGA GGAGATCTTC GGGCCTGTGC TGCCCATCGT GTGCGTGCGC 1080
 AGCCTGGAGG AGGCCATCCA GTTCATCAAC CAGCGTGAGA AGCCCTGGC CCTCTACATG 1140
 TTCTCCAGCA ACGACAAGGT GATTAAGAAG ATGATTGCAG AGACATCCAG TGGTGGGGTG 1200
 GCGGCCAAGC ATGTATCGT CCACATCACC TTGCACCTC TGCCCTTCGG GGGCGTGGGG 1260
 AACAGCGGCA TGGGATCCCTA CCATGGCAAG AAGAGCTTGG AGACTTTCTC TCACCGCGCG 1320
 TCTTGCTCTG TGAGGCTCTCT GATGAATGAT GAAGGCCTGA AGGTGAGATA CCCCCGAGC 1380
 CCGGCCAAGA TGACCCAGCA CTGAGGAGGG GTTGCTCCGC CTGGCTGGC CATACTGTGT 1440
 CCCATCGGAG TGCGGACAC CCTCACTGGC TCTCTGGCC CTGGAGAATC GCTCTGCAG 1500
 CCCCAGCCCA GCCCACTCC TCTGCTGACC TGCTGACCTG TGCACACCCC ACTCCACAT 1560
 GGGCCAGGCG CTCACATTC CAAGTCTCCA CCCCTTTCTA GACCAATAAA GAGACAAATA 1620
 CAATTTTCTA ACTCGG

Seq ID NO: 176 Protein sequence:
 Protein Accession #: NP_000682

1 11 21 31 41 51
 MSKISEAVKR ARAAFSSGRT RPLQFRFQQL EALQRLIQEQ EQELVGALAA DLHKNEWNAY 60
 YEEVVVLEE IEYMIQKLEP WAADEPVEKT PQTQDELYI HSEPLGVVLV IGTWNYPPNL 120
 TIQPMVGATA AGNAVVLKPS ELSENMAALL ATIIQPYLDK DLYPVINGGV PETTELLKER 180
 FDHILYTGST GVGKIIMTAA AKHLTPVTLK LGGKSPCYVD KNCOLDVACR RIAWGFPMNS 240
 GQTCVAPDYI LCDPSIQNQI VEKLKSLKE FYGEDAKKSR DYGRISARH FORVMGLIEG 300
 QKVAYGGTGD AATRYIAPTI LTDVDPQSPV MQEEIFGPVL PIVCVRSLEE AIQFINQREK 360
 PLALVMPSSN DLVVKMLAE TSSGGVAAND VIVHITLHSL PFGGVGNSGM GSYHGKKSFE 420
 TFSHRRSCLV RPLMDEGLK VRYPPSPAKM TQH

Seq ID NO: 177 DNA sequence
 Nucleic Acid Accession #: NM_001067.1
 Coding sequence: 108-4703

1 11 21 31 41 51
 CTAACCGAGC CGCGTCTGTG GAGAAGCGGC TTGGTGGGGG GTGGTCTCGT GGGGTCTCTG 60
 CTGTTTAGTC GCTTTCAGGG TTCTTGAGCC CCTTCACGAC CGTCACCATG GAAGTGTCTC 120
 CATTGCGACC TGTAATGAA AATATGCAAG TCAACAAAAT AAAGAAAAAT GAAGATGCTA 180
 AGAAAAGACT GTCTGTGAA AGAATCTATC AAAAGAAAAC ACAATTGGAA CATATTTTGC 240
 TCCGCCCAGA CACCTACATT GGTCTGTGG AATTAGTGAC CCAGCAAAATG TGGGTTTACG 300
 ATGAAGATGT TGGCATTAACT TATAGGGAAG TCACITTTGT TCCTGGTTTG TACAAAAATCT 360
 TTGATGAGAT TCTAGTTAAT GCTGCGGACA ACAAAACAAAG GGACCCAAAA ATGTCTTTGA 420
 TTAGAGTCAC AATTGATCCG GAAAACAATT TAATTAGTAT ATGGAATAAT GAAAAAGGTA 480
 TTCCTGTTGT TGAACACAAA GTTGAAAAAG TGTATGTCCC AGCTCTCATA TTTGGACAGC 540
 TCCTAACTTC TAGTAACAT GATGATGATG AAAAGAAAAGT GACAGGTGGT CGAAATGGCT 600
 ATGGAGCCAA ATTGTGTAACT ATATTCACTA CCAAAATTTAC TGTGGAATAA GCCAGTAGAG 660
 AATACAAGAA AATAGTCTAAA CAGACATGGA TGGATAATAT GGAAGAGAGT GGTGAGATGG 720
 AACTCAAGCC CTTCAATGGA GAAGATTATA CATGTATCAC CTTTCAGCCT GATTGTCTTA 780
 AGTTTAAAT GCAGAGCCGT GACAAAGATA TTGTTGCACT AATGGTCAGA AGAGCATATG 840
 ATATTGCTGG ATCCACCAAA GATGTCAAAG TCTTCTTAA TGGAAATAAA CTGCCAGTAA 900
 AAGGATTTCC TAGTTATGTG GACATGTATT TGAAGGACAA GTTGGATGAA ACTGGTAAT 960
 CCTGAAAGT AATAGTCAAA CAAGTAAACC ACAGGTGGGA AGTGTGTTTA ACTATGAGTG 1020
 AAAAAAGGCT TCAGCAAAAT AGCTTTGTCA ACAGCATTGC TACATCCAAG GGTGGCAGAC 1080
 ATGTTGATTA TGTACTGTAT CAGATTGTGA CTAACTTGT TGTGTTGTG AAGAAGAAGA 1140
 ACAAGGGTGG TGTGCACTA AAAGCACATC AGGTGAAAAA TCACATGTGG ATTTTGTAA 1200
 ATGCCTTAAT TGAAAACCCA ACCTTTGACT CTCAGACAAA AGAAAACATG ACTTTACAAC 1260
 CCAAGAGCTT TGGATCAACA TGCCAATTGA GTGAAAAAAT TATCAAGACT GCCATTGGCT 1320
 GTGGTATTGT AGAAGACATA CTAACTGGG TGAAGTTTAA GGCCCAAGTC CAGTTAAACA 1380
 AGAAGTGTTC AGCTGTAAAA CATAATAGAA TCAAGGGAAT TCCCAAACTC GATGATGCCA 1440
 ATGATGCAGG GGGCCGAAAC TCCACTGAGT GTACGCTTAT CCTGACTGAG GGAGATTGAG 1500
 CCAAACTTTT GGCTGTTTCA GGCCTTGGTG TGGTTGGGAG AGACAAATAT GGGGTTTTCC 1560
 CTCTTAGAGG AAAAAATCTC AATGTTGAG AGCTTCTCA TAAGCAGATC ATGGAATAATG 1620
 CTGAGATTAA CAATATCATC AAGATTGTGG GTCTTCAGTA CAAGAAAAAC TATGAAGATG 1680
 AAGATTCAAT GAAGACGCTT CGTTATGGGA AGATAATGAT TATGACAGAT CAGGACCAAG 1740
 ATGTTCCCA CATCAAGGC TTGCTGATTA ATTTTATCCA TCACAACTGG CCTCTCTCTC 1800
 TGGGACATCG TTTCTGGAG GAATTTATCA CTCCCATGT AAAGGTATCT AAAACAAGC 1860
 AAGAAATGGC ATTTTACAGC CTTCCTGAAT TTGAAGAGTG GAAGAGTTCT ACTCCAATC 1920
 ATAAAAAATG GAAAGTCAAA TATTACAAAG GTTTGGGCAC CAGCACATCA AAGGAAGCTA 1980
 AAGAATACTT TGCATATGAT AAAAGACATC GTATCCAGTT CAAATATTCT GGTCTGAAG 2040
 ATGATGCTGC TATCAGCCTG GCCTTTAGCA AAAACAGAT AGATGATCGA AAGGAATGGT 2100
 TAACTAATTT CATGGAGGAT AGAAGACAAC GAAAGTTACT TGGGCTTCTT GAGGATTACT 2160
 TGTATGGACA AACTACCACT TATCTGACAT ATAATGACTT CATCAACAAG GAACTTATCT 2220
 TGTCTCAAA TTCTGATAAC GAGAGATCTA TCCCTTCTAT GGTGGATGGT TTGAAACCGG 2280
 GTCAGAGAAA GGTTTTGTGT ACTTGCTTCA AACGGAATGA CAAGCGAGAA GTAAAGGTTG 2340
 CCCAATTAGC TGGATCAGTG GCTGAAATGT CTTCTTATCA TCATGGTGAG ATGTCACTAA 2400
 TGATGACCAT TATCAATTTG GCTCAGAAAT TTGTGGGTAG CAATAATCTA AACCTCTTGC 2460
 AGCCCATTTG TCAGTTTGGT ACCAGGCTAC ATGGTGGCAA GGAATCTGCT AGTCCACGAT 2520
 ACATCTTTAC AATGCTCAGC TCTTTGGCTC GATTGTTATT TCCACCAAAA GATGATCACA 2580
 CGTTGAAGTT TTTATATGAT GACAACACAG GTGTTGAGCC TGAATGGTAC ATTCCTATTA 2640
 TTCCCATGGT GCTGATAAAT GGTGCTGAAG GAATCGGTAC TGGGTGGTCC TGCAAAATCC 2700
 CCAACTTTGA TGTGCGTGAA ATTTGAAATA ACATCAGGCG TTTGATGGAT GGAGAAGAAC 2760
 CTTTGCCAAT GCTTCCAAGT TACAAGAACT TCAAGGGTAC TATTGAAGAA CTGGCTCCAA 2820
 ATCAATATGT GATTAGTGGT GAAGTAGCTA TTCTTAATTC TACAACCAT GAAATCTCAG 2880
 AGCTTCCCGT CAGAACATGG ACCCAGACAT ACAAGAAACA AGTTCTAGAA CCCATGTTGA 2940
 ATGGACCGGA GAGACACCT CCTCTCATA CAGACTATAG GGAATACCAT ACAGATACCA 3000
 CTGTGAAAT TGTGTGTAAG ATGACTGAAG AAAAAGTGGC AGAGGCAGAG AGAGTTGGAC 3060
 TACACAAAGT CTTCAAACTC CAAACTAGTC TCACATGCAA CTCTATGGTG CTTTTTGACC 3120
 ACGTAGGCTG TTTAAAGAAA TATGACACGG TGTGGATAT TCTAAGAGAC TTTTTTGAAC 3180
 TCAGACTTAA ATATTATGGA TTAAGAAAAG AATGGCTCCT AGGAATGCTT GGTGCTGAAT 3240
 CTGCTAAACT GAATAATCAG GCTCGCTTTA TCTTAGAGAA AATAGATGGC AAAATAATCA 3300

	TTGAAAATAA	GCCTAAGAAA	GAATTAATTA	AAGTTCTGAT	TCAGAGGGGA	TATGATTCCG	3360
	ATCCTGTGAA	GGCCTGGAAA	GAAGCCCAGC	AAAAGGTTCC	AGATGAAGAA	GAAAATGAAG	3420
	AGAGTGACAA	CGAAAAGGAA	ACTGAAAAGA	GTGACTCCGT	AACAGATTCT	GGACCAACCT	3480
5	TCAACTATCT	TCTTGATATG	CCCCTTTGGT	ATTTAACCAA	GGAAAAGAAA	GATGAACCTC	3540
	GCAGGCTAAG	AAATGAAAAA	GAACAAGAGC	TGGACACATT	AAAAAGAAAG	AGTCCATCAG	3600
	ATTTGTGGAA	AGAAGACTTG	GCTACATTTA	TTGAAGAATT	GGAGGCTGTT	GAAGCCAAGG	3660
	AAAAACAAGA	TGAACAAGTC	GGACTTCCTG	GGAAAGGGGG	GAAGGCCAAG	GGGAAAAAAA	3720
	CACAAATGGC	TGAAGTTTIG	CCTTCTCCGC	GTGGTCAAG	AGTCATTCCA	CGAATAACCA	3780
10	TAGAAATGAA	AGCAGAGGCA	GAAAAGAAAA	ATAAAAAGAA	AATTAAAGAT	GAAAACTACTG	3840
	AAGGAAGCCC	TCAAGAAGAT	GGTGTGGAAC	TAGAAGGCCT	AAAAACAAGA	TTAGAAAAAG	3900
	AACAGAAAAG	AGAACCAGGT	ACAAAGACAA	AGAAACAAAC	TACATTGGCA	TTTAAGCCAA	3960
	TCAAAAAAGG	AAAGAAGAGA	AATCCCTGGC	CTGATTGAGA	ATCAGATAGG	AGCAGTGACG	4020
	AAAGTAATTT	TGATGTCCCT	CCAGGAGAAA	CAGAGCCACG	GAGAGCAGCA	ACAAAAACAA	4080
15	AATTCACAAT	GGATTCTGGAT	TCAGATGAAG	ATTTCTCAGA	TTTTGATGAA	AAAACTGATG	4140
	ATGAAGATTT	TGTCCCATCA	GATGCTAGTC	CACCTAAGAC	CAAAACTTCC	CCAAAACTTA	4200
	GTAACAAAGA	ACTGAAACCA	CAGAAAAGTG	TCGTGTCAGA	CCTTGAAGCT	GATGATGTTA	4260
	AGGGCAGTGT	ACCACTGTCT	TCAAGCCCTC	CTGCTACACA	TTTCCCAGAT	GAAACTGAAA	4320
	TTACAAAACC	AGTTCTCTAA	AAGAATGTGA	CAGTGAAGAA	GACAGCAGCA	AAAAGTCAGT	4380
20	CTTCCACCTC	CACCTACCGT	GCCAAAAAAA	GGGCTGCCCC	AAAAGGAAAG	AAAAGGGGAT	4440
	CAGCTTTGAA	TTCTGGGTCT	TCTCAAAAGC	CTGATCCTGC	CAAAACCAAG	AATCGCCGCA	4500
	AAAGGAAGCC	ATCCACTTCT	GATGATTCTG	ACTCTAATTT	TGAGAAAATT	GTTTCGAAAG	4560
	CAGTCACAAG	CAAGAAATCC	AAGGGGGAGA	GTGATGACTT	CCATATGGAC	TTTGACTCAG	4620
	CTGTGGCTCC	TCGGGCAAAA	TCTGTACGGG	CAAGAAACCC	TATAAAGTAC	CTGGAAGAGT	4680
25	CAGATGAAGA	TGATCTGGAT	TAAAATGTGA	GGCGATTATT	TAAAGTAATT	ATCTTACCAA	4740
	GCCCAAGACT	GGTTTAAAG	TTACCTGAAG	CTCTTAACTT	CCTCCCCCTC	GAATTTAGTT	4800
	TGGGGAAGGT	TTTTTTAGCA	CAAGACATCA	AAGTGAAGTA	AAGCCCAAGT	GTTCTTTAGT	4860
	TTTTTATAAT	ACTGTCTAAA	TAGTGACCAT	CTCATGGGCA	TTGTTTTCTT	CTCTGCTTTG	4920
	TCGTGTTTTT	GAGTCTGCTT	TCITTTGTCT	TTAAAACCTG	ATTTTAAAGT	TCTTCTGAAC	4980
30	TGTAGAAATA	CACTTCTGAT	CACCTCAGCG	TAAAGCAGTG	TGTTTATTAA	CCATCCCACT	5040
	AGCTAAAACT	AGAGCAGTTT	GATTAAAAAG	TGTCACCTCT	CCTCCTTTTC	TACTTTCAGT	5100
	AGATATGAGA	TAGAGCATAA	TTATCTGTTT	TATCTTAGTT	TTATACATAA	TTTACCATCA	5160
	GATAGAATTT	TATGGTTCTA	GTACAGATAC	TCTACTACAC	TCAGCCTCTT	ATGTGCCAAG	5220
	TTTTTCTTTA	AGCAATGAGA	AATTGCTCAT	GTCTTCTCAT	TTCTCAAATC	ATCAGAGGCC	5280
35	AAAGAAAAAC	ACTTTGGCTG	TGCTATAAAC	TTGACACAGT	CAATGAAGAT	AAGAAAAATTA	5340
	GAGTAGTTAT	GTGATTATTT	CAGCTCTTGA	CCTGTCCCCT	CTGGCTGCCT	CTGAGTCTGA	5400
	ATCTCCCAAA	GAGAGAAACC	AATTCTAAG	AGGACTGGAT	TGCAGAAGAC	TCGGGGACAA	5460
	CATTGTATCC	AAGATCTTAA	ATGTTATATT	GATAACCATG	CTCAGCAATG	AGCTATTAGA	5520
	TTCAATTTGG	GAAATCTCCA	TAATTTCAAT	TTGTAACCTT	TGTTAAGACT	TGCTACATT	5580
40	GTTATATGTG	TGTGACTTGA	GTAATGTTAT	CAACGTTTTT	GTAATATATT	ACTATGTTTT	5640
	TCTATTAGCT	AAATTCACAC	AATTTGTAC	TTAATAAAAA	TGTTCTAAAC	ATTGC	

Seq ID NO: 178 Protein sequence:
Protein Accession #: NP_001058.1

45	1	11	21	31	41	51	
	MEVSPLQPVN	ENMQVNKIKK	NEDAKKRLSV	ERIQKKTQL	EHILLRPTDY	IGSVELVTQO	60
	MWVYDEDVGI	NYREVTFVPG	LYKIFDEILV	NAADNKQRDP	KMSCIRVTID	PENNLISIWN	120
50	NGKGIPVVEH	KYVKMYVPAL	IFGQLLTSSN	YDDDEKKVTG	GRNGYGAKLC	NIPSTKFTVE	180
	TASREYKKNF	KQTWMDNMGR	AGEMELKPFN	GEDYTCITFQ	PDLSKPKMQS	LDKDIVALMV	240
	RRAYDLAGST	KDVVVFLLGN	KLPVKGFRSY	VDMYLQDKLD	ETGNSLVKVIH	EQVNRHWEVC	300
	LTMSEKGFQO	ISFVNSIATS	KGGRHVDYVA	DQIVTKLVDV	VKKKNKGGVA	VKAHVQKNHM	360
	WTFVNALIEN	PTFDSQTKEN	MTLQPKSFGS	TCQLSEKPIK	AAIGCGIVES	ILNWVKFKAQ	420
55	VQLNKKCSAV	KHNRIKGIPI	LDDANDAGGR	NSTECTLILT	EGDSAKTLAV	SGLGVVGRDK	480
	YGVPFLRGLI	LNVREASHKQ	IMENAEINNI	IKIVGLQYKK	NYEEDSLKT	LYGKIMIMT	540
	DQDDQDGHK	GLLNFIIHNN	WPSLLRHRFL	EEPTPIVKV	SKNKQEMAFY	SLPEPEEWKS	600
	STPNHKKWV	KYYKGLGTST	SKEAKYFAD	MKRHRIQFKY	SGPEDDAAIS	LAFSKKQIDD	660
	RKEWLTNFM	DRRQRKLGL	PEDYLYGQTT	TYLTYNDFIN	KELILFSNSD	NERSIPSMVD	720
60	GLKPGQRKVL	PTCFKRNDRK	EVKVAQLAGS	VAEMSSYHHG	EMSLMNTIIN	LAQNFVGSNN	780
	LNLLQPIGQF	GTRLHGGKDS	ASPRYIPTML	SSLARLLFPP	KDDHTLKFY	DDNQREPEW	840
	YPIIIPMVL	NAGBIGTGW	SKIPNFDVR	EIVNNIRRLM	DGEEFLPMLP	SYKNPKGTIE	900
	ELAPNQYVVS	GEVAILNSTT	IEISELPVRT	WTQTYKEQVL	EPMLNGTEKT	PPLITDYREY	960
	HTDITVFKFV	KMTTEKLAE	ERVGLHKVFK	LQTSLTCSNM	VLFHDVGCLE	KYDITVLDILR	1020
65	DPFELRLKY	GLRKEWLLGM	LGAESAKLNN	QARFILEKID	GKII IENPK	KELIKVLIQR	1080
	GYSDFPVKAW	KEAQKVPDE	EENEESDNEK	ETEKSDSVTD	SGPTFNVLDD	MLWYLTKEK	1140
	KDELCLRLNE	KEQELDTLKR	KSPSLWKEK	LATFIEELEA	VEAKEKQDEQ	VGLPGRGKKA	1200
	KGKKTQMAEV	LPSPRGQRTI	PRITIEMKAE	AEKKNKKIK	NENTEGSPQE	DGVELEGLKQ	1260
	RLEKKQKREP	GTKTKKQTTL	AFKPIKKGKK	RNFWDSESD	RSSDESNEFDV	PPRETEPRRA	1320
70	ATKTKFTMDL	DSDEDFSDFD	EKTDDDFVFP	SDASPPKTKT	SPKLSNKKEL	PQKSVVSDLE	1380
	ADDVKGSVPL	SSSPFATHFP	DETEITNFVP	KKNVTVKKTA	AKSQSSTSTT	GAKKRAAPKG	1440
	TKRDPALNSG	VSQKPDPAKT	KNRRKRKPST	SDDSDSNFEK	IVSKAVTSKK	SKGESDDPHM	1500
	DFDSAVAPRA	KSVRAKFKIK	YLESEDEDDL	P			

Seq ID NO: 179 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 148-7095

80	1	11	21	31	41	51	
	CACACATACG	CACGCACGAT	CTCACTTCSA	TCTATACACT	GGAGGATTAA	AACAAAACAA	60
	CAAAAAAAC	ATTTCTCTCG	CTCCCCCTCC	CTCTCCACTC	TGAGAAGCAG	AGGAGCCGCA	120
	CGGCGAGGGG	CCGAGACACG	TCTGGAAATG	CGAATCTTAA	AGCGTTTCTC	CGCTTGCAAT	180
	CAGCTCCTCT	GTGTTTGGCG	CCTGGATTGG	GCTAATGGAT	ACTACAGACA	ACAGAGAAAA	240
85	CTGTGTGAAG	AGATTGGGCTG	GCTCTATACA	GGAGCACTGA	ATCAAAAAAA	TTGGGGAAAG	300
	AAATATCCAA	CATGTAATAG	CCCAAAACAA	TCTCCTATCA	ATATTGATGA	AGATCTTACA	360
	CAAGTAAATG	TGAATCTTAA	GAAACTTAAA	TTTCAGGGTT	GGGTATAAAC	ATCATTGGAA	420

	AACACATTCA	TTCATAACAC	TGGGAAAACA	GTGGAAATTA	ATCTCACTAA	TGACTACCGT	480
	GTCAGCGGAG	GAGTTTCAGA	AATGGTGTIT	AAAGCAAGCA	AGATAACTTT	TCACTGGGGA	540
	AAATGCAATT	TGTCACTCTGA	TGGATCAGAG	CATAGTTTAG	AAGGACAAAA	ATTTCCACTT	600
5	GAGATGCAAA	TCTACTGCTT	TGATGCGGAC	CGATTTTCAA	GTTTTGAGGA	AGCAGTCRAA	660
	GGAAAAGGGA	AGTTAAGAGC	TTTATCCATT	TTGTTTGAGG	TTGGGACAGA	AGAAAATTTG	720
	GATTTCAAAG	CGATTATTGA	TGGAGTCGAA	AGTGTTAGTC	GTTTTGGGAA	GCAGGCTGCT	780
	TTAGATCCAT	TCATACTGTT	GAACCTTCTG	CCAAACTCAA	CTGACAAGTA	TTACATTTAC	840
	AATGGCTCAT	TGACATCTCC	TCCTTGACCA	GACACAGTTG	ACTGGATTGT	TTTTAAAGAT	900
10	ACAGTTAGCA	TCTCTGAAAG	CCAGTTGGCT	GTTTTGTGTG	AAGTTCTTAC	AATGCAACAA	960
	TCTGGTTATG	TCATGCTGAT	GGACTACTTA	CAAAACAATT	TTCCAGAGCA	ACAGTACAA	1020
	TTCTCTAGAC	AGGTGTTTTT	CTCATACACT	GGAAAGGAAG	AGATTCTATG	AGCAGTTTGT	1080
	AGTTCAGAAC	CAGAAAATGT	TCAGGCTGAC	CCAGAGAATT	ATACCAGCCT	TCTTGTTACA	1140
	TGGGAAAGAG	CTCAGAGTGT	TTATGATACC	ATGATTGAGA	AGTTTGCAGT	TTTGTACCAG	1200
	CAGTTGGATG	GAGAGGACCA	AACCAAGCAT	GAATTTTGA	CAGATGGCTA	TCAAGACTTG	1260
15	GGTGCTATT	TCAATAATTT	GCTACCCAAT	ATGAGTTATG	TTCTTCAGAT	AGTAGCCATA	1320
	TGCACATAAT	CTATCTATGG	AAATATACAG	GACCAACTGA	TTGTGACAT	GCCTACTGAT	1380
	AATCCTGAAC	TTGATCTTTT	CCCTGAATTA	ATTGGAAGT	AAGAAATAAT	CAAGGAGGAG	1440
	GAAGAGGGAA	AGACATTTGA	AGAAGGCGCT	ATTGGAATC	CTGGTAGAGA	CAGTGCTACA	1500
20	AACCAATAAT	AAGAAATGGA	ACCCAGATT	TCTACCACAA	CACACTACAA	TCGCTATAGG	1560
	ACGAAATATG	ATGAAGCCAA	GACTAACCGA	TCCCAACAA	GAGGAAGTGA	ATTCTCTGGA	1620
	AAGGGTATG	TCTCCCAAT	ATCTTTAAAT	TCCACTTCCC	AACCACTCAC	TAAATTAGCC	1680
	ACAGAAAAG	ATATTTCTCT	GACTTCTCAG	ACTGTGACTG	AACCTGCCAC	TCACACTGTG	1740
	GAAGGTACTT	CAGCCTCTTT	AAATGATGGC	TCTAAAACCTG	TTCTTAGATC	TCCACATATG	1800
25	AACTTGTGCG	GGACTGACAG	ATCCTTAAAT	ACAGTTTCTA	TAACAGAATA	TGAGGAGGAG	1860
	AGTTTATTGA	CCAGTTTCAA	GCTTGATACT	GGAGTCTAAG	ATTCTTCAGG	CTCCAGTCCC	1920
	GCAACTTCTG	CTATCTCCAT	CATCTCTGAG	AACATATCCC	AAGGGTATAT	ATTTTCTCTC	1980
	GAAGAACCCAG	AGACAATAAC	ATATGATGTC	CTTATACCA	AATCTGCTAG	AAATGCTTCC	2040
	GAAGATTCAA	CTTCACTCAG	TTGAGAGAA	TCATAAAGG	ATCCTTCTAT	GGAGGGAAT	2100
30	GTGTGGTTTC	TAGCTCTAC	AGACATAACA	GCACAGCCCG	ATGTTGGATC	AGGCAGAGAG	2160
	AGCTTTCTCC	AGACTAATTA	CAGTGAGATA	CGTGTGATG	AATCTGAGAA	GACAAACCA	2220
	TCCTTTTCTG	CAGGCCCACT	GATGTACAG	GGTCCCTCAG	TTACAGATCT	GGAAATGCCA	2280
	CATTATTCTA	CCTTTGCTTA	CTTCCCAACT	GAGGTAACAC	CTCATGCTTT	TACCCCATCC	2340
	TCCAGACAA	AGGATTTGGT	CTCCACGGTC	AACGTGGTAT	ACTGCGCAGC	AACCCCAACG	2400
35	GTATACAATG	GTGAGACACC	TCTTCAACCT	TCTTACAGTA	GTGAAAGTCT	TCTCTTAGTC	2460
	ACCCCTTTGT	TGCTTGACAA	TCAGATCCTC	AACACTACCC	CTGCTGCTTC	AAGTAGTGAT	2520
	TGCGCTTGTC	ATGCTACGCC	TGATTTTCCC	AGTGTGATG	TGTCATTGTA	ATCCATCCTG	2580
	TCTTCTATG	ATGCTGACCC	TTTCTTCCA	TTTCTCTCTG	CTTCTTCTAG	TAGTGAATG	2640
	TTTCTGCTAT	TGCTACAGT	TTCTCAAATC	CTTCCCAAG	TTACTTTCAGC	TACCGAGAGT	2700
40	GATAAGGTGC	CTTGCATGTC	TTCTCTGCCA	GTGGCTGGGG	GTGATTTGCT	ATTAGAGCCC	2760
	AGCCTTGCTC	AGTATTCTGA	TGTGCTGTCC	ACTACTCATG	CTGCTTCAGA	GACGCTGGAA	2820
	TTTGTGTAGT	TCTTGTGTGT	TCTTTATAAA	ACGCTTATGT	TTTCTCAAGT	TGAACCAACC	2880
	AGCAGTGATG	CCATGATGCA	TGCACGTTCT	TCAGGGCCTG	AACCTTCTTA	TGCTTGTCT	2940
	GATAATGAGG	GCTCCCAACA	CATCTTCACT	TTTTCTTACA	GTTCGTCAAT	ACCTGTGCAT	3000
45	GATTCTGTGG	GTGTAACCTA	TCAGGGTTCC	TTATTTAGCG	GCCCTAGCCA	TATACCAATA	3060
	CCTAAGTCTT	CGTTAATAAC	CCCAACTGCA	TCATTACTGC	AGCCTACTCA	TGCCCTCTCT	3120
	GGTGATGGGG	AATGGTCTGG	AGCCTCTTCT	GATAGTGAAT	TTCTTTTACC	TGACACAGAT	3180
	GGGCTGACAG	CCCTTAACAT	TTCTTCACT	GTTCGTGATG	CTGAATTTAC	ATATACAA	3240
	TCTGTGTTTG	GTGATGATAA	TAAGGCGCTT	TCTAAAAGTG	AAATAATATA	TGGAAATGAG	3300
50	ACTGAACTGC	AAATTCCTTC	TTTCAATGAG	ATGGTTTACC	CTTCTGAAG	CACAGTCATG	3360
	CCCAACATGT	ATGATAATGT	AAATAAGTTG	AATGCGTCTT	TACAAGAAAC	CTCTGTTTCC	3420
	ATTTCTAGCA	CCAAGGGCAT	GTTTCCAGGG	TCCTTGCTCT	ATACCAACCAC	TAAGGTTTTT	3480
	GATCATGAGA	TTAGTCAAGT	TCCAGAAAAT	AACTTTTCAG	TTCAACCTAC	ACATACCTGC	3540
	TCTCAAGCAT	CTGGTGACAC	TTGCTTAA	CCTGTGCTTA	GTGCAAACTC	AGAGCCAGCA	3600
55	TCCTCTGACC	TCGCTTCTAG	TGAAATGTTA	TCTCCTTCAA	CTCAGCTCTT	ATTTTATGAG	3660
	ACCTCAGCTT	CTTTTAGTAC	TGAAGTATTG	CTACAACTT	CCTTTCAGGC	TTCTGATGTT	3720
	GACACCTTGC	TAAACCTTGC	TCTTCCAGCT	GTGCCCAGTG	ATCCAATATT	GGTTGAAACC	3780
	CCCAAGTTG	ATAAACTATG	TTCTACAATG	TTGCACTCTA	TTGTATCAAA	TTCTGCTTCA	3840
	AGTGAACACA	TGCTGCACTC	TACATCTGTA	CCAGTTTGTG	ATGTGTGCGC	TACTTCTCAT	3900
60	ATGCACTCTG	CTTCACTTCA	AGGTTTGACC	ATTTCTATG	CAAGTGAGAA	ATATGAACCA	3960
	GTTTTGTGTA	AAAGTGAAAG	TTCCCAACCA	GTGGTACCTT	CTTTGTACAG	TAATGATGAG	4020
	TTGTTCCAAA	CGGCCAATTT	GGAGATTAA	CAGGCCCATC	CCCAAAAGG	AAGGCATGTA	4080
	TTTGCTACAC	CTGTTTATC	AATGTATGAA	CCATTAAATA	CACATAATAA	TAAGCTTATA	4140
	CATTCCGATG	AAATTTTAA	CTCCACCAAA	AGTTCTGTTA	CTGGTAAGGT	ATTTGCTGGT	4200
65	ATTCCAACAG	TTGCTTCTGA	TACATTGTTA	TCTACTGATC	ATTCTGTTC	TATAGGAAAT	4260
	GGGCAATGTT	CCATTACAGC	TGTTTCTCCC	CACAGAGATG	GTTCGTGTA	CTCAACAAAG	4320
	TTGCTGTTTC	CTTCTAAGGC	AACCTCTGAG	CTGAGTCATA	GTGCCAAATC	TGATGCCGGT	4380
	TTAGTGGGTG	GTGGTGAAGA	TGGTGACACT	GATGATGATG	GTGATGATGA	TGATGATGAC	4440
	AGAGGTAGTG	ATGGCTTATC	CATTCTAAG	TGTATGTCTAT	GCTCATCTTA	TAGAGAATCA	4500
70	CAGGAAAAGG	TAATGAATGA	TTCAAGACAC	CACGAAAACA	GTCTTATGGA	TCAGAATAAT	4560
	CCAATCTCAT	ACTCACTATC	TGAGAAATCT	GAAGAAGATA	ATAGAGTCAC	AAGTGATATC	4620
	TCAGACAGTC	AAACTGGTAT	GGACAGAAGT	CCTGGTAAAT	CACCATCAGC	AAATGGGCTA	4680
	TCCCAAAAGC	ACAATGATGG	AAAAGAGGAA	AATGACATTC	AGACTGGTAG	TGCTCTGCTT	4740
	CCTCTCAGCC	CTGAATCTAA	AGCATGGGCA	GTTCGACAA	GTGATGAAGA	AAGTGGATCA	4800
75	GGGCAAGGTA	CCTCAGATAG	CCTTAATGAG	AATGAGACTT	CCACAGATT	CAGTTTGTGA	4860
	GACACTAATG	AAAAAGATGC	TGATGGGATC	CTGGCAGCAG	GTGACTCAGA	AATAACTCCT	4920
	GGATTCCCA	AGTCCCAAC	ATCATCTGTT	ACTAGCGAGA	ACTCAGAAGT	GTTCACGTT	4980
	TCAGAGGAG	AGGCCAGTAA	TAGTAGCCAT	GAGTCTCGTA	TTGGTCTAGC	TGAGGGGTTG	5040
	GAATCCGAGT	AGAAGGAGT	TATACCCCTT	GTGATCGTGT	CAGCCCTGAC	TTTTATCTGT	5100
80	CTAGTGGTTC	TTGTGGGTAT	TCTCATCTAC	TGGAGGAAAT	GCTTCCAGAC	TGCACACTTT	5160
	TACTTAGAGG	ACAGTACATC	CCCTAGAGTT	ATATCCACAC	CTCCAACACC	TATCTTTCCA	5220
	ATTTCAAGAT	ATGTCGGAGC	AATTTCAATA	AAGCACTTTC	CAAAGCATGT	TGCAGATTTA	5280
	CATGCAAGTA	GTGGGTTTAC	TGAAGAATTT	GAGACACTGA	AAGAGTTTTA	CCAGGAAGTG	5340
	CAGAGCTGTA	CTGTGTTTAC	CGGATATTACA	GCAGACAGCT	CCAACCAACC	AGACAACAAG	5400
	CACAAGAATC	GATACATAAA	TATCGTTGCC	TATGATCATA	GCAGGGTTAA	GCTAGCACAG	5460
85	CTTGCTGAAA	AGGATGGCAA	ACTGACTGAT	TATATCAATG	CCAATTATGT	TGATGGCTAC	5520
	AACAGACCAA	AAGCTTATAT	TGCTGCCCAA	GGCCCACTGA	AATCCACAGC	TGAAGATTTT	5580
	TGGAGAATGA	TATGGGAACA	TAATGTGGAA	GTATTGTGTA	TGATAACAAA	CCTCGTGAG	5640

WO 02/086443

PCT/US02/12476

5
10
15
20
25
30
35
40

```

AAAGGAAGGA GAAATGTGA TCAGTACTGG CCTGCCGATG GGAGTGAGGA GTACGGGAAC 5700
TTTCTGGTCA CTCAGAAGAG TGTGCAAGTG CTTGCCCTATT ATACTGTGAG GAATTTTACT 5760
CTAAGAAACA CAAAATAAAA AAAGGGCTCC CAGAAAGGAA GACCCAGTGG ACGTGTGGTC 5820
ACACAGTATC ACTACACGCA GTGGCCTGAC ATGGGAGTAC CAGAGTACTC CCTGCCAGTG 5880
CTGACCTTTG TGAGAAAGGC AGCCTATGCC AAGCGCCATG CAGTGGGGCC TGTGTGCTC 5940
CACTGCAGTG CTGAGAGTTG AAGAACAGGC ACATATATTG TGCTAGACAG TATGTTGCA 6000
CAGATTCAAC ACGAAGGAAC TGTCAACATA TTTGGCTTCT TAAACACAT CCGTTCACAA 6060
AGAAATTATT TGGTACAAAC TGAGGAGCAA TATGTCTTCA TTCATGATAC ACTGGTTGAG 6120
GCCATACCTA GTAAAGAAAC TGAGGTGCTG GACAGTCATA TTCATGCCTA TGTTAATGCA 6180
CTCCTCATTC CTGGACCAGC AGGCAAAACA AAGCTAGAGA AACAATTCCA GCTCCTGAGC 6240
CAGTCAATA TACAGCAGAG TGACTATTCT GCAGCCCTAA AGCAATGCAA CAGGGAAAG 6300
AATCGAATT CTCTATCAT CCTGTGGAA AGATCAAGGG TTGGCATTTC ATCCCTGAGT 6360
GGAGAAGGCA CAGACTACAT CAATGCCTCC TATATCATGG GCTATTACCA GAGCAATGAA 6420
TTCATCATTG CCCAGCACCC TCTCCTTCAT ACCATCAAGG ATTTCTGGAG GATGATATGG 6480
GACCATAATG CCCAAGTGGT GGTATGATG CTTGATGGCC AAAACATGGC AGAAGATGAA 6540
TTTGTTTACT GGCACAAATA AGATGAGCCT ATAAATTGTG AGAGCTTTAA GGTCACTCTT 6600
ATGGCTGAAG AACACAAATG TCTATCTAAT GAGGAAAAAC TTATAATTCA GGACTTTATC 6660
TTAGAAGCTA CACAGGATGA TTATGTACTT GAAGTGAGGC ACTTTCAGTG TCCTAAATGG 6720
CCAAATCCAG ATAGCCCCAT TAGTAAAACT TTTGAACTTA TAAGTGTAT AAAAGAAGAA 6780
GCTGCCAATA GGGATGGGCC CTTATGCTAT CATGATGAGC ATGAGGAGAT GACGGCAGGA 6840
ACTTCTGTG CTCTGACCAAC CCTATGCGAC CAACATAGAA AAGAAAAATC CGTGGATGTT 6900
TACCAGGTAG CCAAGATGAT CAATCTGATG AGGCAGGAG TCTTGTCTGA CATTGAGCAG 6960
TATCAGTTTC TCTACAAAGT GATCCTCAGC CTTGTGAGCA CAAGGCAGGA AGAGAATCCA 7020
TCCACCTCTC TGGACAGTAA TGGTGACGCA TTGCCTGATG GAAATATAGC TGAGAGCTTA 7080
GAGTCTTTAG TTTAACACAG AAAGGGGTGG GGGGACTCAC ATCTGAGCAT TGTTCCTC 7140
TTCTAAAAAT TAGGCAGGAA AATCAGTCTA GTTCTGTAT CTGTTGATT CCCATCACCT 7200
GACAGTAATC TTTATGACAT AGGATTCTGC CGCCAAATTT ATATCATTA CAATGTGTGC 7260
CTTTTTGCAA GACTGTATAT TTACTTATTA TGTTTGAAC AAAATGATTG AATTTTACAG 7320
TATTTCTAAG AATGGAATTG TGGTATTTT TTCTGTATTG ATTTTAACAG AAAATTTCAA 7380
TTTATAGAGG TTAGGAATTC CAAACTACAG AAAATGTTTG TTTTATGAT CAAATTTTAA 7440
GCTGTATTTG TAGCAATTC CAGGTTTGCT AGAAATATAA CTTTAAATAC AGTAGCCTGT 7500
AAATAAAACA CTCTTCCATA TGATATTCAA CATTTTACAA CTGCAGTATT CACCTAAAGT 7560
AGAAATAATC TGTACTTAT TTAAATACT GCCCTAGTGT CTCCATGGAC CAAATTTATA 7620
TTTATAATTA TAGATTTTAA TATTTTACTA CTGAGTCAAG TTTTCTAGT CTGTGTAATT 7680
GTTTAGTTTA ATGACGTAGT TCATTAGCTG GTCTTACTCT ACCAGTTTTC TGACATTGTA 7740
TTGTGTTACC TAAGTCATTA ACTTTGTTTC AGCATGTAAT TTTAACTTTT GTGGAAAAA 7800
GAAATACCTT CATTTTGAAA GAAGTTTTTA TGAGAATAAC ACCTTACCAA ACATTGTTCA 7860
AATGGTTTTT ATCCAAGGAA TTGCAAAAAT AAATATAAAT ATTGCCATTA AAAAAAAA 7920
AAAAA AAAA

```

Seq ID NO: 180 Protein sequence:
Protein Accession #: Eos sequence

45
50
55
60
65
70
75
80
85

```

1 11 21 31 41 51
MRILKRFLAC IQLLCVCRID WANGYYRQR KLVEEIGWSY TGALNQKNWG KKYPTCNSPK 60
QSPINIDEDL TQVNVNKLKL KFGGWDKTS LENTFIHNTGK TVEINLTNDY RVSGGVSEMV 120
FKASKITFFW GKCMNSSDGS EHSLEGQKFP LEMQIYCFDA DRFSSEFEAV KKGKLRALS 180
ILFEVTEEN LDFKAIIDGV ESWRFRGKA ALDPPIILLNL LPNSTDKYI YNGSLTSPPC 240
TDTVDWIVEK DTVSISESQL AVFCEVLTMQ QSGYVMLMDY LQNNFREQQY KFSRQVFSY 300
TGKEEHEAV CSSEFENVQA DPENYTSLLV TWERPRVVD TMIEKFAVLY QQLDGEDQTK 360
HEFLTDGYQD LGAILNNLLP NMSYVLQIVA ICTNGLYGY SDQLIVDMPT DNPDLDFPE 420
LIGTEELIKE EEEGKDIEEG AIVNPGRDSA TNQIRKKEPQ ISTTTHYNR GTKYNEAKTN 480
RSPTRGSEFS GKGDPVNTSL NSTSQPVTKL ATEKDISLTS QTVTELPFHT VEGTSASLND 540
GSKTVLRSPH MNLSTABSL NTVSITYEYB ESLTSTFKLD TGAEDSSGSS PATSAIPFIS 600
ENISQGYIFS SENPETITYD VLIPESARNA SEDSTSSGSE ESLKDPMSME NVWFPSSDI 660
TAQPDVGSGR ESFLQNTYTE IRVDESEKTT KSFSAGPVMS QGPSVTDLEM PHYSTFAYFP 720
TEVTPHAFTE SSRQDLVST VNVVYSQTTQ PVYNGETPLQ PSYSSEVFPL VTPLLLDNI 780
LNTTPAASSS DSALHATPVF FSVQVSFESI LSSYDGAPLL PFSSASFSSSE LFRHLHTVSQ 840
ILPQVTSATE SDKVPLHASL PVAGDILLLE PSLAQYSDVL STTHAASETL EFGSESGVLY 900
KTLMFQVPEP PSSDAMMHAR SSGPEPSYAL SDNEGSQHIF TVSYSSAIPV HDSVGVTYQG 960
LPSFGPSHIP IPKSLITPT ASLQPHAL SGDGEWSGAS SDSEFLLPDT DGLTALNIS 1020
PVSVAEFTYT TSVFGDDNKA LSKSEIIYGN ETELQIPSFN EMVYSESTV MPNMYDNVKN 1080
LNASLQETSV SISSTGKMFP GSLAHTTKV FDHEISQVPE NNFSVQPTHT VSQASGDTSL 1140
KPVLSANSE ASSDPASSEM LSPSTQLLFY ETSASFSTEV LLQPSFQASD VDTLLKTVLP 1200
AVPSDPIVLE TPKVDKISST MLHLIVNSA SSENMLRSTS VPVFDVSPTS HMHSASLQGL 1260
TISYASEKEY PVLLKSESSH QVVPSTLYND ELFTANLEI NQAHPPKGRH VFATPVLSID 1320
EPLNTLINKL IHSDEILTST KSSVTGKVFA GIFTVASDTF VSTDHSPVIG NGHVAITAVS 1380
PHRDSVTST KLLFPKATS ELSHSAKSDA GLVGGGEDGD TDDGDGDDDD DRGSDGLSIH 1440
KCMSCSYRE SQEKVMNDSD THENSMDQN NPISYSLSEN SEEDNRVTSV SSSDQTGMDR 1500
SPGKSPSANG LSQKINDGKE ENDIQTGSAL LPLSPESKAW AVLTSDSEESG SGQGTSDSLN 1560
ENETSTDFSF ADTNEKDADG ILAAGDSEIT PGFPQSPTSS VTSENSEVFH VSEAEASNS 1620
HESRIGLAEG LESEKKAIVP LVIVSALTFI CLVVLVGILI YWRKCFQTAH FYLEDSTSPR 1680
VISTPPTPIF PISDDVGAIP IKHFPKHVAD LHASSGFTEE FETLKEFYQE VQSCVLDLGI 1740
TADSSNHPDN KHKNYINIV AYDHSRVKLA QLAEKDGKLT DYINANYVDG YNRPKAYIAA 1800
QQPLKSTAE FWRMIWEHNV EVIVMITNLV EKGRKCDQY WPADGSEBYG NFLVTQKSQV 1860
VLAYYTVRNF TLRNTKIKKG SQKGRPSGRV VTQHYHTQWP DMQVPEYSLP VLTFFVKAAY 1920
AKRHAVGPV VHCASAGVRT GTYIVLDSML QQIQHEGTVN IFGLKHIRS QRNYLVQTE 1980
QYVFIHDTLV EAILSKETEV LDSHIHAYVN ALLIPGPAGK TKLEKQFQLL SQSNIQSDY 2040
SAALKQCNRE KNRTSIIIPV ERSRVGISSL SGEGETDYINA SYIMGYQYNS EPIITQHPLL 2100
HTIKDFWRMI WDHNAQLVVM IPDQNMMAED EFVYWFNKDE PINCESFKVT LMAEEHKCLS 2160
NEEKLIIQDF ILEATQDDYV LEVRHFPQCPK WPNPDSPIBK TFEILSVIKE EANRDGPMI 2220
VHDEHGGVTA GTFCALITLM HQLKENSVD VYQVARMINL MRPGVFADIE QYQFLYKVIL 2280
SLVSTRQEEN PSTSLDSNGA ALPDGNIAES LESLV

```

Seq ID NO: 181 DNA sequence
Nucleic Acid Accession #: Eos sequence

	1	11	21	31	41	51	
5	CACACATACG	CACGCACGAT	CTCACTTCGA	TCTATACACT	GGAGGATTAA	AACAAACAAA	60
	CAAAAAAAGC	ATTTCTCTCG	CTCCCCCTCC	CTCTCCACTC	TGAGAAGCAG	AGGAGCGCGA	120
	CGCGAGGGGG	CGCGAGACCG	TCTGGAAATG	CGAATCCTAA	AGCGTTTCCT	CGCTTGCAAT	180
	CAGCTCCTCT	GTGTTTGGCG	CCTGGATTGG	GCTAATGGAT	ACTACAGACA	ACAGAGAAAA	240
10	CTTGTGTAAG	AGATTGGCTG	GTCTTATACA	GGAGCACTGA	ATCAAAAAAA	TTGGGGAAAG	300
	AAATATCCAA	CATGTAATAG	CCCAAAACAA	TCTCCTATCA	ATATTGATGA	AGATCTTACA	360
	CAAGTAAATG	TGAATCTTAA	GAAACTTAAA	TTTCAGGGTT	GGGATAAAAC	ATCATTGGAA	420
	AAACACATCA	TTCATAACAC	TGGGAAAAACA	GTGGAAATTA	ATCTCACTAA	TGACTACCGT	480
	GTACGCGGAG	GAGTTTCAGA	AATGGTGTTC	AAAGCAAGCA	AGATAACTTT	TCACTGGGGA	540
15	AAATGCAATA	TGTCTATCTG	TGGATCAGAG	CATAGTTTAG	AAGGACAAAA	ATTTCCACTT	600
	GAGATGCAAA	TCTACTGCTT	TGATGCGGAC	CGATTTTCAA	GTTTTGAGGA	AGCAGTCAAA	660
	GGAAAAGGGA	AGTTAAGAGC	TTTATCCATT	TTGTTTGAGG	TTGGGACAGA	AGAAAATTTG	720
	GATTTCAAAG	CGATTATATG	TGGAGTCGAA	AGTGTTAGTC	GTTTTGGGAA	GCAGGCTGCT	780
	TTAGATCCAT	TCTACTCTGT	GAACCTTCTG	CCAAACTCAA	CTGACAAGTA	TTACATTTAC	840
20	AATGGCTCAT	TGACATCTCC	TCCCTGCACA	GACACAGTTG	ACTGGATTGT	TTTTAAAGAT	900
	ACAGTTAGCA	TCTCTGAAGG	CGAGTTGGCT	GTTTTGTGTG	AAGTCTTTAC	AATGCAACAA	960
	TCGTGTTATG	TCAATGCTAT	GGACTACTTA	CAAAACAATT	TTCGAGAGCA	ACAGTACAAG	1020
	TTCTCTAGAC	AGGTGTTTTT	CTCATACACT	GGAAAGGAAG	AGATTTCATG	AGCAGTTTGT	1080
	AGTTCAAGAA	TCTACTCTGT	TCAAGCTGAC	CCAGAGAATT	ATACCAGCTT	TCTTGTTACA	1140
25	TGGGAAGAGC	CTCGAGTCGT	TTATGATACC	ATGATTGAGA	AGTTTGCAGT	TTTGTACCAG	1200
	CAGTTGGATG	GAGAGGACCA	AAACCAAGCAT	GAATTTTGA	CAGATGGCTA	TCAAGACTTG	1260
	GGTGCTATTCT	TCAATAATTT	GCTACCCCAAT	ATGAGTTATG	TTCTTCAGAT	AGTAGCCATA	1320
	TGCATTAATG	GCTTATATGG	AAAATACAGC	GACCAACTGA	TTGTCGACAT	GCCTACTGAT	1380
	AATCTCTGAA	TCTACTCTTT	CCCTGAATTA	ATTGGAACCT	AAGAAATAAT	CAAGGAGGAG	1440
30	GAAGAGGGAA	AAGACATTGA	AGAAGGCGCT	ATTGTGAATC	CTGGTAGAGA	CAGTGTCTACA	1500
	AACCAAAATCA	GGAAAAAGGA	ACCCAGAGAT	TCTACCACAA	CACACTACAA	TCCGATAGGG	1560
	ACGAATAACA	ATGAAGCCAA	GACTAACCGA	TCCCCCAACAA	GAGGAAGTGA	ATTCTCTGGA	1620
	AAGGGTGATG	TTCCCAATAC	ATCTTTAAAT	TCCACTTCCC	AACCAAGTCA	TAAATTAGCC	1680
	ACAGAAAAAG	ATATTCTCTT	GACTCTCAG	ACTGTGACTG	AACCTGCCAC	TCACACTGCT	1740
35	GAAGGTACTT	CAGCTCTTTT	AAATGATGGC	TCTAAACTGT	TTCTTAGATC	TCCACATATG	1800
	AACCTGTGCG	GGAGCTGAGA	ATCCTTAAAT	ACAGTTTCTA	TAACAGAATA	TGAGGAGGAG	1860
	AGTTTATTGA	CGTTGATCTA	GCTTGATCTA	GGAGCTGAAG	ATTCTTCAGG	CTCCAGTCCC	1920
	GCAACTTCTG	CTATCCCAAT	CATCTCTGAG	AACATATCCC	AAGGGTATAT	ATTTTCTCTC	1980
	GAAACCCAG	ATGACATTAAC	ATATGATGTC	CTTATACCAG	AATCTGCTAG	AAATGCTTCC	2040
40	GAAGATTCAA	CTTCATCAGG	TTCAAGAGAA	TCACTAAAGG	ATCCTTCTAT	GGAGGGAAAT	2100
	GTGTGGTTTG	CTAGCTCTAC	AGACATAACA	GCACAGCCCG	ATGTTGGATC	AGGCAGAGAG	2160
	AGCTTTCTCC	AGACTTAATTA	CACGTGAGATA	CGTGTGTATG	AATCTGAGAA	GACAAACCAAG	2220
	TCCCTTTCTG	CAGGCCCACT	GATGTCAACG	GGTCCCTCAG	TTACAGATCT	GGAAATGCCA	2280
	CATTATTCTA	CCCTTGCCCT	TCTCCCAACT	GAGGTAAAC	CTCATGCTTT	TACCCCATCC	2340
45	TCCAGACAAC	AGGATTGGGT	CTCCACGGTC	AACGTGGTAT	ACTCGCAGAC	AACCCCAACCG	2400
	GTATACAATG	CAGAGGCCAG	TAATAGTAGC	CATGAGTCTC	GTATTGGTCT	AGCTGAGGGG	2460
	TTGGAATCCG	AGAAGAAGGC	AGTTATACCC	CTTGTGATCG	TGTCAGCCCT	GACTTTTATC	2520
	TGTTCTAGTGG	TTCTTGTGGG	TATTTCTATC	TACTGGAGGA	AATGCTTCCA	GACTGCACAC	2580
	TTTTACTTAG	AGGACAGTAC	ATCCCTTAGA	GTTATATCCA	CACCTCCAAC	ACCTATCTTT	2640
50	CCAATTTCTG	ATGATGTCGG	AGCAATTTCA	ATAAAGCACT	TTCCAAAGCA	TGTTGCAGAT	2700
	TTACATGCAA	GTAGTGGGTT	TACTGAAGAA	TTTGAGACAC	TGAAGAGGTT	TTACCAGGAA	2760
	GTGCAGAGCT	GTACTGTTGA	CTTAGGTATT	ACAGCAGACA	GCTCCAACCA	CCCAGACAAC	2820
	AAGCAACAAG	ATCATATCAT	AAATATCGTT	GCCTATGATC	ATAGCAGGGT	TAAGCTAGCA	2880
	CAGCTTGTCT	AAAAGGATGG	CAAACTGACT	GATTATATCA	ATGCCAATTA	TGTTGATGGC	2940
55	TACAACAGAG	CAAAAGCTTA	TATTGCTGCC	CAAGGCCCACT	TGAAATCCAC	AGCTGAAGAT	3000
	TTCTGGAGAA	TGATATGGGA	ACATAATGTG	GAAGTTATTG	TCATGATAAC	AAACCTCGTG	3060
	GAGAAAGGAA	GGAGAAAATG	TGATCAGTAC	TGGCCTGCCG	ATGGGAGTGA	GGAGTACGGG	3120
	AACCTTCTGG	TCACCTCAGAA	GAGTGTGCAA	GTGCTTGCCCT	ATTATACTGT	GAGGAATTTT	3180
	ACTCTAAGAA	ACACAAAGAA	AAAAAAGGGC	TCCCAAGAAAG	GAAGACCCAG	TGGACGTGTG	3240
60	GTACACAGCT	ATCACTACAC	GCAGTGGCCT	GACATGGGAG	TACCAGAGTA	CTCCCTGCCA	3300
	GTGCTGACCT	TTGTGAGAAA	GGCAGCCTAT	GCCAAGCGCC	ATGCAGTGGG	GCCTGTGTGT	3360
	GTCCACTGCA	GTGCTGGAGT	TGGAAGAACA	GGCACATATA	TTGTGCTAGA	CAGTATGTTG	3420
	CAGCAGATTCT	AACACGAAAG	AACCTGTCAAC	ATATTGGGCT	TCTTAAACAA	CATCCGTTCA	3480
	CAAAAGAAAT	ATTTGGTACA	AACCTGAGGAG	CAATATGTCT	TCATTCTATG	TACACTGGTT	3540
65	GAGGCCATAC	TTAGTAAAGA	AACCTGAGGAG	CTGGACAGTC	ATATTCTATG	CTATGTTAAT	3600
	GCATCTCTCA	TTCTGTGACC	AGCAGGCCAA	ACAAAGCTAG	AGAAACCAAT	CCAGCTCCTG	3660
	AGCCAGTCAA	ATATACAGCA	GAGTGACTAT	TCTGCAGCCC	TAAAGCAATG	CAACAGGGAA	3720
	ARGAATCGAA	CTTCTCTCTAT	CATCCCTGTG	GAAAGATCAA	GGGTTGGCAT	TTTATCCCTG	3780
	AGTGGAGAGG	GCACAGAGTA	CATCAATGCC	TCTTATATCA	TGGGCTATTA	CCAGAGCAAT	3840
70	GAATTCATCA	TTACCCAGCA	CCCTCTCCTT	CATACCATCA	AGGATTTCTG	GAGGATGATA	3900
	TGGGACCATTA	ATGCCCAACT	GGTGGTTATG	ATTCTGTATG	GCCAAAACAT	GGCAGAAGAT	3960
	GAATTTGTTT	ACTGCCCAAA	TAAAGATGAG	CCTATAAATT	GTGAGAGCTT	TAAGGTCACT	4020
	CTTATGGCTG	AAGAACACAA	ATGCTATATCT	AATGAGGAAA	AACCTTATAAT	TCAGGACTTT	4080
	ATCTTAGAAG	CTACACAGGA	TGATTATGTA	CTTGAAGTGA	GGCACTTTCA	GTGCTCTAAA	4140
75	TGGCCAAATC	CAGATAGCCC	CATTAGTAAA	ACTTTTGAAC	TTATAAGTGT	TATAAAAGAA	4200
	GAAGCTGCCA	ATAGGGATGG	GCCTATGATT	GTTTATGATG	AGCATGGAGG	AGTGACGGCA	4260
	GGAACTTTCT	GTGCTCTGAC	AACCTTATG	CACCAACTAG	AAAAAGAAAA	TTCCGTGGAT	4320
	GTTTACCCAG	TAGCCAAGAT	GATCAATCTG	ATGAGGCCAG	GAGTCTTTGC	TGACATTGAG	4380
	CAGTATCAGT	TTCTCTACAA	AGTGATCCTC	AGCCTTGTGA	GCACAAGGCA	GGAAGAGAA	4440
80	CCATCCACCT	CTCTGGACAG	TAATGGTGCA	GCATTTGCCG	ATGGAAATAT	AGCTGAGAGC	4500
	TTAGAGTCTT	TAGTTTAAAC	CAGAAAGGGG	TGGGGGGGAC	CACATCTGAG	CATTGTTTTC	4560
	CTCTTCTTAA	AATTAGGCAG	GAAATCAGT	CTAGTTCTGT	TATCTGTTGA	TTTCCCATCA	4620
	CCTGACAGTA	ACTTTTATGA	CATAGGATTC	TGCCGCCAAA	TTTATATCAT	TAACATGTG	4680
	TGCCTTTTTG	CAAGACTTGT	AAITTTACTTA	TTATGTTTGA	ACTAAAAATG	TTGAATTTTA	4740
85	CAGTATTTCT	AAGAAATGAA	TTGTGGTATT	TTTTTCTGTA	TTGATTTTAA	CAGAAAAATT	4800
	CAATTTATAG	AGGTTAGGAA	TTCCAAACTA	CAGAAAAATG	TTGTTTTTAG	TGTCAAATTT	4860
	TTAGCTGTAT	TTGTAGCAAT	TATCAGGTTT	GCTAGAAATA	TAACCTTTAA	TACAGTAGCC	4920
	TGTAAATAAA	ACACTCTTCC	ATATGATATT	CAACATTTTA	CAACTGCAGT	ATTCACCTAA	4980

AGTAGAAATA ATCTGTTACT TATTGTAAAT ACTGCCCTAG TGTCTCCATG GACCAAAATT 5040
 ATATTATATA TTGTAGATTT TTATATTTTA CTACTGAGTC AAGTTTCTTA GTTCTGTGTA 5100
 ATTGTTTAGT TTAATGACGT AGTTTCATTAG CTGGTCTTAC TCTACCAGTT TTCTGACATT 5160
 GTATTGTGTT ACCTAAGTCA TTAACCTTGT TTCAGCATGT AATTTTAACT TTTGTGGAAA 5220
 ATAGAAATAC CTTTATTGTT AAAGAAGTTT TTATGAGAAT AACACCTTAC CAAACATTGT 5280
 TCAAATGGTT TTTATCCAAG GAATTGCAAA AATAAATATA AATATTGCCA TTAACAAAAA 5340
 AAAAAAAAAA AAAAAAAAAA AAAAAAA

Seq ID NO: 182 Protein sequence:
 Protein Accession #: Eos sequence

1	11	21	31	41	51	
MRILKRFLAC	IQLLCVCRID	WANGYYRQQR	KLVEEIGWSY	TGALNQKNWG	KKYPTCNSPK	60
QSPINIDEDL	TOVNVNKLKL	KFGGWDKTSL	ENTFIHNTGK	TVEINLTNDY	RVS GGVS EMV	120
FKASKITFWH	GKCNMSSDGS	EHSLEGQKFP	LEMQIYCPDA	DRFSSPEEAV	KGKGLRLALS	180
ILFEVGTENG	LDFKAIIDGV	ESVSRFGKQA	ALDPFILLNL	LPNSTDKYYI	YNGSLTSPFC	240
TDTVDWIVFK	DTVHSISBSQ	AVPCEVLTMQ	QSGYVLMMDY	LQNNFREQQY	KFSRQVFSSY	300
TGKEBIHEAV	CSSEFENVQA	DPENYTSLLV	TWERPRVVDY	TMIEKFAVLV	QQLDGEDQTK	360
HEFLTDGYQD	LGAILNNLLP	NMSYVLQIVA	ICTNGLYKGY	SDQLIVDMPT	DNPELDLFPE	420
LIGTEBIIKE	EEBEGDIEEG	AIVNPGRDSA	TNQIRKKEPQ	ISTTTHYNRI	GTKYNEAKTN	480
RSPTRGSEFS	GKGDVPNTSL	NSTSQPVTKL	ATEKDISLTS	QTVTELPFHT	VEGTSASLND	540
GSKTVLRSPH	MNLGSGTAESL	NTVSITEYEE	ESLLTSFKLD	TGAEDSSGSS	PATSAIPFIS	600
ENISQGYIFS	SENPETITYD	VLIPESARNA	SEDSTSSGSE	ESLKDPSMEG	NVWFPSSTDI	660
TAQPDVGSGR	ESFQWNTYTE	IRVDESEKTT	KSPSAGPVMS	QGPSVTDLEM	PHYSTFAYFP	720
TEVTPHAFPT	SSRQDLVST	VNVVYSQTTQ	PVYNAEASNS	SHESRIGLAE	GLESEKKAVI	780
PLVIVSALTF	ICLVVLVGIL	IYWRKCFQTA	HFYLEDSTSP	RVISTPPTPI	FPISDDVGAI	840
PIKHFPKHVA	DLHASSGTEG	EPETLKEFYQ	EVQSCITVDLG	ITADSSNHDP	NKHKNRYINI	900
VAYDHSRVKL	AQLAEKDGKL	TDVINANYVD	GYNRPKAYIA	AQGPLKSTAE	DFWRMIWEHN	960
VEVIVMITNL	YKGGRRKCDQ	YWPADGSEEE	GNPLVTQKSV	QVLAYYTVRN	FTLRNTKIKK	1020
GSQKGRPSGR	VVTQYHYTQW	PDMGVPEYSL	PULTFVRKAA	YAKRHAVGPF	VVHCSAGVGR	1080
TGTYIVLDSM	QLQIQHEGTV	NIFGFLKHIR	SQRNYLVQTE	BQYVFIHDTL	VEAILSKETE	1140
VLDSHIHAYV	NALLIPGPAG	KTKLEKQFQL	LSQSNIQQSD	YSAALKQCNR	EKNRTSIIIP	1200
VERSRVGISS	LSGEGTDYIN	ASYIMGYYSQ	NEFIITQHPL	LHTIKDFWRM	IWDHNAQLVV	1260
MIPDQNMMAE	DEFYVWPNKD	EPINCESFKV	TLMAEBHKCL	SNEEKLIQD	FILEATQDDY	1320
VLEVRHFQCP	KWPNPDSFIS	KTFELISVIK	EEAANRDGFM	IVHDEHGGVT	AGTFCALITL	1380
MHQLKENSIV	DVYQVAKMIN	LMRPGVFADI	EQYQFLYKVI	LSLVSTRQEE	NPSTSLDSNG	1440
AALPDGNIAE	SLESIV					

Seq ID NO: 183 DNA sequence
 Nucleic Acid Accession #: EOS sequence
 Coding sequence: 148-4494

1	11	21	31	41	51	
CACACATACG	CACGCACGAT	CTCACTTCGA	TCTATACACT	GGAGGATTAA	AACAAACAAA	60
CAAAAAAACC	ATTTCCTTCG	CTCCCCCTCC	CTCTCCACTC	TGAGAAGCAG	AGGAGCCGCA	120
CGGCGAGGGG	CCGAGACACG	TCTGGAAATG	CGAATCCTAA	AGCGTTTCTT	CGCTTGCAAT	180
CAGCTCCTCT	TGTGTTCCCG	CCTGGATTGG	GCTAATGGAT	ACTACAGACA	ACAGAGAAAA	240
CTTGTGAAAG	AGATTGGCTG	GTCTATACAA	GGAGCACTGA	ATCAAAAAAA	TTGGGGAAAG	300
AAATATCCAA	CATGTAATAG	CCCAAAACAA	TCTCCTATCA	ATATTGATGA	AGATCTTACA	360
CAAGTAAATG	TGAATCTTAA	GAACCTTAAA	TTTCAGGGTT	GGGATAAAAC	ATCATTGGAA	420
AACACATTCA	TTCATAACAC	TGGGAAAACA	GTGGAAATTA	ATCTCACTAA	TGACTACCGT	480
GTCAGCGGAG	GAGTTTCAGA	AATGGTGTTC	AAAGCAAGCA	AGATAACTTT	TCACTGGGGA	540
AAATGCAATA	TGTCATCTGA	TGGATCAGAG	CATAGTTTAG	AAGGACAAAA	ATTTCACACT	600
GAGATGCAAA	TCTACTGCTT	TGATGCAGAC	CGATTTTCAA	GTTTGGAGGA	AGCAGTCAAA	660
GGAAAAGGGA	AGTTAAGAGC	TTTATCCATT	TTGTTTGAGG	TTGGGACAGA	AGAAAATTG	720
GATTTCAAAG	CGATTATTGA	TGGAGTCGAA	AGTGTAGTTC	GTTTGGGAA	GCAGGCTGCT	780
TTAGATCCAT	TCATACTGTT	GAACCTTCTG	CCAAACTCAA	CTGACAAAGT	TTACATTTAC	840
AATGGCTCAT	TGACATCTCC	TCCCTGCACA	GACACAGTTG	ACTGGATTGT	TTTAAAGAT	900
ACAGTTAGCA	TCTCTGAAAG	CCAGTTGGCT	GTTTCTTCTG	AAGTCTTCTT	AATGCAACAA	960
TCTGGTTATG	TGATGCTGAT	GGACTACTTA	CAAAACAATT	TTGAGAGACA	ACAGTACAAG	1020
TTCTCTAGAC	AGGTGTTTTT	CTCATACACT	GGAAAGGAAG	AGATTCATGA	AGCAGTTTGT	1080
AGTTCAGAAC	CAGAAAATGT	TCAGGCTGAC	CCAGAGAATT	ATACCAGCCT	TCTTGTTACA	1140
TGGGAAAGAC	CTCGAGTCGT	TTATGATACC	ATGATTGAGA	AGTTTGAGAT	TTGTACCAG	1200
CAGTTGGATG	GAGAGGACCA	AACCAAGCAT	GAATTTTGA	CAGATGGCTA	TCAAGACTTG	1260
GGTGCTATTG	TCAATAATTT	GCTACCCAAT	ATGAGTTATG	TTCTTCAGAT	AGTAGCCATA	1320
TGCACATAATG	GCTTATATGG	AAAATACAGC	GACCAACTGA	TTGTCGACAT	GCCTACTGAT	1380
AATCTGAAC	TTGATCTTTT	CCCTGAATTA	ATTGGAAGTG	AAGAAATAAT	CAAGGAGGAG	1440
GAAGAGGGAA	AAGACATTGA	AGAAGGCGCT	ATTGTGAATC	CTGGTAGAGA	CAGTGCTACA	1500
AACCAAAATCA	GGAAAAAGGA	ACCCAGAGAT	TCTACCACAA	CACACTACAA	TCGCRATAGG	1560
ACGAAATACA	ATGAAGCCAA	GACTAACCGA	TCCCAACAA	GAGGAAGTGA	ATTCTCTGGA	1620
AAGGGTGATG	TTCCCAATAC	ATCTTTAAAT	TCCACTTCCC	AACCAAGTCA	TAAATAGGCC	1680
ACAGAAAAAG	ATATTCTCTT	GACTTCTCAG	ACTGTGACTG	AACCTGCCAC	TCACACTGTG	1740
GAAGGTACTT	CAGGCTCTTT	AAATGATGGC	TCTAAACTGT	TTCTTAGATC	TCCACATATG	1800
AACTTGTCCG	GGACTGCGAA	ATCCTTAAAT	ACAGTTTCTA	TAACAGAAAT	TGAGGAGGAG	1860
AGTTTATTGA	CCAGTTTCAA	GCTTGATACT	GGAGCTGAAG	ATTCTTCAGG	CTCCAGTCCC	1920
GCAACTTCTG	CTATCCCAAT	CATCTCTGAG	AACATATCCC	AAGGGTATAT	ATTTTCTCTC	1980
GAAAACCCAG	AGACAATAAC	ATATGATGTC	CTTATACCAG	AATCTGCTAG	AAATGCTTCC	2040
GAAGATTCAA	CTTCATCAGG	TTTCAAGGAA	TCACTAAAGG	ATCCTTCTAT	GGAGGGAAT	2100
GTGTGGTTTC	CTAGCTCTAC	AGACATAACA	GCACAGCCCG	ATGTTGGATC	AGGCAGAGAG	2160
AGCTTCTCTC	AGCTAATTA	CACCTGAGATA	CGTGTGATG	AATCTGAGAA	GACAAACCAA	2220
TCCTTTCTCT	CAGGCCCACT	GATGTACAG	GGTCCCTCAG	TTACAGATCT	GGAAATGCCA	2280
CATTATTCTA	CCTTTGCCTA	CTTCCCAACT	GAGGTAACAC	CTCATGCTTT	TACCCCATCC	2340
TCCAGACAA	AGGATTGGT	CTCCACGGTC	AACGTGGTAT	ACTCGCAGAC	AACCAACCG	2400
GTATACAAATG	AGGCCAGTAA	TAGTAGCCAT	GAGTCTCGTA	TTGGTCTAGC	TGAGGGGTG	2460

5	GAATCCGAGA AGAAGGCAGT TATACCCCTT GTGATCGTGT CAGCCCTGAC TTTTATCTGT 2520
	CTAGTGGTTC TTGTTGGTAT TCTCATCTAC TGGAGGAAAT GCTTCCAGAC TGCACACTTT 2580
	TACTTAGAGG ACAGTACATC CCCTAGAGTT ATATCCACAC CTCCCAACACC TATCTTTCCA 2640
	ATTTAGAGT ATGTCGAGC AATTCCAATA AAGCACTTTC CAAAGCATGT TGCAGATTTA 2700
	CATGCAAGTA GTGGGTTTAC TGAAGAATTT GAGGAAGTGC AGAGCTGTAC TGTGACTTA 2760
	GGTATTACAG CAGACAGCTC CAACCAACCA GACAACAAGC ACAAGAAATCG ATACATAAAT 2820
	ATCGTTGCCT ATGATCATAG CAGGGTTAAG CTAGCACAGC TTGCTGAAAA GGATGGCAAA 2880
	CTGACTGATT ATATCAATGC CAATTATGTT GATGGCTACA ACAGACCAAA AGCTTATATT 2940
10	GCTGCCAAG GCCCACTGAA ATCCACAGCT GAAGATTTCT GGAGAAATGAT ATGGGAACAT 3000
	AATGTGGAAG TTATGTTCAT GATAACAAAC CTCGTGGAGA AAGGAAGGAG AAAATGTGAT 3060
	CAGTACTGGC CTGCCGATGG GAGTGAGGAG TACGGGAAC TCTGGTCAC TCAGAGAGT 3120
	GTGCAAGTGC TTGCCTATTA TACTGTGAGG AATTTTACTC TAAGAAACAC AAAAATAAAA 3180
	AAGGGCTCCC AGAAGGAAG ACCCAGTGGG CGTGTGGTCA CACAGTATCA CTACACGCAG 3240
	TGGCTTGACA TGGGAGTACC AGAGTACTCC CTGCCAGTGC TGACCTTTGT GAGAAAGGCA 3300
15	GCCTATGCCA AGCCCATGTC AGTGGGGCCT GTTGTCTGCC ACTGCAGTGC TGGAGTTGGA 3360
	AGAACAGGCA CATATATTGT GCTAGACAGT ATGTTGCAGC AGATTCAACA CGAAGGAACT 3420
	GTCAACATAT TTGGCTTCTT AAAACACATC CGTTCACAAA GAAATTATTT GGTACAACT 3480
	GAGGAGCAAT ATGTCTTCAT TCATGATACA CTGGTTGAGG CCATACCTAG TAAAGAACT 3540
20	GAGGTGCTGG ACAGTCTATAT TCATGCCTAT GTTAATGCAC TCCTCATTCG TGGACAGCA 3600
	GGCAAAACAA AGCTAGAGAA ACAATCCAG CTCCTGAGCC AGTCAAATAT ACAGCAGAGT 3660
	GACTATTCTG CAGCCCTAAA GCAATGCAAC AGGGAAGAAG ATCGAACTTC TTCTATCATC 3720
	CCTGTGAAAA GATCAAGGGT TGGCATTTCA TCCCTGAGTG GAGAAGGCAC AGACTACATC 3780
	AATGCCTCCT ATATCATGGG CTATTACCAG AGCAATGAAT TCATCATTAC CCAGCACCTC 3840
25	CTCCTTCATA CCCTGATGGG TTCTGGAGG ATGATATGGG ACCATAATGC CCAACTGGTG 3900
	GTATGATTC CTGATGGCCA AAACATGGCA GAAGATGAAT TTGTTTACTG GCCAAATAAA 3960
	GATGAGCCTA TAAATTGTGA GAGCTTTAAG GTCACCTTTC TGGCTGAAGA ACACAAATGT 4020
	CTATCTAATG AGGAAAAACT TATAATTCAG GACTTTATCT TAGAAGCTAC ACAGGATGAT 4080
	TATGTACTTG AAGTGAGGCA CTTCAGTGT CCTAAATGGC CAAATCCAGA TAGCCCCATT 4140
30	AGTAAACTTT TTGAACTTAT AAGTGTATATA AAAGAAGAAG CTGCCAATAG GGATGGGGCT 4200
	ATGATTGTTT ATGATGAGCA TGGAGGAGTG ACGGCAGGAA CTTTCTGTGC TCTGACAAAC 4260
	CTTATGCACC AACTAGAAAA AGAAATTTCC GTGGATGTTT ACCAGGTAGC CAAGATGATC 4320
	AATCTGATGA GGCCAGGAGT CTTTGTCTGAC ATTGAGCAGT ATCAGTTTCT CTACAAAGTG 4380
	ATCCTCAGCC TTGTGAGCAC AAGGCAGGAA GAGAATCCAT CCACCTCTCT GGACAGTAAT 4440
35	GGTGAGCAT TTGCTGATGG AATATAGCT GAGAGCTTAG AGTCTTTAGT TTAACACAGA 4500
	AAGGGGTGGG GGGACTCACA TCTGAGCATT GTTTTCTCTC TCCTAAATTT AGGCAGGAAA 4560
	ATCAGTCTAG TCTGTATTC GTTGTATTC CCATCACCTG ACAGTAACCT TCATGACATA 4620
	GGATTCTGCC GCCAAATTTA TATCATTAA AATGTGTGCC TTTTGTCAAG ACTTGTAAAT 4680
	TACTTATTAT GTTTGAACATA AAATGATTGA ATTTTACAGT ATTTCTAAGA ATGGAATTGT 4740
40	GGTATTTTTT TCTGTATTGA TTTTAACAGA AAATTTCAAT TTATAGAGGT TAGGAATTTC 4800
	AAACTACAGA AAATGTTTGT TTTTAGTGTC AAATTTTAG CTGTATTGT AGCAATTATC 4860
	AGGTTTGACA GCAATGAATT TTTTAATACA GTAGCCTGTA AATAAACAC TCTTCCATAT 4920
	GATATTCAAC ATTTTACAAC TGCAGTATTC ACCTAAAGTA GAAATAATCT GTTACTTATT 4980
	GTAAATACCT CCCTAGTGTC TCCATGGACC AAATTTATAT TTATAATTGT AGATTTTTAT 5040
45	ATTTTACTAC TGTCTAAGT TTTCTAGTTC TGTGTAATTG TTTAGTTTAA TGACGTAGTT 5100
	CATTAGCTGG TCTTACTCTA CCAAGTTTCT GACATTGTAT TGTGTTACCT AAGTCATTAA 5160
	CTTTGTTTCA GCAATGAATT TTAACITTTG TGGAAAATAG AAATACCTTC ATTTTGAAAG 5220
	AAGTTTTTAT GAGAAATAAC CCTTACCAAA CATTTGTTCAA ATGTTTTTTA TCCAAGGAAT 5280
50	TGCAAAAATA AATATAATA TTGCCATTAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 5340
	AAA

Seq ID NO: 184 Protein sequence:
Protein Accession #: EOS sequence

55	1 11 21 31 41 51	MRILKRFLAC IQLLCVCRLD WANGYYRQQR KLVEEIGWSY TGALEQKNWG KKYPTCNSPK 60
		QSPINIDEDL TQVNVNKKL KPGWDKTSI ENTFIHNTGK TVEINLTNDY RVSGGVSEMV 120
		FKASKITFHW GKCMNSDGS EHSLEGKFP LEMQIYCPDA DRFSSFEAV KKGKLRALS 180
60		ILFEVGTEN LDFKAIIDGV ESVSFRGKQA ALDPPILLNL LPNSTDKYYI YNGSLTSPPC 240
		TDVVDWIVFK DTVSISESQI AVFCEVLTMQ QSGYVLMQDY LQNNFREQQY KFSRQVSSY 300
		TGKEEIHFAV CSSEFENVQA DPENYTSLLV TWERPRVVD TMIEKFAVLV QQLDGEDQTK 360
		HEFLTQGYQD LGAILNNLLP NMSYVLQIVA ICTNGLYGY SDQLIVDMPT DNFELDLFPE 420
		LIGTEEIKE EEEGKDIEEG AIVNPGRDSA TNQIRKKEPO ISTTHYNRI GTKYNEAKTN 480
65		RSPTRGSEPS GKGDVPNTSL NSTSQPVTKL ATEKDISLTS QTVTELPHT VEGTSASLND 540
		GSKTVLRSFH MNLSTAESL NTVSITEYEE ESLLTSFKLD TGAEDSSGSS PATSAIPFIS 600
		ENISQGYIFS SENPETITYD VLIPESARNA SEDSTSSGSE ESLKOPSMEG NVWPPSTDI 660
		TAPQDVGSGR ESFLQNTYTE IRVDESEKTT KSFSAGPVM QGPSVTDLEM PHYSTFAYFP 720
		TEVTPHAFPT SSRQDLVST VNVVYSQTTQ PVYNEASNS HESRIGLAEG LESEKKAVIP 780
70		LVIIVSALTFI CLVVLVGLI YWRKCFQTAH FYLEDSTSPR VISTPPTPI PISDDVGAIP 840
		IKHFPKHVAD LHASSGFTFE FEEVQSCVTD LGITADSSNH PDNKHKNRYI NIVAYDHSRV 900
		KLAQLAEKDG KLTIDYINANY VDGYNRPKAY IAAQGLPKST AEDFWRMIWE HNVEIVMIT 960
		NLVEKGRKRC DQYWPADGSE EYGNFLVTQK SVQVLAYTV RNFTLRNTKI KKGSGKGRPS 1020
		GRVVTQYHYT QWPDGVPYV SLFVLTFVRK AAYAKRHAVG PVVHCSAGV GRTGTIVLD 1080
75		SMLQQIQHEG TVNIFGFLKH IRSQRNYLVQ TEEQVVFHID TLVEAILSKE TEVLDSHIHA 1140
		YVNALLIPGP AGKTKLEKQF QLLSQSNIQQ SDYSALKQC NREKQRTSSI IPVERSRVGI 1200
		SSLSGEGTDF INASYIMGYI QSNFIIITQH PLLHTIKDFW RMIWDHNAQL VVMIPDQGNM 1260
		AEDEFVYWN KDEPINCBSF KVTLMABEHK CLSNEEKLI QDFILEATQD DVVLEVRHFQ 1320
		CPKWNPDSP ISKTFELSV IKEEAANRDG PMIVHDEHGG VTAGTFCAL TLMHOLEKEN 1380
80		SVDVYQVAKM INLMRPGVFA DIEQYQFLYK VILSLVSTRQ EENPSTSLDS NGAALPDGNI 1440
		AESLESV

Seq ID NO: 185 DNA sequence
Nucleic Acid Accession #: EOS sequence
Coding sequence: 501-4514

85	1 11 21 31 41 51
----	------------------

	CACACATACG	CACGCACGAT	CTCAGCTCGA	TCTATACACT	GGAGGATTAA	AACAAACAAA	60
	CAAAAAAAC	ATTTCTCTCG	CTCCCCCTCC	CTCTCCACTC	TGAGAAGCAG	AGGAGCCGCA	120
5	CGGCGAGGGG	CGCGAGACCG	TCTGGAAATG	CGAATCCTAA	AGCGTTTCTC	CGCTTGCATT	180
	CAGCTCCTCT	GTGTTTGCCG	CCTGGATTGG	GCTAATGGAT	ACTACAGACA	ACAGAGAAAA	240
	CTTGTTGAAG	AGATTGGCTG	GTCTATACA	GGAGCACTGA	ATCAAAAAAT	TGGGGAAGA	300
	AATATCCAAC	ATGTAATAGC	CCAAAACAAT	CTCCTATCAA	TATTGATGAA	GATCTTACAC	360
	AAGTAAATGT	GAATCTTAAG	AAACTTAAAT	TTCAGGGTTG	GGATAAAACA	TCATTGGAAA	420
10	ACACATTTCAT	TCATAACACT	GGGAAAAACAG	TGGAAATTAA	TCTCACTAAT	GACTACCGTG	480
	TCAGCGGAGG	AGTTTCAGAA	ATGGTGTTTA	AAGCAAGCAA	GATAACTTTT	CACTGGGGAA	540
	AATGCAATAT	GTCACTCGAT	GGATCAGAGC	ATAGTTTAGA	AGGACAAAAA	TTTCCACTTG	600
	AGATGCAAAAT	CTACTGCTTT	GATGCGGACC	GAITTTCAAG	TTTTGAGGAA	GCAGTCAAAG	660
	GAAAAGGGAA	GTTAAGAGCT	TTATCCATT	TGTTTGAGGT	TGGGACAGAA	GAAAATTGG	720
15	ATTTCAAAGC	GATTATTGAT	GGAGTCGAAA	GTGTTAGTCG	TTTTGGGAAG	CAGGCTGCTT	780
	TAGATCCATT	CATCTGTGTG	AACCTTCTGC	CAAACTCAAC	TGACAAGTAT	TACATTTACA	840
	ATGGCTCATT	GACATCTCCT	CCCTGCACAG	ACACAGTTGA	CTGGATTGTT	TTTAAAGATA	900
	CAGTTAGCAT	CTCTGAAAGC	CAGTTGGCTG	TTTTTTGTGA	AGTTCTTACA	ATGCAACAAT	960
	CTGTTTATGT	TATGCTGATG	GACTACTTAC	AAAACAATTT	TCGAGAGCAA	CAGTACAAAT	1020
20	TCTCTAGACA	GGTGTTTTCC	TCATACACTG	GAAAGGAAGA	GATTTCATGAA	GCAGTTTGTG	1080
	GTTTCAGAAC	AGAAAAATGTT	CAGGCTGACC	CAGAGAATTA	TACCAAGCCTT	CTTGTTTACAT	1140
	GGGAAAGACC	TCGAGTCGTT	TATGATACCA	TGATTGAGAA	GTTTGCAAGT	TTGTACCAGC	1200
	AGTTGGATGG	AGAGGACCAA	ACCAAGCATG	AATTTTTGAC	AGATGGCTAT	CAAGACTTGG	1260
	GTGCTATTCT	CAATAAATTTG	CTACCCAATA	TGAGTTATGT	TCTTCAGATA	GTAGCCATAT	1320
	GCCTAATGG	CTTATAATGGA	AAATACAGCG	ACCAACTGAT	TGTCGACATG	CCTACTGATA	1380
25	ATCCTGAAC	TGATCTTTTC	CCTGAATTAA	TGGAACATGA	AGAAATAATC	AAGGAGGAGG	1440
	AAGAGGGAAA	AGACATTGAA	GAAGGCGCTA	TTGTGAATCC	TGGTAGAGAC	AGTGTACAA	1500
	ACCAAATCAG	GAAAAAGGAA	CCCCAGATTT	CTACCAACAAC	ACACTACAAT	CGCATAGGGA	1560
	CGAAATACAA	TGAAGCCAAAG	ACTAACCGAT	CCCCAACAAAG	AGGAAGTGAA	TTCTCTGGAA	1620
	AGGGTGATGT	TCCCAATACA	CTTTTAAAT	CCACTTCCCA	ACCACTCACT	AAATTAGCCA	1680
30	CAGAAAAAGA	TATTTCTCTG	ACTTCTCAGA	CTGTGACTGA	ACTGCCACCT	CACACTGTGG	1740
	AAGGTACTTC	AGCCTCTTTA	AATGATGGCT	CTAAAAGTGT	TCTTAGATCT	CCACATATGA	1800
	ACTTGTGCGG	GACTTCCAGAA	TCTTTAAATA	CAGTTTCTAT	AACAGAAATAT	GAGGAGGAGA	1860
	GTTTATTGAC	CAGTTTCAAG	CTTGATACTG	GAGCTGAAGA	TTCTTCAGGC	TCCAGTCCCG	1920
	CAACTTCTGC	TATCCCATTC	ATCTCTGAGA	ACATATCCCA	AGGGTATATA	TTTTCTCCG	1980
35	AAAACCCAGA	GACATAACCA	TATGATGTCC	TTATACCAGA	ATCTGTCTAGA	AATGCTTCCG	2040
	AAGATTCAAC	TTCACTAGGT	TCAGAAGAAT	CACATAAGGA	TCTTCTATG	GAGGGAAATG	2100
	TGTGGTTTCC	TAGCTCTACA	GACATAACAG	CACAGCCCGA	TGTTGGATCA	GGCAGAGAGA	2160
	GCCTTTCTCCA	GACTAATTAC	ACTGAGATAC	GTGTTGATGA	ATCTGAGAAG	ACAACCAAGT	2220
40	CCTTTTCTGC	AGGCCCAAGT	ATGTCCACAG	GTCCCTCAGT	TACAGATCTG	GAAATGCCAC	2280
	ATTATTTCTAC	CTTTGCCCTC	TTCCCAACTG	AGGTAACACC	TCATGCTTTT	ACCCCATCCT	2340
	CCAGACAACA	GGATTGTGTC	TCCACGGTCA	ACGTGGTATA	CTCGCAGACA	ACCCCAACGG	2400
	TATACAATGA	GAAGGCAGTT	ATACCCCTTG	TGATCGTGTC	AGCCCTGACT	TTTATCTGTC	2460
	AATCCGAGAA	GAAGGCAGTT	ATACCCCTTG	TGATCGTGTC	AGCCCTGACT	TTTATCTGTC	2520
45	TAGTGGTTCT	TGTGGGTATT	CTCATCTACT	GGAGGAAATG	CTTCCAGACT	GCACACTTTT	2580
	ACTTAGAGGA	CAGTACATCC	CCTAGAGTTA	TATCCACACC	TCCAACACCT	ATCTTTCCAA	2640
	TTTCAGATGA	TGGGTTTACT	GAAGAATTTG	AGACACTGAA	AGAGTTTAC	CAGGAAGTGC	2700
	ATGCAAGTAG	TGTTGACTTA	GGTATTACAG	CAGACAGCTC	CAACCAACCA	GACAAACAGC	2760
	AGAGCTGTAG	TGTTGACTTA	GGTATTACAG	CAGACAGCTC	CAACCAACCA	GACAAACAGC	2820
50	ACAGAATCG	ATACATAAAT	ATCGTTGCC	ATGATCATAG	CAGGGTTAAG	CTAGCACAGC	2880
	TTGCTGAAAA	GGATGCTAAA	CTGACTGATT	ATATCAATGC	CAATTATGTT	GATGGCTACA	2940
	ACAGACCAAA	AGCTTATATT	GCTGCCCAAG	GCCCCACTGA	ATCCACAGCT	GAAGATTTCT	3000
	GGAGAATGAT	ATGGGAACAT	AATGTGGAAG	TTATTGTGAT	GATAACAAAC	CTCGTGGAGA	3060
	AAGGAAGGAG	AAAATGTGAT	CAGTACTGTC	CTGCCGATGG	GAGTGAGGAG	TACGGGAAGT	3120
55	TTCTGGTCA	TCAGAGAGAT	GTGCAAGTGC	TTGCCCTATTA	TACTGTGAGG	AATTTTACTC	3180
	TAAAGAACAC	AAAAATAAAA	AAGGGCTCCC	AGAAAGGAAG	ACCCAGTGA	CGTGTGGTCA	3240
	CACAGTATCA	CTACAGCGAG	TGGCCTGACA	TGGGAGTACC	AGAGTACTCC	CTGCCAGTGC	3300
	TGACCTTTGT	GAGAAAGGCA	GCCTATGCCA	AGCGCCATGC	AGTGGGGCCT	GTGTGCTGCC	3360
	ACTGCAGTGC	TGGAGTTGGA	AGAACAGGCA	CATATATTGT	GCTAGACAGT	ATGTTGCAGC	3420
60	AGATTCAACA	CGAAGGAATC	GTCAACATAT	TTGGCTTCTT	AAAAACATC	CGTTTCAAAA	3480
	GAAATATTAT	GGTACAAACT	GAGGAGCAAT	ATGCTTTCAT	TCATGATACA	CTGGTTGAGG	3540
	CCATACTTAG	TAAAGAAACT	GAGGTGCTGG	ACAGTCATAT	TCATGCCCTAT	GTTAATGCAC	3600
	TCCTCATTC	TGGACCAGCA	GGCAAAACAA	AGCTAGAGAA	ACAATTCAG	CTCCTGAGCC	3660
	AGTCAAAAT	ACAGCAGAGT	GACTATTCTG	CAGCCCTAAA	GCAATGCAAC	AGGGAAAAAG	3720
	ATCGAACTTC	TTCTATCATC	CCTGTGGAAA	GATCAAGGGT	TGGCATTTC	TCCCTGAGTG	3780
65	GAGAAGGCAC	AGACTACATC	AATGCCTCCT	ATATCATGGG	CTATTACCAG	AGCAATGAAT	3840
	TCATCATTAC	CCAGCAACCT	CTCCTTCATA	CCATCAAGGA	TTTCTGGAGG	ATGATATGGG	3900
	ACCATAATGC	CCAATGTTG	GTTATGATTC	CTGATGGCCA	AAACATGGCA	GAAGATGAAT	3960
	TTGTTTACTG	GCCAAATAAA	GATGAGCCTA	TAAATTGTGA	GAGCTTTAAG	GTCACTCTTA	4020
70	TGGCTGAAGA	ACACAAATGT	TATGTAATG	AGGAAAAACT	TATAATTGAG	GACTTTATCT	4080
	TAGAAGCTAC	ACAGGATGAT	TATGTAATG	AGGAAAAACT	TATAATTGAG	GACTTTATCT	4140
	CAAAATCCAGA	TAGCCCCATT	AGTAAAACTT	TTGAACTTAT	AAGTGTATTA	AAAGAAAGAG	4200
	CTGCCAATAG	GGATGGGCCCT	ATGATTGTTT	ATGATGAGCA	TGGAGGAGTG	ACGCCAGGAA	4260
	CTTTCTGTGC	TCTGCAACCC	CTTATGACCC	AACTAGAAAA	AGAAAATTCC	GTGGATGTTT	4320
75	ACCAGGTAGC	CAAGATGATC	AATCTGATGA	GGCCAGGAGT	CTTTGCTGAC	ATTGAGCAGT	4380
	ATCAGTTTCT	CTACAAAGTG	ATCCTCAGCC	TTGTGAGCAC	AAGGCAGGAA	GAGAAATCCAT	4440
	CCACCTCTCT	GGACGTAAT	GGTGACGAT	TGCCTGATGG	AAATATAGCT	GAGAGCTTAG	4500
	AGTCTTTAGT	TAAACACAGA	AAGGGGTGGG	GGGACTCACA	TCTGAGCATT	GTTTTCTCTT	4560
	TCCTAAAAAT	AGGCAGGAAA	ATCAGTCTAG	TTCTGTTATC	TGTTGATTTC	CCATCACTTG	4620
80	ACAGTAACCT	TCATGACATA	GGATTCTGCC	GCCAAATTTA	TATCATTAA	AATGTGTGCC	4680
	TTTTTGCAAG	ACTTGTAAAT	TACTTATTAT	GTTTGAACCT	AAATGATTGA	ATTTTACAGT	4740
	ATTTCTAAGA	ATGGAATTTG	GGTATTTTTT	TCTGTATTGA	TTTTAACAGA	AAATTTCAAT	4800
	TTATAGAGGT	TAGGAATTTCC	AAACTACAGA	AAATGTTTGT	TTTTAGTGTG	AAATTTTATG	4860
	CTGTATTGTT	AGCAATTTAT	AGGTTTGCTA	GAAATATAAC	TTTTAATACA	GTAGCCGTGA	4920
	AATAAAACAC	TCTTCCATAT	GATATTCAAC	ATTTTACAAC	TGCAGTATTC	ACCTAAAGTA	4980
85	GAAATAATCT	GTTACTTATT	GTAAATACCT	CCCTAGTGTG	TCCATGGACC	AAATTTATAT	5040
	TTATAATTGT	AGATTTTTAT	ATTTTACTAC	TGAGTCAAGT	TTTCTAGTTC	TGTGTAATTG	5100
	TTTAGTTTAA	TGACGTAGTT	CATTAGCTGG	TCTTACTCTA	CCAGTTTCTT	GACATTGTAT	5160

WO 02/086443

PCT/US02/12476

TGTGTTACCT AAGTCATTA CTTTGTTC CA GCATGTAATT TTAACCTTTG TGGAAATAG 5220
 AAATACCTTC ATTTTGAAAG AAGTTTTTAT GAGAATAACA CCTTACCAA CATTTGTC AA 5280
 ATGTTTTTTA TCCAAGGAAT TCAAAAAATA AATATAAATA TTGCCATTAA AAAAAAATA 5340
 AAAAAAATA AAAAAAATA AAA

5

Seq ID NO: 186 Protein sequence:
 Protein Accession #: EOS sequence

10 1 11 21 31 41 51
 MVFKASKITP HWGKCNMSSD GSEHSLEGQK FPLEMQIYCF DADRFSSFE AVKGKGLRA 60
 LSILFEVGTB ENLDFKAIID GVESVSRFGK QALDPPFILL NLLPNSTDKY YIYNGSLTSP 120
 PCTDTVDWIV FKDTVSISES QLAVFCEVLT MQQSGYVMLM DYLNQNFREQ QYKFSRQVFS 180
 15 SYTGKEEIEH AVCSSEPEPV QADPENYTSI LVTWERPRV YDTMIEKFAV LYQQLDGEDQ 240
 TKHEFLTGGY QDGLAILNNL LPNMSYVLQI VAITCNGLYG KYSDQLIVDM PTNPELDF 300
 PELIGTEBII KEBEEGKDIE EGAIIVNPGRD SATNQIRKKE PQISTTTHYN RIGTKYNEAK 360
 TNRSPTRGSE FSGKGDVPNT SLNSTSQPV T KLATEKDLS TSQVTLELTP HTVEGTSASL 420
 NDGSKTVLRS PHMNLSTGAE SLMTVSITEY EESLSTSFK LDTGAEDSSG SSPATSAIPP 480
 20 ISENIQGYI FSSSENPETIT YDVLIPESAR NASEDSTSSG SEESLKDPSM EGMVNFPSST 540
 DITAQPDVGS GRESFLQNTY TEIRVDESEK TTKSFSAGPV MSQGPSVTDL EMPHYSTFAY 600
 PFTEVTPHAF TPSSRQQLDV STVNVSYSQT TQPVYNEASN SSHESTRIGLA EGLESEKKAV 660
 IPLVIVSALT FICLVVLVGI LIYWRKCFQT AHFYLEDSTS PRVISTPPTP IFPIISDDVGA 720
 IPIKHFPKHV ADLHASSGTA EEFETLKEFY QEVQSCVLDL GITADSNHNP DNKHKNRYIN 780
 25 IVAYDHSRVK LAQLAEKDGK LTDYINANYV DGYNRPKAYI AAQGPLKSTA EDFWRMIWEH 840
 NVEVIVMITN LVEKGRKRC D QYWPADGSEB YGNFLVTQKS VQVLAYYTVR NFTLRNTKIK 900
 KGSQKGRPSG RVETQYHYTQ WPDMDGVPEYS LPVLTFFVRKA AYAKRHAVGP VVVHCSAGVG 960
 RTGTYIVLDS MLQIQHEGT VNIFFGLKHI RSQRNYLVQT EEQYVFIHDT LVBAILSKET 1020
 EVLDSHIAHY VNALLIPGA KTKLEKQFO LLSQGNIQSS DYSALKQCN REKNRTSSII 1080
 30 PVERSRVGIS SLSEGEGDYI NASYIMGYQ SNEFIITQHP LLHTIKDFWR MIWDHNAQLV 1140
 VMIPDQNMCA EDEFVYWPNK DEPINCESFK VTLMAEEHKC LSNEEKLIQ DFIEATQDD 1200
 YVLEVRHFQC PKWPNPDSPI SKTFELISVI KEEAANRDGP MIVHDEHGGV TAGTFCALTT 1260
 LMHQLKENS VDVYQVAKMI NLMRPGVFAD IEQYQFLYKV ILSLVSTRQE ENPSTSLDSN 1320
 GAALPDGNIA ESLBSLV

35

Seq ID NO: 187 DNA sequence
 Nucleic Acid Accession #: EOS sequence
 Coding sequence: 148-4632

40 1 11 21 31 41 51
 CACACATACG CACGCACGAT CTCACCTCGA TCTATACACT GGAGGATTAA AACAAACAAA 60
 CAAAAAATAC ATTTCCCTCG CTCCTCCCTCC CTCTCCACTC TGAGAAGCAG AGGAGCCGCA 120
 CGGCGAGGGG CCGCAGACCG CTCGGAATG CGAATCCTAA AACGTTTCCT CGCTTGCAAT 180
 45 CAGCTCCTCT GTGTTTCCCG CTTGGATTGG GCTAATGGAT ACTACAGACA ACAGAGAAAA 240
 CTTGTTGAAG AGATTGGCTG GTCCCTATACA GGAGCACTGA ATCAAAAAA TTGGGGAAAG 300
 AAATATCCAA CATGTAATAG CCCAAACAAA TCTCCTATCA ATATTGATGA AGATCTTACA 360
 CAAGTAAATG TGAATCTTAA GAAACTTAAA TTTCAGGGTT GGGATAAAAC ATCATTTGAA 420
 AACACATTCG TGCATTAACAC GTGGAAAAACA ATCTCACTAA TGACTACCGT 480
 50 GTCAGCGGAG GAGTTTCAGA AATGGTGTIT AAAGCAAGCA AGATAACTTT TCACTGGGGA 540
 AAATGCAATA TGTCATCTGA TGGATCAGAG CATAGTTTAG AAGGACAAA ATTTCCACTT 600
 GAGATGCAAA TCTACTGCTT TGATGCGGAC CGATTTCCTA GTTTTGAGGA AGCAGTCAAA 660
 GGAAAAGGGA AGTTAAGAGC TTTATCCATT TTGTTTGAGG TTGGGACAGA AGAAAATTGT 720
 GATTTCAAGC CGATTATTGA TGGAGTCCGA AGTGTATGTC GTTTTGAGGA CGAGGCTTGT 780
 55 TTAGATCCAT TCATACTGTT GAACCTTCTG CCAAACTCAA CTGACAGTA TTACATTTAC 840
 AATGGCTCAT TGACATCTCC TCCCTGCACA GACACAGTTG ACTGGATTGT TTTTAAAGAT 900
 ACAGTTAGCA TCTCTGAAAG CCAGTTGGCT GTTTTTTGTG AAGTCTTAC AATGCAACAA 960
 TCTGTTATG TCATGCTGAT GGACTACTTA CAAAACAATT TTCGAGAGCA ACAGTACAG 1020
 TTCTCTAGAC AGGTGTTTTC TCATACACT GGAAGGAAG AGATTCTATG AGCAGTTGT 1080
 60 AGTTCAAGAC CAGAAAATG TCAGGCTGAC CCAGAGAATT ATACCAGCT TCTTGTATCA 1140
 TGGAAAGAGC CTCAGTCTGT TTATGATACC ATGATTGAGA AGTTTGCACT TTTGTACCAG 1200
 CAGTTGGATG GAGAGGACCA AACCAAGCAT GAATTTTGA CAGATGGCTA TCAAGACTTG 1260
 GGTGCTATTC TCAATAATTT GCTACCCAAT ATGAGTTATG TTCTTCAGAT AGTAGCCATA 1320
 TGCATAATG GCTTATATGG AAAATACAGC GACCAACTGA TTGTCCAGAT GCCTACTGAT 1380
 65 AATCCTGAAC TTGATCTTTT CCCTGAATTA ATTGGAACAG AAGAAATAAT CAAGGAGGAG 1440
 GAAGAGGGAAT TACATTTGA AGAAGGCGCT ATTGTGAATC CTGGTAGAGA CAGTGCTACA 1500
 AACCAATCA GGAAGGAAG ACCCCAGATT TCTACCACAA CACACTACAA TCGCATAGGG 1560
 ACGAATACAA ATGAAGCCAA GACTAACCGA TCCCAACAAA GAGGAAGTGA ATTCTCTGGA 1620
 AAGGCTGATG TTCCCAATAC ATCTTTAAAT TCCACTTCCC AACCACTCAC TAAATTAGCC 1680
 70 ACAGAAAAAG ATATTTCTTT GACTTCTCAG ACTGTGACTG AACTGCCACC TCACACTGTG 1740
 GAAGGTACTT CAGCTTCTTT AAATGATGGC TCTAAAACAG TTCTTAGATC TCCCATATG 1800
 AACTTGTCTG GACTGTCAGA ATCTTAAAT ACAGTTCTTA TAACAGAATA TGAGGAGGAG 1860
 AGTTTATGTA CAGTTTTCAG GCTTGATACT GGAGCTGAAG ATTCTTCAGG CTCCAGTCCC 1920
 GCAACTTCTG CTATCCCAT T CATCTCTGAG AACATATCCC AAGGATATAT ATTTCTCTCC 1980
 75 GAAAAACCCAG AGCAATAAAC ATATGATGTC CTTATACAG AATCTGCTAG AAATGCTTCC 2040
 GAAGATTCAA CTTTATCAGG TTCAGAAAG TCACTAAAAG ATCCTTCTAT GGAGGGAAT 2100
 GTGTGTTTTC CTAGCTCTAC AGACATAACA GCACAGCCCG ATGTTGGATC AGGCAGAGAG 2160
 AGCTTCTCTC AGACTAATTA CACTGAGATA CGTGTGATG AATCTGAGAA GACAACCAAG 2220
 TCCCTTCTCG CAGCCCCAGT GATGTCACAG GGTCCCTCAG TTACAGATCT GGAAATGCCA 2280
 80 CATTATCTA CTTTGGCTA CTTCCCACT GAGGTAAAC CTCTGCTTT TACCCCATCC 2340
 TCCAGACAA AGGATTTGGT CTCCACGGTC AACGTGGTAT ACTCGCAGAC AACCCCAACC 2400
 GFATACAATG AGGCCAGTAA TAGTAGCCAT GAGTCTCGTA TTGGTCTAGC TGAGGGGTTG 2460
 GAATCCGAGA AGAAGGCACT TATACCCCTT GTGATCGTGT CAGCCCTGAC TTTTATCTGT 2520
 CTAGTGGTTC TTGTGGGTAT TCTCATCTAC TGGAGGAAAT GCTTCCAGAC TGCACACTTT 2580
 85 TACTTAGAGG ACAGTACATC CCCTAGAGTT ATATCCACAC CTCACACACC TATCTTTCCA 2640
 ATTTGAGATG ATGTCCGAGT AATTCCAATA AAGCACTTTC CAAAGCATGT TGCAGATTTA 2700
 CATGCAAGTA GTGGGTTTAC TGAAGAATTT GAGACACTGA AAGAGTTTTA CCAGGAAGTG 2760
 CAGAGCTGTA CTGTTGACTT AGGTATTACA GCAGACAGCT CCAACCAACC AGACAACAG 2820

	CACAGAATC	GATACATAAA	TATCGTTGCC	TATGATCATA	GCAGGGTTAA	GCTAGCACAG	2880
	CTTGCTGAAA	AGGATGGCAA	ACTGACTGAT	TATATCAATG	CCAATTATGT	TGATGGCTAC	2940
	AACAGACCAA	AAGCTTATAT	TGCTGCCCAA	GGCCCACTGA	AATCCACAGC	TGAAGATTTC	3000
5	TGGAGAAATGA	TATGGGAACA	TAATGTGGAA	GTTATTGTCA	TGATAACAAA	CCTCGTGGAG	3060
	AAAGGAAGGA	GAATAATGTGA	TCAGTACTGG	CCTGCCGATG	GGAGTGAGGA	GTACGGGAAC	3120
	TTTCTGGTCA	CTCAGAAGAG	TGTGCAAGTG	CTTGCTTATT	ATACTGTGAG	GAATTTTACT	3180
	CTAAGAAACA	CAAAAAATAA	AAAGGGCTCC	CAGAAAGGAA	GACCCAGTGG	ACGTGTGGTC	3240
	ACACAGTATG	ACTACACGCA	GTGGCCTGAC	ATGGGAGTAC	CAGAGTACTC	CCTGCCAGTG	3300
10	CTGACCTTTG	TGAGAAAGGC	AGCCTATGCC	AAGCGCCATG	CAGTGGGGCC	TGTTGTGCTC	3360
	CACGTGCAGTG	CTGGAGTTGG	AAGAACAGGC	ACATATATTG	TGCTAGACAG	TATGTTGCAG	3420
	CAGATTCAAC	ACGAAGGAAC	TGTCAACATA	TTTGGCTTCT	TAAAACACAT	CCGTTACAAA	3480
	AGAAATTATT	TGGTACAAAC	TGAGGAGCAA	TATGCTTCA	TTCATGATAC	ACTGGTTGAG	3540
	GCCATACTTA	GTAAAGAAAC	TGAGGTGCTG	GACAGTCATA	TTCATGCCCTA	TGTTAATGCA	3600
15	CTCCTCACTT	CTGGACAGC	AGGCAAAACA	AAGCTAGAGA	AACAATTCCA	GGGTCTCACT	3660
	CTGTACCCCA	GGCTGGAGTG	CAGAGGCACA	ATCTCGGCTC	ACTGCAACCT	TCCTCTCCCT	3720
	GGCTTAATCG	ATCCTCTCAT	CTCAGCCTCC	CGAGTGGCTG	GGACTATACT	CCTGAGCCAG	3780
	TCAAATATAC	AGCAGAGTGA	CTATTCTGCA	GCCCTAAAGC	AATGCAACAG	GGAAAGAAT	3840
	CGAATCTCTT	CTATCATCCC	TGTGGAAAGA	TCAAGGGTTG	GCATTTTCATC	CCTGAGTGGG	3900
20	GAAGGCACAG	ACTACATCAA	TGCTCCTCAT	ATCATGGGCT	ATTACCAGAG	CAATGAATTC	3960
	ATCATTACCC	AGCACCCTCT	CCTTCATACC	ATCAAGGATT	TCTGGAGGAT	GATATGGGAC	4020
	CATAATGCCC	AACTGGTGGT	TATGATTCTT	GATGGCCAAA	ACATGGCAGA	AGATGAATTT	4080
	GTTTACTGGC	CAAAATAAGA	TGAGCCTATA	AAATGTGAGA	GCTTTAAGGT	CACCTTATG	4140
	GCTGAAGAAG	ACAAATGTCT	ATCTAATGAG	GAAAACTTA	TAATTTCAGGA	CTTTATCTTA	4200
25	GAAGCTACAC	AGGATGATTA	TGTACTTGAA	GTGAGGCAC	TTCAGTGCTC	TAAATGGCCA	4260
	AATCCAGATA	GGCCCACTAG	TAAACTTTT	GAACTTATAA	GTGTTATAAA	AGAAGAAGCT	4320
	GCCAATAGGG	ATGGGCCCTAT	GATTGTTTCT	GATGAGCATG	GAGGAGTGAC	GGCAGGAATC	4380
	TCTGTGCTC	TGACAACCTT	TATGCACCAA	CTAGAAAAG	AAAATTCCTG	GGATGTTTAC	4440
	CAGGTAGCCCA	AGATGATCAA	TCTGATGAGG	CCAGGAGTCT	TTGCTGACAT	TGAGCAGTAT	4500
30	CAGTTTCTCT	ACAAAGTGAT	CCTCAGCCTT	TGGGGCACAA	GGCAGGAAGA	GAATCTCACT	4560
	ACCTCTCTGG	ACAGTAATGG	TGCAGCATTG	CCTGATGGAA	ATATAGCTGA	GAGCTTAGAG	4620
	CTTTTAGATT	AACACAGAAA	GGGGTGGGGG	GACTCACATC	TGAGCATTGT	TTTCTCTTTC	4680
	CTAAAATTAG	GCAGGAAAT	CAGTCTAGTT	CTGTTATCTG	TTGATTTCCC	ATCACCTGAC	4740
	AGTAACTTTT	ATGACATAGG	ATTCTGCCGC	CAAATTATA	TCATTAACAA	TGTGTGCTCT	4800
35	TTTGCAAGAC	TGTAAATTTA	CTTATTATGT	TGAACTAAA	ATGATTGAAT	TTTACAGTAT	4860
	TTCTAAGAA	GGAAATGTGG	TATTTTITTC	TGTATTGATT	TTAACAGAAA	ATTTCAATTT	4920
	ATAGAGGTTA	GGAAATCCAA	ACTACAGAAA	ATGTTTGTIT	TTAGTGTCAA	ATTTTAGCTT	4980
	GTATTGTAG	CAATTATCAG	GTTTGCTAGA	AATATAACTT	TTAATACAGT	AGCCTGTAAA	5040
	TAAACACCT	TTCCATATGA	TATTCAACAT	TTTACAACCT	CAGTATTCAC	CTAAAGTAGA	5100
40	AATAATCTGT	TACTTATTGT	AAATACTGCC	CTAGTGTCTC	CATGGACCAA	ATTTATATTT	5160
	ATAATTGTAG	ATTTTATAT	TTTACTACTG	AGTCAAGTTT	TCTAGTTCTG	TGTAATTTGT	5220
	TAGTTTAAAT	ACGTAGTTCA	TTAGCTGGTC	TTACTCTACC	AGTTTCTGTA	CATTGTATTG	5280
	TGTTACCTAA	GTCATTAACT	TGTGTTACAG	ATGTAATTTT	AACTTTTGTG	GAATAAGAAA	5340
	ATACCTTCAT	TTTGAAGAAA	GTTTTATATG	GAATAACACC	TTACCAACAA	TTGTTTCAAT	5400
45	GGTTTATATC	CAAGGAATTG	CAAAAATAAA	TATAATATAT	GCCATTAAAA	AAAAAATAAA	5460
	AAAAAATAAA	AAAAAATAAA	A				

Seq ID NO: 188 Protein sequence:
Protein Accession #: EOS sequence

50	1	11	21	31	41	51	
	MRILKRFLAC	IQLLCVCRLD	WANGYYRQOR	KLVEEIGWSY	TGALNQKNWG	KKYPTCNSPK	60
	QSPINIDEDL	TQVNVNLKLL	KPQGWDXTSL	ENTFIHNTGK	TVEINLTNDY	RVSGGVSEMV	120
	FKASKITFFHW	GKCNMSSDGS	EHSLEGQKFP	LEMQIYCFDA	DRFSSFEEAV	KGKGLRLALS	180
55	ILFEVGTTEEN	LDFKATIDGV	ESVSRFGKQA	ALDPFILLNL	LPNSTDKYYI	YNGSLTSPPC	240
	TDYDWDVIFK	DTVSISESQ	AVFCEVLTMQ	QSGYVLMMDY	LQNNFREQQY	KFSRQVFSSY	300
	TGKEEIHAEV	CSSEPENVQA	DPENYTSLLV	TWERPRVVDY	TMIEKFAVLY	QQLDGEDQTK	360
	HEFLTDGYQD	LGAILMNLPL	NMSYVLQIVA	ICTNGLYKGY	SDQLIVDMPT	DNPELDLPPE	420
60	LIGTEBIIKE	EEEGKDIEEG	AIVNPGRDSA	TNQRKKEPQ	ISTTTHYNRI	GTYKNEAKTN	480
	RSPTRGSEFS	KGQDVPNTSL	NSTSQPVTKL	ATEKDILSTS	QTVTELPPHT	VEGTSASLND	540
	GSKTVLRSPH	MNLSGTAESE	NTVSITEYEE	ESLLTSFKLD	TGAEDSSGSS	PATSAIPFIS	600
	ENISQGVIPS	SENPETITYD	VLIPESARNA	SEDSTSSGSE	ESLKDPSMEG	NVWFPSSTDI	660
	TAQPDVSGSR	ESPLQNTYTE	IRVDESEKIT	KSFAGPVMS	QGFVTDLEM	PHYSTPAYFP	720
65	TEVTPHAFPT	SSRQQLVST	VNVVYSQTTQ	PVYNEAGNS	HESRIGLAEG	LESEKKAVIP	780
	LVIVSALTPI	CLVVLVGILI	YWRKCFQTAH	FYLEDDSTSP	VISTPPTPIF	PISDDVGAIP	840
	IKHFFKHVAD	LHASSGFTTE	FETLKEFYQE	VQSCVTDLGI	TADSSNHPDN	RKKNRYINIV	900
	AYDHSRVKLA	QLAEKDGKLT	DYINANYVDG	YNRPKAYIAA	QGPLKSTAE	FWRMIWEHNV	960
	EVIVMITNVL	EKGRRKCDQY	WPADGSEYEG	NFLVTQKSVQ	VLAYYTVRNF	TLRNTKIKKG	1020
70	SQKGRPSGRV	VTQYHYTQWP	DMGVPEYSLP	VLTFRKAAY	AKRHAVGPVV	VHCAGVGRV	1080
	GTYIVLDSML	QQIQHEGTVN	IFGFLKHIRS	QRNYLVQTEE	QYVFIHDTLV	EAILSKBTEV	1140
	LDSDIHAYVN	ALLIPGPAGK	TKLEKQFQGL	TLSPRLRCRG	TISAHCNLPL	PGLTDPPTSA	1200
	SRVAGTILLS	QSNIQQSDYS	AALKQCNREK	NRTSSIIPE	RSRVGISSLS	GEGTDYINAS	1260
	YIMGYQSQNE	FIITQHPLHL	TIKDFWRMIW	DHNAQLVVM	PDGQNMAGE	FVYWFNKDEP	1320
75	INCESPKVTL	MAEHEKCLSN	EELIIQDFI	LEATODDYVL	EVRRHFCQPKW	PNPDSPISKT	1380
	FELISVIKEE	AANRDGPMIV	HDEHGGVTAG	TFCALTTLMH	QLEKENSVDV	YQVAKMINLM	1440
	RPGVFADIEQ	YQFLYKVILS	LVGTRQEENP	STSLDSNGAA	LPDGNIAESL	ESLV	

Seq ID NO: 189 DNA sequence
Nucleic Acid Accession #: NM_002820
Coding sequence: 304..831

85	1	11	21	31	41	51	
	CCGGTTCGCA	AAGAAGCTGA	CTTCAGAGGG	GGAAACTTTC	TTCTTTTAGG	AGGCCGTTAG	60
	CCCTGTTCCT	CGAACCAGG	AGAAGCTGCT	GCCAGATTAA	TTAGACATTG	CTATGGGAGA	120
	CGTGTAACAA	CACACTATTAT	CATTGATGCA	TATATAAAAC	CATTTTATTT	TGCTATTAT	180

5
10
15
20
25

```
TTCAGAGGAA GCGCCTCTGA TTTGTTTCTT TTTTCCCTTT TTGCTCTTTC TGGCTGTGTG 240
GTTTGGAGAA AGCAGAGTTG GAGTAGCCGG TTGCTAAATA AGTCCCGAGC GCGAGCGGAG 300
ACGATGCAGC GGAGACTGGT TCAGCAGTGG AGCGTCGCGG TGTTCCCTGCT GAGCTACGGG 360
GTGCCCTCCT GCGGGCGCTC GGTGGAGGGT CTCAGCGCGC GCCTCAAAAG AGCTGTGTCT 420
GAACATCAGC TCCTCCATGA CAAGGGGAAG TCCATCCAAG ATTTACGGCG ACGATTCTTC 480
CTTCACCATC TGATCGCAGA AATCCACACA GCTGAAATCA GAGCTACCTC GGAGGTGTCC 540
CCTAACTCCA AGCCCTCTCC CAACACAAAG AACCACCCCG TCCGATTTGG GTCTGATGAT 600
GAGGGGAGAT ACCTAACTCA GGAACCTAAC AAGGTGGAGA CGTACAAAGA GCAGCCGCTC 660
AAGACACCTG GGAAGAAAAA GAAAGGCAAG CCCGGGAAAC GCAAGGAGCA GGAAAAGAAA 720
AAACGGCGAA CTCGCTCTGC CTGGTTAGAC TCTGGAGTGA CTGGGAGTGG GCTAGAAGGG 780
GACCACCTGT CTGACACCTC CACAACGTGG CTGGAGCTCG ATTCACGGTA ACAGGCTTCT 840
CTGGCCCGTA GCCTCAGCGG GGTGCTCTCA GCTGGGTTTT GGAGCCTCCC TTCTGCCTTG 900
GCTTGGACAA ACCTAGAATT TTCTCCCTTT ATGTATCTCT ATCGATTGTG TAGCAATTGA 960
CAGAGAATAA CTCAGAAAT TGTCTGCCTT AAAGCAGTAC CCCCTACCA CACACACCCC 1020
TGTCCTCCAG CACCATAGAG AGGCGCTAGA GCCCATTCCT CTTTCTCCAC CGTACCCCAA 1080
CATCAATCCT TTACCACTCT ACCAAATAAT TTCATATTCA AGCTTCAGAA GCTAGTGACC 1140
ATCTTCATAA TTGCTGGAG AAGTGTATTT CTTCCTCTTA CTCTCACACC TGGGCAAACT 1200
TTCTTCAGTG TTTTTCATTT CTACGTTCTT TTCACTTCAA GGGAGAAATAT AGAAGCATTT 1260
GATATTATCT ACAAACTAG CAGAACAGCA TCATGTCTAA AACGATTCTG AGCCATTCTC 1320
ACTTTTATAT TAATTAATG TATTAATTA ATCTCAAT TTATTTTAAT GTAAAGAACT 1380
TAAATATATG TTTAAACACA TGCCCTAAAT TTGTTTAATT AAATTTAACT CTGGTTTCTA 1440
CCAGCTCATA CAAAATAAAT GGTTCCTGAA AATGTTTAAG TATTAACCTA CAAGGATATA 1500
GGTTTTCTCT ATGTATCTTT TTGTTCAATG GCAAGATGAA ATAATTTTTC TAGGGTAATG 1560
CCGTAGGAAA AATAAACTT CACATTTAAA AAAAA
```

Seq ID NO: 190 Protein sequence:
Protein Accession #: NP_002811

30
35

```
1 11 21 31 41 51
| | | | |
MQRRRLVQWS VAVFLSYAV PSCGRSVEGL SRRLKRAVSE HQLLHDKGKS IQDLRRRFFL 60
HHLIAEIHIA EIRATSEVSP NSKPSPTNKN HPVRFSGSDE GRYLQTQENK VETYKEQPLK 120
TPGKKKKKGP GKRKEQEKKK RRTSAWLDS GVTGSGLEGD HLSDTSTSL ELDSR
```

Seq ID NO: 191 DNA sequence
Nucleic Acid Accession #: XM_059328
Coding sequence: 52..1023

40
45
50
55
60
65

```
1 11 21 31 41 51
| | | | |
GGGCTGTCCG GCCCACTCCC CTGGGAGCGC GAGCGGTGGA CCCAGGCGGC CATGTCCCGC 60
CCTCGCATGC GCCTGGTGGT CACCGCGGAC GACTTTGGTT ACTGCCCGCG ACGCGATGAG 120
GGTATCGTGG AGGCCCTTCT GGCGGGGGCT GTGACCAGCG TGTCCTCTGCT GGTCAACGGT 180
GCGGCCACCG AGAGCGCGGC GGAGCTGGCC CGCAGGCACA GCATCCCCAC GGGCCTCCAC 240
GCCAACCTGT CCGAGGGCGC CCCCGTGGGT CCGGCCCGCC GTGGCGCCTC ATGCTGTCTC 300
GGCCCGGAAG GCTTCTTCTT TGCCCAAGATG GGATTCGGGG AGGCGGTGGC GGCCGGAGAC 360
GTGGATTTCG CTCAGGTGCG GGAGGAGCTC GAGGCCCAAC TAAGCTGCTT CCGGGAGCTG 420
TGTGGGAGGG CCCCCACGCA CGCGGACGGG CACCAGCACG TGCACGTGCT CCCAGGCGTG 480
TGCCAGGTGT TCGCCGAGGC GCTCAGGCC TATGGGGTGC GCTTTACGCG ACTGCCGCTG 540
GAGCGCGGTG TGGGTGGCTG CACTTGGCTG GAGGCCCGCG CGCGTGCTTT CGCCTGCGCC 600
GTGGAGCGCG ACGCCCGGGC CGCGGTGGGC CCCTTCTCCC GCCACGCGCT GCCTGGAACA 660
GACGCGCTTG TGGGCTGAG CACTTGGCGC CGGCACATGT CCGCTCACCG CGTGTCCGGG 720
GCCCTGGCGC GGGTCTCTGA AGGTACCTTA GCGGGCCACA CCCTGACAGC CGAGCTGATG 780
GCGCACCCCG GCTACCCCTG GTGCTCTCCC ACCGGCGGCT GCGGTGAAGG CCCCAGCGCT 840
TTCTCTTGCT CTGCGGAGCG GCTGCATGAG CTGCGGTGCC TCACCGGCGC CACGCTGCGG 900
GCCCACTTTC CCCAGGATGG CGTGCACTTT TGCCTCCCTG ACGACCTGGA CTCCAAGAGG 960
CCAGGGGAGG AGGTCCCTTG TGAGCCCACT CTGGAACCTT TCCTGGAACC CTCCTTACTC 1020
TGACCCCTTA CAGACAACCA AGCACTAATC CCCTTAGTAC CAAGAAAGGG GAGCCAGGAT 1080
TTAGTCTGCG CCCAGCCGAG AGCTGGGACC TGGAGCACGA TCTGTTGACT TCCCTGGGTA 1140
GGACACTGCC ACCTCTGGGC TCAGGTCTCT ATGCTCCCAA ATGGCATCTA GAGTTTGAGC 1200
AGCCTTCTTG GCTGCAGGCA GGCCTAGCCT GTGGCAGCGG GCTAGGGCCC GCAGAGCATT 1260
TGGTGCCCTT CCATGTTGCA ATGCAAAACAC CTTACCACT GGGGCAGTGG GGAGAGATGG 1320
CTATATTAAT AAAATAACGT GTGTCTTTC
```

Seq ID NO: 192 Protein sequence:
Protein Accession #: XP_059328

70
75
80

```
1 11 21 31 41 51
| | | | |
MSRPRMRLV TADDFGYCPR RDEGIVEAPL AGAVTSVSLV VNGAATESAA ELARRHSIPT 60
GLHANLSEGR PVGPARRGAS SLLGPEGFFL GKMGPREAVA AGVDLPQVR EELEAQLSCF 120
RELLGRAPTH ADGHQHVHVL PGVCQVFAEA LQAYGVRFTR LFLERGVGGC TWLEAPARAF 180
ACAVERDARA AVGPFSRHGL RWTDAPVGLS TCGRHMSAHR VSGALARVLE GTLAGHTLTA 240
ELMAHFGYFS VPPTGGCGEG PDAFSCSWER LHELRLVTAP TLRAQLAQDG VQLCALDDLD 300
SKRPGEEVPC EPTLEPPLEP SLL
```

Seq ID NO: 193 DNA sequence
Nucleic Acid Accession #: NM_005688.1
Coding sequence: 126..4439

85

```
1 11 21 31 41 51
| | | | |
CCGGGCGAGT GGCTCATGCT CGGGAGCGTG GTTGAGCGGC TGGCGCGGTT GTCCTGGAGC 60
AGGGGCGCAG GAAATCTGAT GTGAAACTAA CAGTCTGTGA GCCCTGGAAC CTCGCTCAG 120
```

	AGAAAGATGAA	GGATATCGAC	ATAGGAAAAG	AGTATATCAT	CCCCAGTCTC	GGGTATAGAA	180
	GTGTGAGGGA	GAGAACCCAGC	ACTTCTGGGA	CGCACAGAGA	CCGTGAAGAT	TCCAAGTTCA	240
	GGAGAACTCG	ACCGTTGGAA	TGCCAAGATG	CCTTGGAAAC	AGCAGCCCGA	GCCGAGGGCC	300
5	TCTCTCTTGA	TGCCTTCATG	CATTCTCAGC	TCAGAAATCCT	GGATGAGGAG	CATCCCAAGG	360
	GAAAGTACCA	TCATGGCTTG	AGTGCTCTGA	AGCCCCATCG	GACTACTTCC	AAACACCAGC	420
	ACCCAGTGGA	CAATGCTGGG	CTTTTTTCCT	GTATGACTTT	TTCGTGGCTT	TCTTCTCTGG	480
	CCCGTGTGGC	CCACAAGAAG	GGGAGCTCTC	CAATGGAAGA	CGTGTGGTCT	CTGTCCAAGC	540
	ACGAGTCTTC	TGACGTGAAC	TGCAGAAGAC	TAGAGAGACT	GTGGCAAGAA	GAGCTGAATG	600
10	AAGTTGGGCC	AGACGCTGCT	TCCCTGCGAA	GGTGTGTGTG	GATCTTCTGC	CGCACCAGGC	660
	TCATCTGTGC	CATCGTGTGC	CTGATGATCA	CGCAGCTGGC	TGGCTTCAGT	GGACCAGCCT	720
	TCATGGTGAA	ACACCTCTTG	GAGTATACCC	AGGCAACAGA	GTCTAACCTG	CAGTACAGCT	780
	TGTTGTAGT	GCTGGGCTTC	CTCCTGACCG	AAATCGTGGC	GTCTTGGTGG	CTTGCACTGA	840
	CTTGGGCATT	GAAITACCGA	ACCGGTGTCC	GCTTGGCGGG	GGCCATCCTA	ACCATGGCAT	900
15	TTAAGAAGAT	CCTTAAGTTA	AAGAACATTA	AAGAGAAATC	CCTGGGTGAG	CTCATCAACA	960
	TTTGTCTCAA	CGATGGGAG	AGAATGTTTG	AGGCAGCAGC	CGTTGGCAGC	CTGCTGGCTG	1020
	GAGGACCCGT	TGTTGCCATG	TTAGGCATGA	TTTATAATGT	AATTATTCTG	GGACCAACAG	1080
	GCTTCTCTGG	ATCAGCTGTT	TTTATCTCTC	TTTACCCAGC	AATGATGTTT	GCATCACGGC	1140
	TCACAGCATA	TTTCAGGAGA	AAATGCGTGG	CCGCCACCGA	TGAACGTGTC	CAGAAGATGA	1200
20	ATGAAGTTCT	TACTACATT	AAATTTATCA	AAATGTATGC	CTGGGTCAAA	GCATTTTCTC	1260
	AGAGTGTTC	AAAAATCCGC	GAGGAGGAGC	GTCCGATATT	GGAAAAAGCC	GGGTACTTCC	1320
	AGGGTATCAT	TGTGGCTGTG	GCTCCCATTG	TGGTGGTGAT	TGCCAGCGTG	GTGACCTTCT	1380
	CTGTTCAAT	GACCTGGGCG	TTCGATCTGA	CAGCAGCACA	GGCTTTCACA	GTGGTGACAG	1440
	TCTTCAATT	CATGACTTTT	GCTTTGAAAG	TAACACCGTT	TTCAGTAAAG	TCCCTCTCAG	1500
25	AAGCCTCAGT	GACTTGTGAC	AGATTTAAGA	GTTTGTTTCT	AATGGAAGAG	GTTCAATGA	1560
	TAAAGAACCA	ACCAGCCAGT	CCTCACATCA	AGATAGAGAT	GAAAAATGCC	ACCTTGGCAT	1620
	GGGACTCCTC	CACCTCCAGT	ATCCAGAATC	CGCCCAAGCT	GACCCCAAAA	ATGAAAAAAG	1680
	ACAAGAGGGC	TTCAGGGGCG	AAGAAAGAGA	AGGTGAGGCA	GCTGCAGCGC	ACTGAGCATC	1740
	AGCGGTGCTC	GGCAGAGCAG	AAAGGCCACC	TCTTCTTGGA	CAGTGACGAG	CGGCCCACTC	1800
30	COGAAGAGGA	GAAAGAGGCA	CACATCCACC	TGGGCCACCT	CGCTTACAG	AGGACACTGC	1860
	ACAGCATCGA	TCTGAGATC	CAAGAGGGTA	AACTGCTTGG	AATCTGCGGC	AGTGTGGGAA	1920
	GTGGAAAAAC	TCTCTCAT	TCAGCCATT	TAGGCCAGAT	GACGCTTCTA	GAGGCGCAGA	1980
	TTGCAATCAG	TGGAACCTTC	GCTTATGTGG	CCCAGCAGGC	CTGGATCCTC	AATGCTACTC	2040
	TGAGAGACAA	CATCTGTTT	GGGAAGGAAT	ATGATGAAGA	AAGATACAAC	TCTGTGCTGA	2100
35	ACAGCTGCTG	CCCTGAGGCT	GACCTGGCCA	TTCTTCCCAG	CAGCGACCTG	ACGGAGATTG	2160
	GAGAGCGAGG	AGCCAACTCG	AGCGGTGGGC	AGCGCCAGAG	GATCAGCCTT	GCCCGGGCCT	2220
	TGTATAGTGA	CAGGAGCATC	TACATCCTGG	ACGACCCCTC	CAGTGCCTTA	GATGCCCATG	2280
	TGGGCAACCA	CATCTTCAAT	AGTGCTATCC	GGAAACATCT	CAAGTCCAAG	ACAGTTCTGT	2340
	TGTTATCCCA	CGAGTTACAG	TACCTGGTTG	ACTGTGATGA	AGTGATCTTC	ATGAAAGAGG	2400
40	GCTGTATTAC	GGAAAGAGGC	ACCATGAGG	AACTGATGAA	TTTAAATGGT	GACTATGCTA	2460
	CCATTTTAA	TAACCTGTTG	CTGGGAGAGA	CACCCGCAAT	TGAGATCAAT	TCAAAAAAGG	2520
	AAACCAAGTG	TTCACAGAAG	AAGTCAACA	ACAAGGGTCC	TAAACACGGA	TCAGTAAAGA	2580
	AGGAAAAAGC	AGTAAAGCCA	GAGGAAGGGC	AGCTTGTGCA	GCTGGAAGAG	AAAGGGCAGG	2640
	GTTCAAGTGC	CTGGTCAGTA	TATGGTGTCT	ACATCCAGGC	TGCTGGGGGC	CCCTTGGCAT	2700
45	TCTGTGTTAT	TATGGCCCTT	TTCATGCTGA	ATGTAGGCAG	CACCGCCTTC	AGCACCTGGT	2760
	GGTTGAGTTA	CTGGATCAAG	CAAGGAAGCG	GGAAACACCAC	TGTGACTCGA	GGGAACGAGA	2820
	CCTCGGTGAG	TGCAGCATG	AAGGACAATC	CTCATATGCA	GTACTATGCC	AGCATCTACG	2880
	CCCTCTCCAT	GGCAGTCAAG	CTGATCTCTG	AAGCCATTCC	AGGAGTTGTC	TTTGTCAAGG	2940
	GCACGCTGCG	AGCTTCTCTC	CGGCTGCATG	ACGAGCTTTT	CCGAAGGATC	CTTCGAAGCC	3000
50	CTATGAAGTT	TTTTGACACG	ACCCCCACAG	GGAGGATTCT	CAACAGGTTT	TCCAAAGACA	3060
	TGGATGAAGT	TGACGTGGCG	CTGCCGTTC	AGGCCGAGAT	GTTCATCCAG	AACGTTATCC	3120
	TGGTGTCTCT	TGCTGTGGGA	ATGATCGCAG	GAGTCTTCCC	GTGGTTCTCT	GTGGCAGTGG	3180
	GGCCCTCTGT	CATCTCTTTT	TCAGTCTCTG	ACATTGTCTC	CAGGTCCTGT	ATTGCGGAGC	3240
	TGAAGCGTCT	GGACAATATC	ACGCAGTCAC	CTTCTCTCTC	CCACATCAG	TCCAGCATA	3300
55	AGGGCCTTGC	CACCATCCAC	GCCTACAATA	AAGGGCAGGA	GTTCCTGCAC	AGATACCAGG	3360
	AGCTGCTGGA	TGACAAACCA	GCTCCTTTT	TTTTGTTTAC	GTGTGCGATG	CGGTGGCTGG	3420
	CTGTGCGGCT	GGACCTCATC	AGCATCGCCC	TCATCACACC	CACGGGGCTG	ATGATCGTTC	3480
	TTATGCAAGG	GCAGATTCCC	CCAGCCTATG	CGGGTCTCGC	CATCTCTTAT	GCTGTCCAGT	3540
	TAAAGGGGCT	GTTCCAGTTT	ACGGTCAGAC	TGGCATCTGA	GACAGAAGCT	CGATTCAACT	3600
60	CGGTGGAGAG	GATCAATCAC	TACATTAAGA	CTCTGTCTCT	GGAAAGCACT	GCCAGAATTA	3660
	AGAACAAAGC	TCCCTCCCTC	GACTGGCCCC	AGGAGGGAGA	GGTGACCTTT	GAGAACGAG	3720
	AGATGAGGTA	CCGAGAAAC	CTCCCTCTTG	TCCTAAAGAA	AGTATCCTTC	ACGATCAAAC	3780
	CTAAAGAGAA	GATTGGCATT	GTGGGGCGGA	CAGGATCAGG	GAAATCCTCG	CTGGGGATGG	3840
	CCCTCTTCCG	TCTGTTGGAG	TTATCTGGAG	GCTGCATCAA	GATTGATGGA	GTGAGAATCA	3900
65	GTGATATTGG	CCTTGCCGAC	CTCCGAAGCA	AACTCTCTAT	CATTCTCTCA	GAGCCGGTGC	3960
	TGTTCAAGTG	CATGTCTAGA	TCAAATTGG	ACCCCTTCAA	CCAGTACACT	GAAGACCAGA	4020
	TTTGGGATGC	CCCTGGAGAGG	ACACACATGA	AAGAATGTAT	TGCTCAGCTA	CCTCTGAAAC	4080
	TGAATCTGTA	AGTGTGGAG	AATGGGGATA	ACTTCTCAGT	GGGGGAACGG	CAGCTCTTGT	4140
	GCATAGCTAG	AGCCCTGCTC	CGCCACTGTA	AGATTCTGAT	TTTAGATGAA	GCCACAGCTG	4200
70	CCATGGACAC	AGAGACAGAC	TTATTGATTC	AAGAGACCAT	CCGAGAAGCA	TTTGCAAGCT	4260
	TGACCATGCT	GACCATTGCC	CATCGCCTGC	ACACGGTCTC	AGGCTCCGAT	AGGATTATGG	4320
	TGCTGGCCCA	GGGACAGGTG	GTGGAGTTTG	ACACCCCATC	GGTCTTCTGT	TCCAACGACA	4380
	GTTCGCGATT	CTATGCCATG	TTTGCTGCTG	CAGAGAACAA	GGTCCGTGTC	AAGGGCTGAC	4440
	TCCTCCCTGT	TGACGAAGTC	TCTTTTCTTT	AGAGCATTGC	CATTCCCTGC	CTGGGGCGGG	4500
75	CCCTCATCG	CGTCTCTCTA	CCGAAACCTT	GCCTTTCTCG	ATTTTATCTT	TGCGACAGCA	4560
	GTTCGCGATT	GGCTTGTGTG	TTTCACTTTT	AGGSAGAGTC	ATATTTTGTAT	TATTTATTTT	4620
	ATTCCATATT	CATGTAAACA	AAATTTAGTT	TTTGTCTCTA	ATTGCACCTC	AAAAGGTTCA	4680
	GGGAACCGTT	ATTATAATTG	TATCAGAGGC	CTATAATGAA	GCTTTATACG	TGTAGCTTATA	4740
	TCTATATATA	ATTCTGTACA	TAGCCTATAT	TTACAGTGAA	AATGTAAGCT	GTTTATTTTA	4800
80	TATTAAAAA	AGCACTGTGC	TAATAACAGT	GCATATTCTC	TTCTATCATT	TTTGTACAGT	4860
	TTGCTGTACT	AGAGATCTGG	TTTGTCTATT	AGACTGTAGG	AAGAGTAGCA	TTTCACTTCT	4920
	TCCTAGCTGG	TGGTTTCAGG	GTGCCAGGTT	TTCTGGGTGT	CCAAAGGAAG	ACGTGTGGCA	4980
	ATAGTGGGCC	CTCCGACAGC	CCCCCTGTCC	GCCTCCCCAC	AGCCGCTCCA	GGGGTGGCTG	5040
	GAGACGGGTG	GGCGGCTGGA	GACCATGCAG	AGCGCGGTGA	GTTCTCAGGG	CTCCTGCCCT	5100
	CTGTCTGTGT	GTCACTTACT	GTTTCTGTCA	GGAGAGCAGC	GGGGCGAAGC	CCAGGCCCTC	5160
85	TTTCACTCCC	TCCATCAAGA	ATGGGGATCA	CAGAGACATT	CCTCCGAGCC	GGGGAGTTTC	5220
	TTTCTGCTCT	TCTTCTTTT	GCTGTTGTTT	CTAAACAAGA	ATCAGTCTAT	CCACAGAGAG	5280
	TCCACTGCTC	TCAGTTCCT	ATGGCTGGCC	ACTGCACAGA	GCTCTCCAGC	TCCAAGACCT	5340

GTTGGTTCCA AGCCCTGGAG CCAACTGCTG CTTTGTGAGG TGGCACTTTT TCATTTGCCT 5400
 ATTCCACAC CTCCACAGTT CAGTGGCAGG GCTCAGGATT TCGTGGGTCT GTTTTCCTTT 5460
 CTACCCGAG TCGTCGCACA GTCTCTCTCT CTCTCTCCCC TCAAAGTCTG CAACCTTAAG 5520
 CAGCTCTTGC TAATCAGTGT CTCACACTGG CGTAGAAGTT TTTGTACTGT AAAGAGACCT 5580
 ACCTCAGGTT GCTGTTGTCT GTGTGGTTTG GTGTGTCTCC GCAAAACCCC TTTGTGCTGT 5640
 GGGGCTGGTA GCTCAGGTGG GCGTGGTCAC TGCTGTCATC AGTTGAATGG TCAGCGTTGC 5700
 ATGTCTGTGAC CAACTAGACA TTCTGTGCGC TTAGCATGTT TGCTGAACAC CTTGTGGAAG 5760
 CAAAAAATCTG AAAATCTGAA TAAATATTATT TTGGATTTTG TAAAAAATAA AAAAAAATAA 5820
 AAAAAAATAA AAAAAAATAA

Seq ID NO: 194 Protein sequence:
 Protein Accession #: NP_005679.1

1 11 21 31 41 51
 MKDIDIGKEY IIPSPGYRSV RERTSTSGTH RDREDSKFRF TRPLECQDAL ETAARAEGLS 60
 LDASMHSQLR ILDEEHPKKG YHHGLSALKP IRTTSKHQHP VDNAGLFSCM TFSWLSLAR 120
 VAHKKGELSM EDVWSLSKHE SSDVNCRRLE RLWQEEELNEV GPDAASLRV VWIFCRTRLI 180
 LSIVCLMTIQ LAGFSGPAFM VKHLLLEYTQA TESNLQYSL LVLGLLLTEI VRSWSLALTW 240
 ALNYRTGVRL RGAILTMAPK KILKLNKIKE KSLGELINIC SNDGQRMFEA AAVGSLLAGG 300
 PVVAILGMIY NVIILGPTGF GSAVFILFY PAMMFASRLT AYFRRKCVAA TDERVQKME 360
 VLTYYIKFKM YANVKAFPSQ VQKIREEERR ILEKAGYFQG ITVGVAPIV VIASVVTFSV 420
 HMTLGFDLTA AQFTVVTVF NSMTFALKVT PFSVKSLSSEA SVAVDRFKSL FLMEVHMIK 480
 NKPASPHIKI EMKNATLAWD SSHSSIQNSP KLTPKMKDKK RASRGKKEKV RQLQRTEHQA 540
 VLAEQKGHLL LDSDERPSP EEEGKHILG HLRLQRTLHS IDLEIQEGKL VGICGSVSG 600
 KTSLSAILG QMTLLEGSIA ISGTFAYVAQ QAWILNATLR DNILFGKEYD EERYNSVLNS 660
 CCLRPDLAIL PSSDLTEIGE RGNALSGGQR QRISLARALY SDRSIYLLD PLSALDAHV 720
 NHIFNSAIRK HLKSKTVLFV THQLQYLVD DEVIFMKEGC ITERGTHEEL MNLNGDYATI 780
 PNNLLGETP PVEINSKKT SSGSKKSQDK GPKTGSVKKE KAVKPEEGQL VQLEEKGGQS 840
 VPSVYGVYI QAAGCPILAF VIMALEMLNV GSTAFSTWWL SYWIKQSGSN TTVTRGNETS 900
 VSDSMKDNPH MQYYSIYAL SMAVMLILKA IRGVVFVKG TLRASSRLHDE LFRILRLSPM 960
 KFFDTPPTGR ILNRFSKDM EVDVRLPFQA EMFIQNVILV FFCVGMIAVG PFWFLVAVGP 1020
 LVILFSLVHI VSRVLIRELK RLDNITQSPF LSHITSSIQG LATIHAYNKG QEFLHRYQEL 1080
 LDDNQAPFPL SETCAMRLAV RLDLISIALI TTTGLMIVLM HGQIPPAYAG LAISYAVQLT 1140
 GLFQPTVRLA FTEEARFTSV ERINHVIKTL SLEAPARIKN KAPSPDWQGE GEVTFENAEM 1200
 RYRENLPVLV KKVSTFIKPK EKIGIVGRTG SSKSSLMGAL FRLVELSGGC IKIDGVRI 1260
 IGLADLRSLK SIIPQEPVLF SGTVRSNLDP FNQYTEDQIW DALERTHMKC CIAQLPLKLE 1320
 SEVMENGDNF SVGSRQLLCI ARALLRHCKI LILDEATAAM DTETDLLEI QREAPADCT 1380
 MLTIAHRLHT VLGS DRIMVL AQGVVEFDT PSVLLSNDSS RPYAMFAAAB NKVAVKG

Seq ID NO: 195 DNA sequence
 Nucleic Acid Accession #: NM_006470
 Coding sequence: 228..1922

1 11 21 31 41 51
 GCTGTCCTGA GCCTGAGTAC TCTAGCTGCC TTGTGCGCAT CGCATCTGGC TGCCATCCAG 60
 CGCCAGCACA CAGTAATGAG TGGCCGAGCT TCCTCTGGGA GGGAGGAAAC AGTTAAATC 120
 TTGACGACAG TCGATCATC TAGGCGTGGT TCTCTGTCT GACTTGGGCT GCACAGATCC 180
 TGGGCCAAGG GACAGAAGAA AGACAGCCTA GGAGCAGAGC CTCCAGATG GCTGAGTTGG 240
 ATCTAATGCG TCCAGGGCCA CTGCCAGGG CCACTGCTCA GCCCCAGCC CCTCTCAGCC 300
 CAGACTCTGG GTACCCAGC CCAGATTCTG GGTGAGCCAG CCCAGTGGAA GAAGAGGAGC 360
 TGGGCTCCTC GGAGAAGCTT GGCAGGGAGA CGGAGGAACA GGACAGCGAC TCTGCAGAGC 420
 AGGGGGATCC TGCTGGTGAG GGGAAAGAGG TCCTGTGTGA CTTCTGCCTT GATGACACCA 480
 GAAGAGTGAA GGCAGTGAAG TCCTGTCTAA CTGTGATGGT GAATTAATCT GAAGAGCACT 540
 TGCAGCCGCA TCAGGTGAAC ATCAAACCTG AAGGCCACCT GCTGACCGAG CCAGTGAAGG 600
 ACCACAACCT GCGATACATG CCTGCCACAC ACAGCCCACT GTCTGCTTTC TGCTGCCCTG 660
 ATCAGCAGTG CATCTGCCAG GACTGTTGCC AGGAGCACAG TGGCCACACC ATAGTCTCCC 720
 TGGATGCAGC CCGCAGGAGC AAGGAGGCTG AACTCCAGTG CACCCAGTTA GACTTGGAGC 780
 GGAAACTCAA GTTGAATGAA AATGCCATCT CCAGGCTCCA GGCTAACCAA AAGTCTGTTC 840
 TGGTGTCCGT GTCAGAGTGC AAAGCGGTGG CTGAAATGCA GTTTGGGGAA CTCCTTGCTG 900
 CTGTGAGGAA GGCCAGGACC AATGTGATGC TCTTCTTAGA GGAGAAGGAG CAAGTGCCTG 960
 TGAGCCAGGC CAACGGTATC AAGGCCACAC TGGAGTACAG GAGTGCCGAG ATGGAGAAGA 1020
 GCAAGCAGGA CTGGAGAGG ATGGCGGCCA TCAGCAACAC TGTCCAGTTC TTGGAGGAGT 1080
 ACTGCAAGTT TAAGAACCTC GAAGACATCA CCTTCCCTAG TGTTCACGTA GGGCTGAAGG 1140
 ATAACTCTC GGGCATCCGC AAGTTATCA CGGAATCCAC TGTACACTTA ATCCAGTTGC 1200
 TGGAGAACTA TAAGAAAAAG CTCCAGGAGT TTTCCAAGGA AGAGGAGTAT GACATCAGAA 1260
 CTCAAGTGTG TGCGTTGTT CAGCGCAAAT ATTGGACTTC CAAACCTGAG CCCAGCACCA 1320
 GGGAAACAGT CCTCCAATAT GCGTATGACA TCACGTTTGA CCGGACACA GCACACAAGT 1380
 ATCTCGGCT GCGAGGAGG AACCGCAAGG TCACCAACAC CACGCCCTGG GAGCATCCCT 1440
 ACCCGGACCT CCCAGCAGG TTCTGCACT GCGGCGAGGT GCTGTCCCAG CAGAGTCTGT 1500
 ACCTGCACAG GTACTATTTT GAGGTGGAGA TCTTCGGGGC AGGCACCTAT GTTGGCCTGA 1560
 CCTGCAAGG CATCGACCGG AAGGGGGAGG AGCGCAACAG TTGCATTTC GGAACAACCT 1620
 TCTCCTGGAG CCTCCAATGG AACGGGAAGG AGTTCACGGC CTGGTACAGT GACATGGAGA 1680
 CCCCACTCAA AGCTGGCCCT TTCCGGAGGC TCGGGGTCTA TATCGACTTC CCGGGAGGGA 1740
 TCCTTTCCTT CTATGGCTGA GAGTATGATA CCATGACTCT GGTTCACAA TTTGCTGCA 1800
 AATTTCAGA ACCAGTCTAT GCTGCCCTCT GGCTTCCAA GAAGGAAAC GCCATCOGGA 1860
 TTGTAGATCT GGGAGAGGAA CCCGAGAGC CAGCACCGTC CTTGGGGGTG ACTGCTCCCT 1920
 AGACTCCAGG AGCCATATCC CAGACCTTTG CCAGCTACAG TGATGGGATT TGCAATTTAG 1980
 GGTGATTGTT GGGCAGAAAT AACTGCTGAT GGTAGCTGGC TTTTGAAATC CTATGGGGTC 2040
 TCTGAATGAA AACATCTCC AGCTGCTCTC TTTTGCTCCA TATGGTGTCT TTCTATGT 2100
 GTTTCAGTA ATTCTTTT TTTTTCCTGA GACGGAGTCT CGCACTGTTC CCCAGGCTGG 2160
 AGAGCAGTGG CCGATCTTG GCTCACTGCA AGCTCCGCTC CCGAGTTTCA AGCAATTCTC 2220
 CTGCTCAGC CTCCCGAGTA GCTGGGATTA CAGGTGCTTG CCACCAACAC CAGCTAATGT 2280
 TTTGTATTT TAGTAGAGAT GGGGTTTCAC CATGTTGGCC AGGCAGATCT CAAACTCCTG 2340

ACCTCGTGAT GCACCCACCT CGGCCTCCCA AAGTGCTGGG ATTACATGCG TGAGCCACTG 2400
 CGCCCTGCCT GTTTGTAGTA ATTTTGTAGC ACCAAATCTC CCTCATCTTC TAGTGCCATT 2460
 CTCCTCTCTG TTCAGGTAAA TGTCACACTG TGCCCAAGAT GGATGACCAG GAACCTTAAA 2520
 GAGTGGCTGA AAAGATTGCA GAGTTATCAT AATAAATTGC TAACCTGCGT

5

Seq ID NO: 196 Protein sequence:
 Protein Accession #: NP_006461

10 1 11 21 31 41 51
 MAELDLMAPG PLPRATAQPP APLSPDSGSP SPDSGSSAPV EEDVGSSEK LGRETEEQDS 60
 DSAEQDQDPAG EGKEVLCDFC LDDTRRVKAV KSCLTCMVNY CEEHLQPHQV NIKLQSHLLT 120
 EPVKDHNWRY CPAHHSPLSA FCCPDQQCIC QDCQEHSGH TIVSLDAARR DKEAELQCTQ 180
 15 LDLEKRLKLN ENAISRLQAN QKSVLVSVE VKAVAEMQFG ELLAAVRKAQ ANVMLFLEEK 240
 EQAALSQANG IKAHLEYRSA EMKSKQELE RMAAISNTVQ FLEBYCKFKN TEDITFPSVY 300
 VGLKDKLSGI RKVITESTVH LIQLLENYKK KLQEPSKEEE YDIRTQVSAV VQRKYWTSKP 360
 EPSTREQFLQ YAYDITDPDP TAHKYLRLOE ENRKVTINTP WEHPYPDLPS RFLHWRQVLS 420
 20 QQSLYLHRYF FEVEIFGAGT YVGLTCKGID RKGEERNSCI SGNNFWSLQ WNGKEFTAWY 480
 SDMETPLKAG PFRLGLVYID FPGILSFYG VEYDTMTLVH KFACKFSEPV YAAFVLSKKE 540
 NAIRIVDLGE EPEKPAPSLG VTAP

Seq ID NO: 197 DNA sequence
 Nucleic Acid Accession #: NM_004316
 Coding sequence: 433-1149

25 1 11 21 31 41 51
 CCGGAGACCC GGCAGCAAGAG AGCGCAGCCT TAGTAGGAGA GGAACGCGAG ACGCGGCAGA 60
 GCGCGTTCCG CACTGACTTT TGCTGCTGCT TCTGCTTTT TTTTCTTAG AAACAAGAAG 120
 GCGCCAGCGG CAGCCTCACA CGCGAGCGCC ACGCGAGGCT CCCGAAGCCA ACCCGCGAAG 180
 GGAGGAGGGG AGGGAGGAGG AGCGCGCGTG CAGGGAGGAG AAAAAGCATT TTCACCTTTT 240
 TTGCTCCAC TCTAAGAAGT CTCCCGGGGA TTTGTATAT ATTTTAAAC TTCCGTCAGG 300
 GCTCCCGCTT CATATTTCTT TTTCTTTCCC TCTCTGTTCC TGCACCCAAG TTCTCTCTGT 360
 35 GTCCCCCTCG CGGGCCCGCG ACCTCGCGTC CCGGATCGCT CTGATTCGCG GACTCCTTGG 420
 CGCGCGCTGC GCATGGAAG CTCTGCCAAG ATGGAGAGCG GCGGCGCGCG CCAGCAGCCC 480
 CAGCCGCGAG CCCAGCAGCC CTTCTGCGG CCGCAGCCT GTTCTTTGC CACGCGCGCA 540
 GCGCGCGCGG CCGCAGCGCG CGCAGCGGCA GCGCAGAGCG CGCAGCAGCA GCAGCAGCAG 600
 CAGCAGCAGC AGCAGCAGCA GCAGCGCGCG CAGCTGAGAC CGCGCGCCGA CGGCCAGCCC 660
 40 TCAGGGGGCG GTCAACAAGT AGGCGCCAAG CAAGTCAAGC GACAGCGCTC GTCTTCGCCC 720
 GAACTGATGC GCTGCAACAG CCGGCTCAAC TTCAGCGGCT TTGGCTACAG CCGTCCGCG 780
 CAGCAGCGCG CCGCGTGGC GCGCGCAAC GAGCGCGAGC GCAACCGCGT CAAGTTGGTC 840
 AACCTGGGCT TTGCCACCTT TCGGGAGCAC GTCCCCAAG CCGCGGCCAA CAAGAAGATG 900
 AGTAAGGTGG AGACACTGCG CTGCGCGGTC GAGTACATCC GCGCGCTGCA GCAGCTGCTG 960
 45 GACGAGCATG ACGCGGTGAG CGCGCGCTTC CAGGCAGGCG TCCTGTGCGC CACCATCTCC 1020
 CCAACTACT CCAACGACTT GAACTCCATG GCGGCTCGC CGGTCTCATC CTACTCGTCG 1080
 GACGAGGCT CTTACGACCC GTCTAGCCCC GAGGAGCAGG AGCTTCTCGA CTTACCAAC 1140
 TGGTTCTGAG GGGCTCGGCC TGGTCAGGCC CTGGTGCAG TGGACTTGG AAGCAGGGTG 1200
 50 ATCGCACAA CTGCATCTTT AGTGTCTTCT TGTAGTGGC GTTGGGAGG GGAGAAAAGG 1260
 AAAAGAAAAA AAAAGAAGAA GAAGAAGAAA AGAGAAGAA AAAAAACGA AAACAGTCAA 1320
 CCAACCCCTA CCAAGACTAA GCGAGGCATG CCTGAGAGAC ATGGCTTCA GAAAACGGGA 1380
 AGCGCTCAGA ACAGTATCTT TGCACTCAA TCATTACGAG AGATATGAG AGCAACTGGG 1440
 ACCTGAGTCA ATGCGCAAAA TGCAGCTTGT GTGCAAAAGC AGTGGGCTCC TGGCAGAAAG 1500
 55 GAGCAGCACA CGCGTTATAG TAACCTCCAT CACCTCTAAC ACGCACAGCT GAAAGTCTCT 1560
 GCTCGGGTCC CTTACCTCC CCGCCCTTTC TTAGAGTGCA GTTCTTAGCC CTGTAGAAAC 1620
 GAGTTGGTGT CTTTC

Seq ID NO: 198 Protein sequence:
 Protein Accession #: NP_004307

60 1 11 21 31 41 51
 MESSAKMESG GAGQQPQPQP QQPFLPPAAC FPATAAAAAA AAAAAAQSA QQQQQQQQQQ 60
 65 QQQAPQLRP AADQPPSGGG HKSAPKQVKR QRSSSPFLMR CKRRLNFSGF GYSLPQQQPA 120
 AVARENRENER NRVLVNLGF ATLREHVPNG AANKKMSKVE TLRSAVEYIR ALQQLLDEHD 180
 AVSAAFQAGV LSPTISPNYS NDLNSMAGSP VSSYSSDEGS YDPLSPEEQE LLDFTNWF

Seq ID NO: 199 DNA sequence
 Nucleic Acid Accession #: NM_007015
 Coding sequence: 1-1005

70 1 11 21 31 41 51
 75 ATGACAGAGA ACTCCGACAA AGTTCCTCATT GCCCTGGTGG GACCTGATGA CGTGGGAATTC 60
 TGCAGCCCCC CGGCTACGCG TACGCTGACG GTGAAGCCCT CCAGCCCCCG CGGGCTGCTC 120
 AAGGTGGGAG CCGTGGTCTT CATTTGCGGA GCTGTGCTGC TGCTCTTTGG GGCCATCGGG 180
 GCCTTCTACT TCTGGAGAGG GAGCGACAGT CACATTACA ATGTCCATTA CACCATGAGT 240
 ATCAATGGGA AACTACAAGA TGGGTCAATG GAAATAGACG CTGGGAACAA CTGGAGAGCC 300
 80 TTTAAATGG GAAGTGAGG TGAAGAAGCA ATTGCAGTTA ATGATTTCCT GAATGGCATC 360
 ACAGGAATTC GTTTTGTCTG AGGAGAGAAG TGCTACATTA AAGCGCAAGT GAAGGCTCGT 420
 ATTCTGTAGG TGGCGCGCGT GACCAACAG AGCATCTCCT CCAACTGGA AGGCAAGATC 480
 ATGCCAGTCA AATATGAGA AAATCTCTT ATCTGGGTGG CTGTAGATCA GCCTGTGAAG 540
 85 GACCAACAGT TCTTGAGTTC TAAGGTGTTA GAACTCTCG GTGACCTTCC TATTCTCTGG 600
 CTTAAACCAA CCTATCCAAA AGAAATCCAG AGGGAAGAA GAGAAGTGGT AAGAAAAATT 660
 GTTCCAACCTA CCACAAAAAG ACCACACAGT GGACCCAGGA GCAACCCAGG CGCTGGAAGA 720
 CTGAATAATG AAACCAGACC CAGTGTTCAG GAGGACTCAC AAGCCTTCAA TCCTGATAAT 780

CCTTATCATC AGCAGGAAGG GGAAGCATG ACATTGACC CTAGACTGGA TCACGAAGGA 840
 ATCTGTTGTA TAGAATGTAG GCGGAGCTAC ACCCACTGCC AGAAGATCTG TGAACCCCTG 900
 GGGGGCTATT ACCCATGGCC TTATAATTAT CAAGGCTGCC GTTCGGCTG CAGAGTCATC 960
 5 ATGCCATGTA GCTGGTGGGT GGCCGATATC TTGGGCATGG TGTGAATCA CTTCATATAT 1020
 CACGTGCTGT AAAATAAGAA CTAGCTGAAG AGACAACCAA AGAAGCATT AAGCAGGTTG 1080
 ATGCTGATGG GACCATAAAA TATTTTACA CGCAGCCTGA GCGGTTATTC TTGACACTCT 1140
 TAACAGAAAT TTTTAAATCG TTTTCCAGAA CTTTAGTATA TGCAAATGA CTGAAAGGGT 1200
 AGTTCAAGTC TAAATGCCA TAACCCGTT ATTTGTTATT TTTTATTGTC ATTGATTGTC 1260
 10 CATAAGTCTT CCCTTGCTTG CATCTCCAA AGCTATTTCG AAATAAACAC GAAATTTTAC 1320
 AGTTTGCC

Seq ID NO: 200 Protein sequence:
 Protein Accession #: NP_008946

1 11 21 31 41 51
 MTENS DKVPI ALVGPDDVEF CSPPAYATLT VKPSSPARLL KVGAVVLISG AVLLLFGAIG 60
 AFYFWKSDS HIYNVHYTMS INGKLQDGS EIDAGNNLET PKMGSGAEEA IAVNDFQNGI 120
 20 TGIRFAGGEK CYIKAQVKAR IPEVGAVTQ SISKLEKGI MPVKYEENSL IWVAVDQPVK 180
 DNSPLSSKVL ELCGDLPIFW LKPTYPKEIQ RERREVVRI VPTTTKRPHS GFRSNFGAGR 240
 LNNETRPVQ EDSQAFNPDN PYHQEGESM TFDPRLDHEG ICCIECRSY THCQKICEPL 300
 GGYYPWPYNY QGCRSACRVI MPCSMWVARI LGMV

Seq ID NO: 201 DNA sequence
 Nucleic Acid Accession #: NM_000728.2
 Coding sequence: 112..495

1 11 21 31 41 51
 GTAATAAGAG CGGGGTCTCC GCGGGGAAGG CGCCCAAGC AGGTGTGGTG TTCATCCCGG 60
 GTCGACCGGC CGCTCGCGCT GCCCTGAAAC TCTAGTCGCC AGAGAGGCGG CATGGGTTTC 120
 CGGAAGTTCT CCCCTTCTCT GGCTCTCAGT ATCTTGGTCC TGTACCAGGC GGGCAGCCTC 180
 35 CAGGCGGCGC CATTCAAGTC TGCCCTGGAG AGCAGCCAG ACCCGGCCAC ACTCAGTAAA 240
 GAGGACGCGC GCTTCTGCT GGCTGCACTG GTGCAGGACT ATGTGCAGAT GAAGGCCAGT 300
 GAGCTGAAGC AGGAGCAGGA GACACAGGGC TCCAGCTCCG CTGCCAGAA GAGAGCCTGC 360
 AACACTGCCA CCTGTGTGAC TCATCGGCTG GCAGGCTTGC TGAGCAGATC AGGGGGCATG 420
 GTGAAGAGCA ACTTCGTGCC CACCAATGTG GGTTCCAAAG CCTTTGGCAG GCGCCGAGG 480
 GACCTTCAAG CCTGAGCAGA TGAATGACTC CAGGAAGAAG GTGTGTCTCA AATCCAATGA 540
 40 CATATCTTA TAAGAGATT ACTCAGAAGA CACATGTGGA GAAGGTGACA TGACAGAGGC 600
 AAGGAGGCAC AAGCCAAGGA AGTCTGTGTC TACCAGAAGC CAGAATCACA GAACAGTCTC 660
 TGAAGAAGA GCAGCCCTGC TGACACCTAG AGTTTGGACT TCCAGCTTCC AGAAGTGTGA 720
 GAGAATAATT TCTGTGTGTT TAAGCCACAA AGTTTGTGGT AATTGTGTTAT GACAGCCCTA 780
 GGAATACTAAT ACAATACATT TTCAATTATT TTGGGTAAT GCCTTGGAGT GGGATTGCTG 840
 45 GTTATTGTTG AAGTGTGTTA TTTAACTCTG TAAGAACTG CCAAACTATT TTCTGAAGTG 900
 ACTGTACCAC TTGCGCTTCT TGCCAGCCAC ATATGAGAGC TCTAGTATT CCACAAATAG 960
 GTATGTAGCA GTATCTCATT GCTGTTTAA TTGTATTTC CCCAATGACT AATGACGTTG 1020
 AGCATCTATT TTACCATATG TTTATCACCT TTATTGAAG GTCTGTGTTA ATCTTCTGCT 1080
 50 AAATTTTGTG TGGCTTGCTT GCTTATTAG TGTGAGTTT TTAGAGCTCT TTATATGTTG 1140
 TGGATCTAAG ATTGTTTTCA GATATATAGT TTGGAACCTT CCTTCCCTG AATCTGCGGA 1200
 TTGCTTTTTC ATTTTCTTAG CAGTGTCTCT CACAGAGAAA AAGTTGTAAT TTGAATAAGA 1260
 TCCAATTCAT CTTTTTTTTT CTTTTATGTA TTGTGCTTT AGTTCATGTC TAAGAACTCT 1320
 TTGCCTAATC AAGGTCCCAA GGTCAATA ACCTTATTCT ATACTTCTT GTAAAAAGTT 1380
 55 TATAGTTTAT TATTTTATAT GTAGATTAGT GATCTATTT GAGTTAATT TTGTATAAGG 1440
 TTGAGAGGTG AGGTGAAAT TCATACCTGT GAATATAGAT ACCCAATTGT TTCAGTGCCA 1500
 TTTGTTAAAA AGACTCTTAT TTCACATTT AATTGCCCC GCACCTTGT CAAAAAGCAA 1560
 CTGATCATAT TTGTGTGGGT ATATTCTGG GTTCTCAAT CTGTCTCATT GATTGATTTG 1620
 ACCATTCTTT TGCCAATGTC ATACTGCTT GATTAGTGA GTGTAAAGT GAATCTCAAA 1680
 60 ACCAGATAAT GTGGGTCTAC CAACATTGTT CATTCTGTT CAAAAGATT TTAGCTACAT 1740
 CTAAATATTT TTCTACATCT TTTATACATT TTAGAATCAG TGTGTTACTA TCTACAAAAT 1800
 TTCTGATGAG ATTTTAAATG GGAATGTGTT AAATCAGTGG GTTAATTTG GGAGAATTAG 1860
 CATATTAATA ATATTAAGTC GTTCAATCA TGAACCAAT ACATGTTTT ACTTATTTAG 1920
 GTTTCTCTG TTTTTTTTT TTTAACAGTG TTCTCAGTT TCAACAGAAA TATTCTACAC 1980
 65 ATATCTTGT AGATTTTTAA CTATTTTATT TTTTGTGCT AATGTAAAT GTACTTAAAC 2040
 ATTTTGTGT TTAATGTTC ATTGCTAGTA GATAGAAATA CAATATTAA AATATTAGGA 2100
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA

Seq ID NO: 202 Protein sequence:
 Protein Accession #: NP_000719.1

1 11 21 31 41 51
 MGPRKFPFPL ALSILVLVQA GSLQAAPFRS ALESSPDPAT LSKEDARLLL AALVQDYVQM 60
 75 KASELKQEQE TQSSSSAAQK RACNTATCVT HRLAGLLSRG GGMVKS NFVP TNVGSKAFGR 120
 RRRDLQA

Seq ID NO: 203 DNA sequence
 Nucleic Acid Accession #: NM_001741
 Coding sequence: 71..496

1 11 21 31 41 51
 CTCTGGCTGG ACGCCGCGCC CGCCGCTGCC ACCGCTCTG ATCCAAGCCA CCTCCCGCCA 60
 GAGAGGTGTC ATGGGCTTCC AAAAGTTCTC CCCCTTCTG GCTCTCAGCA TCTTGGTCTC 120
 85 GTTGACAGCA GGCAGCCTCC ATGCAGCACC ATTCAGGTCT GCCCTGGAGA GCAGCCAGC 180
 AGACCCGGCC ACGCTCAGTG AGGACGAAGC GCGCTCTCT CTGGCTGCAC TGGTGCAGGA 240
 CTATGTGCAG ATGAAGGCCA GTGAGCTGGA GCAGGAGCAA GAGAGAGAGG GCTCCAGCCT 300

5 GGACAGCCCC AGATCTAAGC GGTGCGGTAA TCTGAGTACT TGCAATGCTGG GCACATACAC 360
 GCAGGACTTC AACAGTTTC ACACGTTCCC CCAAAGTGA ATTGGGTTG GAGCACTGG 420
 AAAGAAAAGG GATATGTCCA GCGACTTGA GAGAGACCAT CGCCCTCATG TTAGCATGCC 480
 CCAGAAATGCC AACTAACTC CTCCCTTCC TTCTTAATTT CCCTTCTTGC ATCCTTCCTA 540
 TAACTTGATG CATGTGTTT GGTTCCTCTC TGGTGGCTCT TTGGGCTGGT ATTGGTGGCT 600
 TTCCTTGTGG CAGAGGATGT CTCAAATTC AGATGGGAGG AAAGAGAGCA GGAATCACAG 660
 GTTGAAGAG AATCACTGG GAAAATACCA GAAAATGAGG GCCGCTTTGA GTCCCCCAGA 720
 GATGTCATCA GAGCTCTCT GTCTGCTTC TGAATGTGCT GATCATTTGA GGAATAAAAT 780
 TATTTTCCC C

Seq ID NO: 204 Protein sequence:
Protein Accession #: NP_001732

15 1 11 21 31 41 51
 MGFKQFSPFL ALSILVLLQA GSLHAAPFRS ALESSPADPA TLSEDEARLL LAALVQDYVO 60
 MKASELEQEQ EREGSSLDSP RSKRCGNLST CMLGTYTQDF NKFHTFPQTA IGVGAPGKKR 120
 DMSSDLERDH RPHVSMQNA N

Seq ID NO: 205 DNA sequence
Nucleic Acid Accession #: NM_005361
Coding sequence: 1-945

25 1 11 21 31 41 51
 ATGCCTCTTG AGCAGAGGAG TCAGCACTGC AAGCCTGAAG AAGGCCTTGA GGCCCGAGGA 60
 GAGGCCCTGG GCCTGGTGGG TGCAGAGGCT CCTGCTACTG AGGAGCAGCA GACCCGCTCT 120
 TCCTCTTCTA CTCTAGTGA AGTTACCTTG GGGGAGGTGC CTGCTGCCGA CTCACCGAGT 180
 30 CCTCCGCCCA GTCCCTCAGG AGCCTCCAGC TTCTCGACTA CCATCAACTA CACTCTTTGG 240
 AGACAATCCG ATGAGGGCTC CAGCAACCAA GAAGAGGAGG GGCCAAGAAT GTTTCCCGAC 300
 CTGGAGTCCG AGTTCCAAGC AGCAATCAGT AGGAAGATGG TTGAGTTGGT TCATTTTCTG 360
 CTCTCAAGT ATCAGCCAG GAGGCCGCTC ACAAAGGCAG AAATGTCTGA GAGTGTCTCT 420
 AGAAATTGCC AGGACTTCTT TCCTCGATC TTCAGCAAG CCTCCGAGTA CTTCAGCTG 480
 35 GTCTTTGGCA TCGAGGTGGT GGAAGTGGTC CCCATCAGCC ACTTGATACAT CCTTGTCAAC 540
 TGCCTGGGCC TCTCTACGA TGGCCTGCTG GCGACAATC AGGTCAATGCC CAAGACAGGC 600
 CTCCTGATAA TCGTCTGGC CATAATCGCA ATAGAGGGCG ACTGTGCCCC TGAGGAGAAA 660
 ATCTGGGAGG AGCTGAGTAT GTTGGAGGTG TTTGAGGGGA GGGAGGACAG TGTCTTCGCA 720
 CATCCAGGA AGCTGCTCAT GCAAGATCTG GTGCAGGAAA ACTACCTGGA GTACCGGCAG 780
 40 GTGCCCGGCA GTGATCTCTG ATGCTACGAG TTCTGTGGG GTCCAAGGGC CCTCATTTGA 840
 ACCAGCTATG TGAAGTCTT GCACCATACA CTAAAGATCG GTGGAGAACC TCACATTTC 900
 TACCCACCCC TGCATGAACG GGCTTTGAGA GAGGGAGAAG AGTGA

Seq ID NO: 206 Protein sequence:
Protein Accession #: NP_005352

45 1 11 21 31 41 51
 MPLEQRSQHC KPBEGLAARG EALGLVGAQA PATEEQQTAS SSSTLVEVTL GEVPAADSPS 60
 50 PPHSPQGASS PSTTINTYTLW RQSDGESSNQ EEEGPRMPFD LESEFQAAS RKMVELVHFL 120
 LKRYRAREPV TRAMLESVL RNQDFFPVI FSKASEYLQL VFGIEVVEVV PISHLYILVT 180
 CLGLSYDGLL GDNQVMPKTG LLIIVLAIIA IEGDCAPEEK IWELSLMLEV FEGRSDSVFA 240
 HPRKLLMQDL VQENYLEYRQ VPGSDPACYE FLWGPRALIE TSYVKVLHHT LKIGGBPHIS 300
 YPFLHERALR EGEE

Seq ID NO: 207 DNA sequence
Nucleic Acid Accession #: NM_021115
Coding sequence: 743-2893

60 1 11 21 31 41 51
 AAAGGAAGGG AGGGAGGGAG AAAGGAGAAG TTGGTTTAGA GGCCAGCCGG ACGAGCTTTG 60
 GGCACCGCCC TTAGGAGGGC CACCCTCAGA GTCTGACAGC AGGTGAAGGT CCTAAATCTC 120
 65 CCCAACTAA CTGGTGTCTT TTCTCTCTCT CCAAGATGCT CTTCOCGAGG GAGATGCTAG 180
 CCTTTGGGT CCTTACCTCC TGCCCTCAGG AGCCCCGGAG AGAGGCAGTC CTGGCAAGA 240
 GCACCTGAA GAGAGAGTGG TAACAGCGCC CCCAGTTCC TCACAGTCGG CGGAAGTGCT 300
 GGGCAGCTG GTGCTGGATG GGCAGCGACC CTCTGCACAT CACGACATCC CAGCCCTGTC 360
 ACCGCTGCTT CCAGAGGAGG CCGGCCCAA GCACGCCTTG CCCCCCAAGA AGAAACTGCC 420
 70 TTCGCTCAAG CAGGTGAAC CTGCCAGGAA GCAGCTGAGG CCCAAGGCCA CTTCGCGAGC 480
 CACTGTCCAA AGGGCAGGGT CCCAGCCAGC GTCCAGGGC CTAGATCTCC TCTCTCTCTC 540
 CACGGAGAAG CTTGGCCAC CGGGGACCC GGACCCCATC GTGGCTCCG AGGAGGCATC 600
 AGAAGTGCCC CTTTGGCTGG ACCGAAAGGA GAGTGCGGTC CCTACAACAC CCGCACCCCT 660
 GCAATCTCC CCTTCACTT CGCAGCCCTA TGTGGCCAC ACACTCCCC AGAGGCCAGA 720
 75 ACCCGGGAG CTTGGGCTG ACATGGCCCA GGAGGCCCCC CAGGAGGACA CCAGCCCCAT 780
 GGCCCTGATG GACAAAGGTG AGAATGAGCT GACTGGGTCA GCCTCAGAGG AGAGCCAGGA 840
 GACCACTACC TCCACATTA TCACCAACAC GGTCTATCAC ACCGAGCAGG CACCACTCT 900
 CTGCACTGTG AGCTTCTCCA ATCTGAGGG GTACATTGAC TCCAGCGACT ACCCACTGCT 960
 GCGCCCTCAAC AACTTTCTGG AGTGACATA CAACGTGACA GTCTACACTG GCTATGGGGT 1020
 80 GGAGCTCCAG GTGAAGAGTG TGAACCTGTC CGATGGGGA CTGCTCTCCA TCCGCGGGGT 1080
 GGAAGGCCCT ACCCTGACCG TCTTGGCCAA CAGACACTC CTGGTGGAGG GGCAGTAAT 1140
 CCGAAGCCCC ACCAACACCA TCTCCGTCTA CTTCGGACC TTCCAGGAGC ACGGCCCTTG 1200
 GACCTTCCAG CTTCACTACC AGGCCTTCAT GCTGAGCTGC AACTTTCCCC GCGGCGCTGA 1260
 CTCTGGGGAT GTCACGGTGA TGGACCTGCA CTCAGGTGGG GTGGCCCACT TTCAGTGCCA 1320
 85 CTGTGGCTAT GAGCTCCAGG GCGCTAAGAT GCTGACATGC ATCAATGCCT CCAAGCCGCA 1380
 CTGGAGCAGC CAGGAGCCCA CTGTCTCAGC TCCTTGTGGA GGGGCACTGC ACAATGCCAC 1440
 CATCGGCGCG CTCCTCTCCC CAAGTTACCC TGAACAACA AATGGGAGCC AATTCTGCAT 1500
 CTGGACGATT GAAGCTCCAG AGGGCCAGAA GCTGCACCTG CACTTTGAGA GGCTGTGTCT 1560

WO 02/086443

PCT/US02/12476

5
10
15
20
25

```

GCATGACAAG GACAGGATGA CGGTTACAG CGGGCAGACC AACAAAGTCAG CTCTTCTCTA 1620
CGACTCCCTT CAAACCGAGA GTGTCCCTTT TGAGGGCCTG CTGAGCGAAG GCAACACCAT 1680
CCGCATCGAG TTCAGTCCG ACCAGGCCCG GGCGGCCTCC ACCTTCAACA TCCGATTGGA 1740
AGCGTTTGAG AAAGGCCACT GCTATGAGCC CTACATCCAG AATGGGAAGT TCACTACATC 1800
CGACCCGACC TATAACATTG GGAATATAGT GGAGTTCACC TGCGACCCCG GCCACTCCCT 1860
GGAGCAGGGC CCGGCCATCA TCGAATGCAT CAATGTGGCG GACCCATACT GGAATGACAC 1920
AGAGCCCTCG TGCAGAGCCA TGTGTGGTGG GGAGCTCTCT GCTGTGGCTG GGGTGGTATT 1980
GTCCCAAAAC TGGCCCGAGC CTTACGTGGA AGGTGAAGAT TGTATCTGGA AGATCCACGT 2040
GGGAGAAGAG AAACGGATCT TCTTAGATAT CCAGTTCCTG AATCTGAGCA ACAGTGACAT 2100
CTTGACCATC TACGATGGCG ACAGGGTCAT GCCCACATC TTGGGGCAGT ACCTTGGGAA 2160
CAGTGGCCCT CAGAAACTGT ACTCCTCCAC GCCAGACTTA ACCATCCAGT TCCATTCCGA 2220
CCCTGCTGGC CTCATCTTTG GAAAGGGCCA GGGATTATC ATGAACTACA TAGAGGTATC 2280
AAGGAATGAC TCCTGCTCGG ATTTACCCGA GATCCAGAAAT GGCTGGAAAA CCACTTCTCA 2340
CACGGAGTTG GTGCGGGGAG CCAGAATCAC CTACCAAGTG GACCCCGGCT ATGACATCGT 2400
GGGGAGTGAC ACCCTACCT GCCAGTGGGA CCTCAGCTGG AGCAGCGACC CCCCATTTTG 2460
TGAGAAAAAT TGTACTCTG AGAGGTTGGT CACTCGACCC GCTTAATTTT 2520
GGATCTCTGT CTGCTGGTGG GGAACCCAT CCAATACACC TGCAACCCCG GTTTTGTGCT 2580
TGAAGGAGT TCTCTTCTGA CTTGCTACAG CCGTGAAACA GGAAGTCCCA TCTGGACGTC 2640
TCGCTGCCCC CACTGCGTTT CAGAAGCGGC AGCAGAGAGC TCGCTGGAAG GGGGGAACAT 2700
GGCCCTGGCT ATCTTCATCC CGTCTCTCAT CATCTCCTTA CTGCTGGGAG GAGCCTACAT 2760
TTACATCACA AGATGTCCGT ACTATTCCAA CCTCCGCTG CCTCTGATGT ACTCCACACC 2820
CTACAGCCAG ATCACCCTGG AACCAGAGTT TGACAACCCC ATTTACGAGA CAGGGGGAAC 2880
CCAAAAAGTT TAGGTTTCCA TTTAAAAAGA GGTACCCCTT AAAAAAGGGC TTGTGAATCT 2940
AACCCCAATT TCCCCGAGAC ATTTATCCAA AGGCCCTGGG GGCCTTGATT TAAACCCCA 3000
AAAGGCGGCT GTTTTGTGTT TAAACTTTTT AACAAAGGAT TACGGGTTTT TTCCCGGAT 3060
TTTATAAAT TTTAAAGTG

```

Seq ID NO: 208 Protein sequence:
Protein Accession #: NP_066938

30
35
40
45

```

1 11 21 31 41 51
MAQEAPEQEDT SPMALMDKGE NELTGSASEE SQETTTSTII TTTVITTEQA PALCSVSFSN 60
PEGYIDSSDY PLLPLNNFLE CTYNVTVYTG YGVELQVKS V NLSDGELLSI RGV DGP LTV 120
LANQTLLVEG QVIRSEPTNTI SVYFRTFQDD GLGTFQLHYQ AFMLSCNPPR RPD SG DVTVM 180
DLHSGGVAIF HCHLGYELQG AKMLTCTINAS KPHWSSQEP I CSAPCGGAVH NAT IGRV LSP 240
SVPE NTNGSG FCIW TIEARE GQKLHLHFER LLLHDKDRMT VHSQGTN KSA LLYDSLQTES 300
VPEFGLLSEG NTIRIEFTSD QARAASTFNI RFEAFKGH C YEPYIQNGNF TTS DPTYNIG 360
TIVEFTCDPF HSLEQGPAIL ECINVRDPY W NDTEPLCRAM CGS ELSAVAG VVLS PNWPEP 420
YVEGEDCIWK IHVGEKRIP LDIQFLNLSN SDILTIYDGD EVMPHILQY LGNS GPQKLY 480
SSTPDLTIQF HSDPAGLIFG KGQGFIMNYI EVSRNDS CSD LPEIQNGWKT TSHT ELVRGA 540
RTTYQCDPGY DIVGSDTLTC QWDLWS SDDP PFCEKIMYCT DPEGEVDHSTR LISDPVLLVG 600
TTIQT CNPG FVLESGSLLT CYSRETGTPI WTSRLPHCVS EAAAE TSLEG GNMALAI FIP 660
VLIISLLLG AYIYITRCRY YSNLRLPLMY SHPYSQITVE TEFDNPIYET GGTQKV

```

Seq ID NO: 209 DNA sequence
Nucleic Acid Accession #: NM_001327.1
Coding sequence: 89-631

50
55
60
65

```

1 11 21 31 41 51
AGCAGGGGGC GCTGTGTGTA CCGAGAATAC GAGAATACCT CGTGGGCCCT GACCTTCTCT 60
CTGAGAGCCG GGCAGAGGCT CCGGAGCCAT GCAGGCCGAA GGCCGGGGCA CAGGGGGTTC 120
ACGCGCGCAT GCTGATGGCC CAGGAGGCC C TGGCATTCT GATGGCCAG GGGGCAATGC 180
TGGCGGCCCA GGAGAGCGCG GTGCCACGGG CGGCAGAGGT CCCC GGGGCG CAGGGGCAGC 240
AAGGGCCTCG GGGCGGGAG GAGGCGCCCC GCGGGGTCCG CATGGCGGCG CGGCTTCAGG 300
GCTGAATGGA TGCTGCAGAT GCGGGGCCAG GGGGCCGGAG AGCCGCTGCT TTGAGTTCTA 360
CCTCGCCATG CCTTTCGGCA CACCATGGA AGCAGAGCTG GCCCGCAGGA GCCTGGCCCA 420
GGATGCCCA CGCTTTCGG TGCCAGGGGT GCTTCTGAAG GAGTTCAGT TGTCCGGCAA 480
CATACTGACT ATCCGACTGA CTGCTGCAGA CCACCGCCAA CTGCAGCTCT CCATCAGCTC 540
CTGTCTCCAG CAGCTTTCCT TGTGATGTG GATCAGCAG TGCTTTCCTG CCGTGTTTTT 600
GGCTCAGCCT CCTCAGGGC AGAGGCGCTA AGCCAGCCT GGCGCCCTCT CCTAGGTCAT 660
GCCTCCTCCC CTAGGGAATG GTCCAGCAC GAGTGGCCAG TTCATTGTGG GGGCCTGATT 720
GTTTGTGCTG GAGAGGAGAC GGCTTACATG TTTGTTCTG TAGAAAAATAA AACTGAGCTA

```

Seq ID NO: 210 Protein sequence:
Protein Accession #: NP_001318.1

70
75

```

1 11 21 31 41 51
MQAEGRGTTG STGDADGPGG POIPDGPQGN AGGPGEAGAT GGRGFRGAGA ARASGPGGGA 60
PRGPHGGAAS GLNGCCRGGA RGPESRLLEF YLAMPFATPM EAELARRSLA QDAPPLFPVG 120
VLLKEFTVSG NILTIRLTAA DHRQLQLSIS SCLQLSLLM WITQCFLPVF LAQPPSGQRR

```

Seq ID NO: 211 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 52-459

80
85

```

1 11 21 31 41 51
CCTCGTGGGC CCTGACCTTC TCTCTGAGAG CCGGGCAGAG GCTCCGGAGC CATGCAGGCC 60
GAAGGCCAGG GCACAGGGGG TTCTACGGGC GATGCTGATG GCCCAGGAGG CCTTGGCATT 120
CCTGATGGCC CAGGGGGCAA TGCTGGCGGC CCAGGAGAGG CGGGTGCCAC GGGCGGCAGA 180
GGTCCCCGGG GCGCAGGGGC AGCAAGGGCC TCGGGGCCGA GAGGAGGCGC CCGCGGGGT 240
CCGATGGCG GTGCCGCTTC TGCGCAGGAT GGAAGGTGCC CCTGCGGGC CAGGAGGCCG 300

```

WO 02/086443

PCT/US02/12476

GACAGCGGCC TGCTTCAGTT CCGACTGACT GCTGCAGACC ACCGCCAACT GCAGCTCTCC 360
ATCAGCTCCT GTCTCCAGCA GCTTCCCTG TTGATGTGGA TCACGAGTG CTTTCTGCCC 420
GTGTTTTTGG CTCAGGCTCC CTCAGGGCAG AGGCGCTAAG CCCAGCTTGG CGCCCTTTC 480
TAGGTATGTC TCCTCCCTC AGGGAATGGT CCCAGCACGA GTGGCCAGTT CATTGTGGGG 540
GCCTGATTGT TTGTGCTGG AGGAGGACGG CTTACATGTT TGTTCCTGTA GAAAAATAAG 600
CTGAGCTA

Seq ID NO: 212 Protein sequence:
Protein Accession #: E08 sequence

1 11 21 31 41 51
MQAEGGQGTGG STGDADGPGG PGIPDGPGGN AGGPGEAGAT GGRGPRGAGA ARASGPRGGA 60
PRGPHGGAAS AQDGRPCPGA RRPDSRLQLF RLTAADHRQL QLSISSCLQQ LSLLMWITQC 120
PLPVFLAQAQ SQQRR

Seq ID NO: 213 DNA sequence
Nucleic Acid Accession #: NM_000555
Coding sequence: 416..1498

1 11 21 31 41 51
CTTATTTTTT ATGAATGTCG GATAGCTGCA CCAGCTTGGT GGGGAAAGGG TTTGATGAAT 60
AGCACAAAGA CACTGGCTGT TCCCTGGAGG CTGTCCCTTT AAAGGAGAAT CTTAGTTTAT 120
TCTGGGGGGA GGGGATGCAAC ACATTAGAGT AGGAAAGAGG GCTTGGAATA AAATGAAAAC 180
ACTCCCCCTT CATAGTCATT GTACTGAAAT GCAAAGACTG CTTCTTAAGC TGGAGATGCT 240
AACCTTGGGT AGCTCCTTCT GTTCTCTTCA AGGGGAATTT TGTCAAGGTA TGGATTCTAT 300
TACAACGTGT AGTCATGTGG GCATGTGTGA GGAACAGAT GCCAGTTTAT ATGTATTTAG 360
CCGGAAGTTC CAATTGTGATA GGAGCCACTG TCAGTCTCTG AGGTTCCACC AAAATATGGA 420
ACTTGATTTT GGACACTTTG ACGAAAGAGA TAAGACATCC AGGAACATGC GAGGCTCCCC 480
GATGAATGGG TCGCTGATCC CCACCTACAG CGCCCACTGT AGCTTCTACC GAACCCAGAA 540
CTTGCAAGCA CTGAGTAATG AGAAGAAAGC CAAGAAGGTA CGTTTCTACC GCAATGGGGA 600
CCGCTACTTC AAGGGGATGG TGTACGCTGT GTCTCTGAC CGTTTTCGCA GCTTTGACGC 660
CTTGCTGGCT GACCTGACGC GATCTCTGTC TGACAACATC AACCTGCTTC AGGGAGTGGC 720
TTACATTAC ACCATTGATG GATCCAGGAA GATCGGAAGC ATGGATGAAC TGGAGGAAGG 780
GGAAAGCTAT GTCTGTTCCT CAGACAACTT CTTTAAAGAG GTGGAGTACA CCAAGAAATG 840
CAATCCCAAC TGGTCTGTCA ACCTAAAAGC ATCTGCCAAT ATGAAAGCCC CCCAGTCTCT 900
GGCTAGCAGC AACAGTGCAC AGGCCAGGGA GAACAAGGAC TTTGTGCGCC CCAAGCTGGT 960
TACCATCATC CGCAGTGGGG TGAAGCCTCG GAAGGCTGTG CGTGTGCTTC TGAACAAGAA 1020
GACAGCCCAT CTTTGTGAGC AAGTCTCTAC TGATATCACA GAAGCCATCA AACTGGAGAC 1080
CGGGGTGTCT AAAAATCTCT ACACCTGGA TGGAAACAGG GTAACCTTGT TCCATGATTT 1140
CTTTGGTGAT GATGATGTGT TTATTGCTGT TGGTCTGTA AAATTTCTGT ATGCTCAGGA 1200
TGATTTTTCT CTGGATGAAT ATGAATGCGG AGTCATGAAG GGAACCCAT CAGCCACAGC 1260
TGGCCCAAGG GCATCCCAAA CACCTCAGAA GACTTCAGCC AAGAGCCCTG GTCTATGCG 1320
CCGAAGCAAG TCTCAGCTG ACTCAGCAAA CGGAACCTCC AGCAGCCAGC TCTCTACCCC 1380
CAAGTCTAAG CAGTCTCCCA TCTCTACGCC CACCACTCCT GGCAGCCCTC GGAAGCACAA 1440
GGACCTGTAC CTGCTCTGTG CTTTGGATGA CTGCGACTCG CTTGGTGATT CCAATGTAAG 1500
GAGGGAGAGG TGCTCAGAGT CCAGAGTACA AATCCAAGCC TATCATTGTA GTAGGGTACT 1560
TCTGCTCAAG TGTCCAACAG GGCTATTGGT GCTTTCAGT TTTTATTGTT TGTGTTGTTG 1620
TATTTTGAAA AACACATTGT AATATGTTGG GTTATTTTTC CTGTGATTTC TCCTCTGGGC 1680
CACTGATCCA CAGTATCAAT TTATGAGAGA TAGATTGATA ACCATCTCTT GGGGCAGCAT 1740
TCCAGGGATG CAAAATGTGC TAGTCCATGA CCTTCAATG GAAAGCTTAG GGGCCTGGGG 1800
TAAATTTGCC CTGTTTAAAT TTGCCCAAAC AGTTTCTCTT TGTAGAGGG GTGTTTAAAT 1860
ATACAGCAAT TAAAAGTTT GTGTGGGGA AAAAAAACT CATGGCAGA TCCAAGAATG 1920
ACAAACACAA GTGCCCTTT TCTCTGGATC TCAAGAATGG TGGAGGACCC TGAAGGACA 1980
GCAAGGCAGT TCCCAGCCT CACTCTTAC TCTGTATTGA GGCCCGGTT TGTGTGCCAG 2040
CACCAATCTT GGCTGTCAAT GGGGAGAAAT AAACCAACAA CTTATAATTG TGACACCAGA 2100
TGCTTAGGAT CCTGTGCTGT GGTTAGCTAA GAGAATAGAC AGAATTGGAA AATACTCAG 2160
ACATTTCGGA AGAGTTTATA AAGCAGAGT AATCTCTGGT CAATCTCTCC ACTGAGGCAA 2220
TTTGGAATCA ATAAGCAATT GATAATAGTT TGGAGTAAGG GACTTCATAT ACCTGATTCC 2280
TCTAGAAGGC TGTCTAAGAT ACCACATGAT TACATGAAC GTATGGTATC CATCTATCTC 2340
TGTTCTATTG AATGCTTGT TAACAGCCAA CACTGAAAAC ACTGTGAGAA TTTGTTTCA 2400
GGTCTGACAC CTTTCACTCT CTTTATTAG CAAGAAATCA ATATCCTTTT TATAAAAAAT 2460
CATGTCTGTA TTTCAGGAGC AAACCTCTCA GGCTCCTTTT TTATAAACTG GTGATTTTTC 2520
TTTGTCTAA AAAACACATG AAGAAAATTT ACCAGAAAAA AAAAAAAGG CCGAAGAATA 2580
ATGTTATTTA GAAATTATGC TGTCACTGCC AAACAGTAAC CTCCAGGAGA AAACAAGATG 2640
AATAGCAGAG GCCAATTCAG TAGAATCAGT TTTTGTATAG CTTTTTAACA GTTATGCTTG 2700
CATTAAATAT TTCAATGTGG ACCAGACATT CTAATTATAT TTTAAATGAA ATGTTACAGC 2760
ATATTTTAAG CAACCTTTT TATCTATAAT CCTAATATTT CATACTGAAG ACACAGAAAT 2820
CTTTCACCTG TCTTTAACAT TAGAAAGGAT TTCTCTTAC TAAGGACTGA TCATTTGAAA 2880
TAGTTTTTCA TCTTTTGAGA TACAGGTTTA TAACACTGCT TTTTTTTCC TGTAAACATA 2940
GCCCAATAAT GCAAAAACAA CTAATTTTAA TTGAAGGTCT TGCTTGCCAN TCCTGTGTTG 3000
GCTTTNACCA AATATAAAAA TTCCCTTATT CCTTGTAAT GGTGCAATN TTTGGAAGG 3060
CACAGCATCC AAACCAAGCT GCTGTTTGGC TACTGAATGG CTTGCAGTTG TTCCTCCACT 3120
CTAAATGGAA TGAGCTTGCT GTGTGTGTGT GTGGTGGTGG TGGGAGGGGG TGGTGCAATG 3180
GTGTGTGTGT GTGTGCATCT GCAGCTGCTT CAAAATTAAG AAATACTACA AGACACCCCT 3240
GTAATGGATT GGTGGCACT GGGTGGCACT GCTGATGTGC ACTGTGTAGG GGGGAACCCA 3300
GTGGTGGTGG GGTATCTCAA ATGCCCTTAG ACAAGCTTCA GATGTCTGTA GCTACCAAAA 3360
ACATTTTCGG TTCAAGAAAA GTGAGATGAT GGTAGTACTG GTTCTGCTGT AAATTGAAAA 3420
ACCCCAATG ATGAGGATCT CTTTGTGCC CCTCTCTTT TTTTGTAAAC CCATTCAAAA 3480
CCATTAAATA GCCCATTTTA CTAANCCCTT ATTTCTTTCT AGAAGCTCAG GGTTTNCTTA 3540
GTGCCTCCCA NAACATTTTG TAGTTAATTG GGAAGAAAGT ATACTTGGAT TAGGGGGTGT 3600
GGGCATAAAG AATGTGGGGA GGCTGATTT TAAAATTCAG GCCAGAACCC CCAATGACTC 3660
CACCCATAGT NTCATTTAG GTCTCATTTA GTCCATCACC TTTATTTTAA GTTGAGGAAG 3720
TGGAGGCTGG TAAAGAGCAG GACCAGAGGA AGAATCCAGA TTTCTTATG CTTGGGCTCT 3780
ACACTAGCTC TMTAGATATT TCCTTGATTG CGGTATATGT ACTACTAGAA AATACCAAT 3840
GGATATATT TCTTAGGAT AACCTTTGAA CCAACAATNT TCAATAACAA TAGTACATCT 3900

	TCCATCTTAC	TTTTAATCGA	GTATAAGGAA	ATGTTTCTTT	ATGGCCATT	TGGAGGGAGC	3960
	AGGGGATGAG	GCTTGGCATA	GTCCAAAATT	TAAGNCTCCA	ATAATTAAAT	GCATTTTAAA	4020
5	TTGTTTTTAA	TTGGCCCACT	TTCAAGGCAA	TTTTTTTTTG	GTGCTGTGTA	CTGAGCTCCT	4080
	CCACCCCTGT	CATTCACTTC	CAATTTTACC	CAATCCAATT	TTAGCACTCA	AGTTCCATTG	4140
	TGTTAAATTT	TGCAGGGTCT	ACACACATCA	AGTCAGCAAG	CATTTGCCAC	CACCTCCCTAT	4200
	ACTTCTCCCT	CTTTTTTACA	CACACACACA	CACACACACA	CACATCCAT	CTCTTGCTTG	4260
	TTCTACCTC	CCTGATTTTT	CTTCCCTACA	GAAATAGAAA	TAGGGACAAA	GAAGGGGAAA	4320
	ATGTATATAT	TGGGGCTGGG	CTGAACAACT	AACCTTCATA	GTAGTATTAA	CTAGGGGTAA	4380
10	ATTGAGAGAA	AAGCTCCTTT	TCTCTTCACT	GTTTTGGAAA	GGATAGCCAT	TAGCATGACT	4440
	GCTTTGTGTC	CTTATGGACT	TTAGTATTAG	CCTAGATTGA	ATTATAGCGT	TTTCTTAGCT	4500
	GAAGGAACCT	TAAGATCACA	TCATCTACTC	CTCTACTCCA	AATTTCTCAT	TCTTCAGGCC	4560
	AGGAAACCGA	GACACAGAGG	TAAAGTAATT	TCCCCAAGGT	CACACAGCTG	GCTGGGCGAG	4620
	GATTGGGTTT	ACAACCCACA	TCTCCTGGCT	CTTATTTCCAG	GGCCTTTTCC	CACTAAGTAG	4680
15	TATTGCCTTC	CATTGCTTTT	CTGAGAGTTA	TTTCTCAGGG	TCATGTTGCA	TCTTGGAGCC	4740
	ACATGCTGCT	GGCCTGATCT	CAGTGGGAAA	TNACCACCAGC	AACCTAAATAC	AGCCCCTTTT	4800
	CCCTGCATT	CCTGGTTTCC	CATCCACATG	GGTTGCAGAT	GTCCCTGAAG	AGAGTGAGGC	4860
	ATTGAGGGCC	AATAGGAGCA	ATGGGGTCCC	TGGCCTTGTC	CATCTGATT	AGGAGATCAC	4920
	TGCTCCATCG	TGAGGAGCCC	TCTGAATAGC	CCCCCACTGA	ATGCTTGCCCT	TGCCCAATAG	4980
20	GAATGGAGGA	AGATTGCTTT	TCTCCATCAG	TTCACTTGT	GTCTCTCAT	AATGGTTTGT	5040
	CTTTCCAGGC	TGAGGGAAT	GTCTCTGTT	TCCANAGTAN	AAAAAAGAAA	GAGTGGAACA	5100
	ATANCTTTGT	TCTACTTAC	TTTCTGAGAT	GGCTTTTCAA	CATTTAAAAA	AACTAGTGT	5160
	GGTACCATT	ACTGCGANGA	TTTNTTTTAG	AATATGGGAG	TAAGATGAGG	TAGAGAAAAT	5220
	AACTGGTCT	CAGTGTGGTT	GGCCTCATCC	ACAATGTCCC	CAAAGCCATC	CTGCTNTGAT	5280
25	GAGGACAATT	TCCAGGTATA	AGCAAGGGGC	TTTGTGACAA	AAATGTACCC	TGGCTGATGT	5340
	TAAACATTGG	CTCCTGTGTT	TGCACCAAAA	TAGCAAGCTG	TGTGCTCTAT	ACACTCTTCC	5400
	CATCGTCTTG	TGTACTGTGC	TCTGTGGGCC	TTCCACAGCA	GAAACCAGGG	CAAAAGGGTC	5460
	CAACACATG	GTTCCTCTTG	CTGCAAGGCT	NTTCTGGGA	ACTAAGGGGG	TATTTATTAG	5520
	TTCAGTTNTA	AGAGACCTCC	TTCTGGGCTT	ACCCCACTCC	TCAGTACTT	CTCTCTCCTT	5580
30	CCTCCTTCTC	TCCCACTGTC	ACAAGTAACC	AAGGAACCTG	AAAGTGGATG	TGTAGCTATT	5640
	TGAAGAAGGC	AAGGAACCTT	GAGATCTTTC	TTTGAATCCT	TTAGTCCAAG	TCTTAGACCA	5700
	GTGATTGGTG	CTTACCTTTA	ACAAAATTTT	GTCTGTGTTT	CTAATCCCTT	CAATACNTTG	5760
	GGTACAATGC	TCCCAATCAC	CCTGCACATT	TGATTCTAAA	TGGCTTTTAT	TTTTTAAAAA	5820
	TCCATATCCC	TAGGACAAGA	NAACAGGATG	CCTATATCCC	CAAAATGAGC	TCCAGGACAC	5880
35	TGATGGGAAT	GAATTTGGCC	CCATCTATCC	CTCAGAAAAC	GTCTGTGCCA	ANAGACTTCC	5940
	CCAGATAGAA	NCAGTGGGAC	AGTGGTTTGA	ACGACTTCTT	TTATGGTTGT	CCAGTTTGCT	6000
	ATGGAATAAA	AAGGCTATGA	TTTTTTAAAA	AAGATGATTG	GAACCTGTCT	TTGGCCACAT	6060
	AGGGCCACTT	GGATCCATTT	CCAGGCCCTTA	CTCATATATT	GCCTTCAGTG	AAGGGCTTTG	6120
	GCTTTAAGTC	CCAGACTGGT	CTCCCAAGTG	AACCATAAGT	GTTCCTGGAG	TCATCTGGGG	6180
40	TGAGGCATGA	GAATTTGGCC	CCATCTATCC	CTTCAGGAAA	AGGTGCCTTC	CCTCCCTTTC	6240
	TCCTAAAGCC	TGGTCCCCAA	AAATTTGTTT	TGTCTCCAAA	AGTCTAGTAT	GGTCTTTATA	6300
	CACCCANACT	CTTAGTGTGG	CGTCTGCTTC	TGTTTCTTGG	TAAAGGATCT	ATGCANACTG	6360
	CCCGCTTTGG	CTTAGCTAGC	GTGACATTGG	CTATCATTGG	ACAAGACTAA	CTTTTTTTTT	6420
	TTTTTTTTTG	ACTGAGTCTC	CCTCTGTAC	CTAGGCTGGA	GTGCACTGGC	ACAATCTTGG	6480
45	TCGCTGCAAA	CCCTCACCTT	TCACCTCCCA	GGTCGAAGCG	ATTCCTCTGC	CTCAGTCTCC	6540
	CGAGTAGCTG	GGATTACAGG	CGTGCGCCAC	CRAATCTGGC	TATTTTTTTA	TTATTATTAT	6600
	TTTTAGTAGA	GATGAGGTTT	CACCATGTTG	GCCAGACTGG	TCTTGAACCT	TTGGGCTCAA	6660
	ATTATCTGCC	CACCTCGGCC	TCCCAAGATG	CTGGGATTAC	AGGCATGAGC	ACCATGCCCA	6720
	CGTGACAAGA	CTAATTTTTT	ATCCCTTGGT	TTATTGGCTT	CAACATCTTC	TGGAATCAGA	6780
50	GGTGATTTTT	TCTTACCTTG	GATGCCTGAG	ACTAGGGGAG	TATAGAATTC	CAATTGGTAA	6840
	TTAAGGCATC	TTTCTGCTTC	TGATCAGAAG	GGCAGGTTAG	TTGGGAGAGG	TCAGATGGCA	6900
	CAACAGAAGT	CACCTTGTAA	GTAAGGCAAA	GACTTTGAAG	GCATTAGCGT	TTCTCATTAT	6960
	TAGGTCAAT	AACCTTGAGG	GAATCAATGG	CTTTTTTGCC	GCTCTACCTC	TTTGTGTATC	7020
	TCITTGACTT	CTTCTCTCTC	GTCTAGTTTC	CTCTGTTCTC	AGTTTATATT	CTATGTTATC	7080
55	AGTCTCTCTT	TCCACAGTAC	AAACATCCAT	CCTTCTCTCT	GTGCAATCTC	GTCTCTCCCT	7140
	CTTATTATCT	TTATTGTGAT	TTTTCTCTTC	CTCCCTGTCT	AGGCATTGGG	CATGTGCCTC	7200
	TTCTTAGCCT	GTGATTTTGC	CTTGGGACTG	ATGATAAATT	ATTTCCAGAT	TCAATCAGCC	7260
	CTGGTCTTAC	CCCACTCCAA	TCAGAAGTAT	GTGGTGGGGG	AATCAACCTG	ATCCTGGCCC	7320
	TTCTTCTTTC	TCCATTTTCA	TTCTGAATCC	CCCTCAGCAG	ATCTTTACAA	GCAGTTTCTT	7380
60	TATAGCTCAT	GTATCTTTAG	GTCTTTGCCT	TCCAAGCACT	GTACAGAATA	CTTTGTGGTT	7440
	CCTTTTATAG	CTGACATTTT	GTGGAGCAGT	GAAGCGTGCT	CAGAGACATA	ATCAGCTGAA	7500
	GAGAAAAAAT	CCACCAATGG	ATTTATATCA	GCTAAATACT	AATAATTGAT	TTTGTGTTAT	7560
	GTGCCCATAA	TTTTTAAAGC	TGCAATATAA	TATAATGAGG	GACCACAGGT	AATTTCTCCT	7620
	GTCAATTGTT	TGGCTGGGAT	GGGGGTGGGG	GAGTAATTGC	TTAAAGTTT	ACCATTACAC	7680
65	ATTAAACTCT	CTATAATAAT	CTTGTTTGGG	GCTTGCTAAC	TGTTGAGCTG	TTTAACTAA	7740
	ACTGGTAGGC	AATCGGAGTT	GATTTAAATG	AAAAGATAAT	TTAACAAATC	TATACTATAA	7800
	AAAGAGACAT	TGCTTAAATT	GACATGTATT	TTTCTCTTCT	GAGTCACTTA	AACATTACTT	7860
	CTTGACACCA	ACTGTTCAAT	ATACTGAATA	GACAGTCCAT	ATAAGAGAAA	TTAGTGGACC	7920
	TAAAGAAGCC	AGATTGTATG	TGTTAATTTA	TTAAACAGAA	TTGCAAGGCC	CTTGGAAATG	7980
70	TCAGTGCTTG	GCAATACCAT	ATGGCATGCC	AAAATTTACA	ATGACTTTTC	TTTATAAGTT	8040
	ATCCAAAAGG	GATTTTGAACA	AGTAAGAGGT	TATGCCAAA	TGCTCTCAAT	GTATGGTCTT	8100
	GTAATATATT	GCAGCTTGAA	GCCAATGATC	CCTTATGACT	TGTATACAAC	TAATGCATGT	8160
	TTTATTGAAT	TTTGCAATTC	CCACGTGTGG	TAAGTCTTTA	AAATGTTTTT	GATCACCTTT	8220
	NTGTGCCATT	AAACTTGTAC	AGAAAATGTT	TTTATGGCCA	TTTTCAAAGG	GAGAAAAGTT	8280
75	AAAATGGAAA	CAGCCCAACC	TTTCTGCCCT	ATAGCTGTAG	TAGAATTGA	GTACCTGTAG	8340
	CAAAACAGCT	GTAATTTGGT	GTGTAGTGT	TAGAGGTGTT	AGCTTGCTAG	TGACTAGCTT	8400
	TGGAGAGTAA	ATGATGTGTA	TTGTACATCA	CATTTCCTAA	CTCGTTTAA	CCTCTGAAAA	8460
	GAATATATTC	TTCTTTGTAG	TCCTTCTTCC	CACCCCTTTC	CCCTCTCCCT	CTCCCTGTCT	8520
	CCAGTTGTCT	TACAGTTGTA	AATATCTGAT	TTGAGGCCCA	ATAACTCTTG	CCAAGTAAAG	8580
80	TCAGCAAAAC	ACAAACAAAC	CAAAATGTGG	GGAAAAGGCA	TTTCTCAACC	ATCTCTCAGC	8640
	AGTTATTGAT	CATTTCTTAA	GGAAACAGCAT	TGTGATCAAA	GACTCAACTT	TACGTAAAAA	8700
	TCAGTGGTAA	ATTGGGGTTG	TATTGGCCAT	TGATTACATT	CAGGATTGAA	TAGTTTTTCA	8760
	AATCATGATG	AATCCAAAGA	CAGTAGGTAG	TGATGTCCCT	TATCCCTGCA	GCTGTTTTAA	8820
	GATAGAGACC	TCAGAAGACT	CTGCTTGACC	GATGACCAAT	AATATTGTA	AAAAAAGAGA	8880
	AAAAATGAGA	GAAATAAAC	AGATATTATA	GAACCTTAGC	CACCTATTTA	GAATAGTTAT	8940
85	AGCCAGAAAA	AAAAACAAGG	GCATGAGTTC	AAATGCATTA	CTATCAGTGT	CCTAGGCAAT	9000
	ACCTAACCTA	CTCTGAAATT	GTGATTCAAA	AGCAGTATTT	CAAGAGGCAT	TCTCCTTTTT	9060
	TGGTTTGCTG	ACCCCACTTG	GACTGGTAGG	TTTGGTGAGG	CCCCCATAAA	CCAGCTGGAG	9120

CAGACCCCTT TCATCTCCTG TGCCTGTAAC ACCCCTCTTC CCCCACCCCC TCCGCAATTC 9180
 AATGAGGGCT TTCTTGGGTC AGAGGACTTC AAGGTTGTCT AGAGAAGTTT GCCATGTGTG 9240
 TAAGGTGCTG TGAAGCTGTA GTGCTGAAGA TTCGCAGCAT TCAATACCAG GCAGCCAAAG 9300
 AGCTGCTCTT GCAATTATTT TGGCTCTCAA GCTCTGTTCT TCATCGCATT CTCAATTCTG 9360
 TGTACATTG CAAGATGTGT GTAATGTCAT TTTCACAAA TAAATTTGA TTTCAAT

Seq ID NO: 214 Protein sequence:
 Protein Accession #: NP_000546

1 11 21 31 41 51
 MELDFGHFDE RDKTSRNRMG SRMNGLPSP T HSAHCSFYRT RTLQALSNEK KAKKVRFYRN 60
 GDRYFKGIVY AVSSDRFRSF DALLADLTRS LSDNINLPQG VRYIYITDGS RKIGSMDELE 120
 EGESYVCSDD NFFPKVEYTK NVNPNWSVNV KTSANMKAPQ SLASSNSAQ A RENKDFVRPK 180
 LVTIIRSGVK PRKAVRVLLN KKTAKHSEFQV LTDITEAIKL ETGVVVKLYT LDGKQVTCLEH 240
 DFFGDDDVFI ACPGPKFRYA QDDPSLDENE CRVMKGNPSA TAGPKASPTP QKTSKSPGP 300
 MRRSKSPADS ANGTSSSQLS TPKSKQSPIS TPTSPGSLRK HKDLYLPLSL DSDSLGDSM

Seq ID NO: 215 DNA sequence
 Nucleic Acid Accession #: NM_130467
 Coding sequence: 312..644

1 11 21 31 41 51
 GGCACGAGGC AGAGCTCTGC AAGGAGAGGT TGTGCTCTCG TTCTTTCCGC CATCTTCGTT 60
 CTTTCCAACA TCTTCGTCTT TTCTCACTGA CCGAGACTCA GCCGGTAGGT CTGCAGAGTG 120
 GTCTTCTCTG TAATTTAGTT GTGAGTGAAT GTGTGGAGGA GCCAGCGGGC TTAGGACAGG 180
 TCTGTGGCA CAGTCCGTGG CTTTGAAGGA AAAGGCCCTC GCGGTGGTCC TCGCCTTCC 240
 CCCAGGTCTG GATGCAGCGC CCATGGGCGG GTAATCGTGG CTGGGCTGGA ACGAGGGAGG 300
 AAGTGAGAGA TATGAGTGAG CATGTAACAA GATCCCAATC CTCAGAAAGA GGAAATGACC 360
 AAGAGTCTTC CCAGCCAGTT GGACCTGTGA TTGTCCAGCA GCCCACTGAG GAAAAACGTC 420
 AAGAAGAGGA ACCACCAACT GATAATCAGG GTATTGCACC TAGTGGGGAG ATCAAAAATG 480
 AAGGAGCACC TGCTGTTCAA GGGACTGATG TGGAGCTTT TCAACAGGAA CTGGCTCTGC 540
 TTAAGATAGA GGATGCACCT GGAGATGGTC CTGATGTGAG GGAGGGGACT CTGCCCACTT 600
 TTGATCCAC TAAAGTGCTG GAAGCAGGTG AAGGGCAACT ATAGGTTTAA ACCAAGACAA 660
 ATGAAGACTG AAACCAAGAA TATTGTTCTT ATGCTGGAAG TTTGACTGCT AACATTCTCT 720
 TAATAAGATT TTACAGTTTT CTGCAAAAAA AAAAAAAAAA AAA

Seq ID NO: 216 Protein sequence:
 Protein Accession #: NP_569734

1 11 21 31 41 51
 MSEHVTRSQS SERGNDQESS QPVGPFVIVQ PTEBKQEEE PPTDNQGIAP SGEIKNEGAP 60
 AVQGTDEAF QQELALLKIE DAPGDGPDVR EGTLPFTDPT KVLEAGEGQL

Seq ID NO: 217 DNA sequence
 Nucleic Acid Accession #: NM_001476.1
 Coding sequence: 82..435

1 11 21 31 41 51
 GCCAGGGAGC TGTGAGGCAG TGCTGTGTGG TTCTGCGCGT CCGGACTCTT TTTCCTCTAC 60
 TGAGATTTCAT CTGTGTGAAA TATGAGTTGG CGAGGAAGAT CGACCTATTA TTGGCCTAGA 120
 CCAAGGCGCT ATGTACAGCC TCCTGAAGTG ATTGGGCCTA TGCGGCCCGA GCAGTTCACT 180
 GATGAAGTGG AACCAGCAAC ACCTGAAGAA GGGGAACCAG CAACTCAACG TCAGGATCCT 240
 GCAGTGTCTC AGGAGGGAGA GGATGAGGGA GCATCTGCAG GTCAGGGGCC GAAGCCTGAA 300
 GCTGATAGCC AGGAACAGG TCACCCACAG ACTGGGTGTG AGTGTGAAGA TGGTCTCTGAT 360
 GGGCAGGAGG TGGACCCGCC AAATCCAGAG GAGGTGAAAA CGCCTGAAGA AGGTGAAAAG 420
 CAATACAGT GTTAAAGAA GACACGTTGA AATGATGCAG GCTGCTCTTA TGTGGAAAT 480
 TTGTTTACATTA AATTCTCTCC AATAAAGCTT TACAGCCTTC TGCAAAA

Seq ID NO: 218 Protein sequence:
 Protein Accession #: NP_001467.1

1 11 21 31 41 51
 MSWRGRSTYY WPRPRRYVQF PEVIGPMRPE QFSDEVEPAT FEEGEPATQR QDPAAQEGE 60
 DEGASAGQGP KPEADSQEQG HPQTGCCEED GPDGGQEVDFP NPEVKTPEE GEKQSQC

Seq ID NO: 219 DNA sequence
 Nucleic Acid Accession #: NM_001476
 Coding sequence: 90-3671

1 11 21 31 41 51
 ACAGCGGAGC GCAGAGTGAG AACCACCAAC CGAGGCGCGG GGCAGCGACC CTGCAGCGG 60
 AGACAGAGAC TGAGCGGCCC GGCACCGCCA TGCCCTGCGCT CTGGCTGGGC TGCTGCCTCT 120
 GCTTCTCGCT CCTCTGCCC GCAGCCCGGG CCACCTCCAG GAGGGAAGTC TGTGATTGCA 180
 ATGGGAAGTC CAGGCAAGTG ATCTTTGATC GGGAACTTCA CAGACAAATC GGTAATGGAT 240
 TCCGCTGCGCT CAACTGCAAT GACAACACTG ATGGCATTCA CTGCGAGAAG TGCAAGAAATG 300
 GCTTTTACCG GCACAGAGAA AGGGACCGCT GTTTGCCCTG CAATTGTAAC TCCAAAGGTT 360

	CTCTTAGTGC	TCGATGTGAC	AACCTCTGGAC	GGTGACGCTG	TAAACCAAGGT	GTGACAGGAG	420
	CCAGATGCGA	CCGATGTCTG	CCAGGCTTCC	ACATGCTCAC	GGATGCGGGG	TGCACCCAAG	480
	ACCAGAGACT	GCTAGACTCC	AAGTGTGACT	GTGACCCAGC	TGGCATCGCA	GGGCCCTGTG	540
5	ACGCGGGCCG	CTGTGTCTGC	AAGCCAGCTG	TTACTGGAGA	ACGCTGTGAT	AGGTGTGATG	600
	CAGGTTACTA	TAAATCTGGAT	GGGGGGAACC	CTGAGGGCTG	TACCCAGTGT	TTCTGCTATG	660
	GGCATTACAG	CAGCTGCCGC	AGCTCTGCAG	AATACAGTGT	CCATAAGATC	ACCTCTACCT	720
	TTATCAAGA	TGTTGATGGC	TGGAAGGCTG	TCCAACGAAA	TGGGTCTCCT	GCAAAGCTCC	780
	AATGGTCACA	GCGCCATCAA	GATGTGTTTA	GCTCAGCCCA	ACGACTAGAC	CCTGTCTATT	840
10	TTGTGGCTCC	TGCCAAATTT	CTTGGGAATC	AACAGGTGAG	CTATGGGCAA	AGCCTGTCTT	900
	TTGACTACCG	TGTGGACAGA	GGAGGCAGAC	ACCCATCTGC	CCATGATGTG	ATTCTGGAAG	960
	GTGCTGGTCT	ACGGATCACA	GCTCCCTTGA	TGCCACTTGG	CAAGCACTG	CCTGTGGGCG	1020
	TCACCAAGAC	TTACACATTC	AGGTTAAATG	AGCATCCAAG	CAATAATTGG	AGCCCCCAGC	1080
	TGAGTTACTT	TGAGTATCGA	AGGTTACTGC	GGAACTCTAC	AGCCCTCCGC	ATCCGAGCTA	1140
	CATATGGAGA	ATACAGTACT	GGGTACATTG	ACAATGTGAC	CCTGATTTC	GCCCCCCTTG	1200
15	TCTCTGGAGC	CCCAGCACCC	TGGGTTGAAC	AGTGATATAT	TCCTGTGTGG	TACAAGGGGC	1260
	AATTCTGCCA	GGATTGTGCT	TCTGGCTACA	AGAGAGATTG	AGCGAGACTG	GGGCTTTTGG	1320
	GCACCTGTAT	TCCTTGTAA	TGTCAAGGGG	GAGGGGCTGT	TGATCCAGAC	ACAGGAGATT	1380
	GTTATTACAG	GGATGAGAAT	CCTGACATTG	AGTGTGCTGA	CTGCCCAATT	GGTTTCTACA	1440
	ACGATCCGCA	AGCAGCTGAC	AGCTGCAAGC	CATGTCCCTG	TCATAACGGG	TTGAGCTGCT	1500
20	CAGTGATGCC	GGAGACCGAG	GAGGTGGTGT	GCAATAACTG	CCCTCCCGGG	GTCAACGGTG	1560
	CCCGCTGTGA	GCTCTGTGCT	GATGGCTACT	TTGGGGACCC	CTTTGGTGAA	CATGGCCAG	1620
	TGAGGCCCTT	TCAGCCCTGT	CAATGCAACA	ACAAATGTGA	CCCCAGTGCC	TCTGGGAATT	1680
	GTGACCCGGT	GACAGGCAGG	TGTTTGAAGT	GTATCCACAA	CACAGCCGGC	ATCTACTCGG	1740
	ACCAGTGCAA	ATCAGGTACT	TTGCGGGACC	CATTGGCTCC	CAACCCAGCA	GACCAAGTGC	1800
25	GAGCTTGCAA	CTGTAAACCC	ATGGGCTCAG	AGCCTGTAGG	ATGTGCAAGT	GATGGCACCT	1860
	GTGTTTGCAA	GCCAGGATTT	GGTGGCCCCA	ACTGTGAGCA	TGGAGCATTC	AGCTGTCCAG	1920
	CTTGCTATAA	TCAAGTGAAG	ATTGAGATGG	ATCAGTTTAT	GCAGCAGCTT	CAGAGAATGG	1980
	AGGCCCTGAT	TTCAAAGGCT	CAGGGTGGTG	ATGGAGTAGT	ACCTGATACA	GAGCTGGAAG	2040
	GCAGGATGCA	GCAGGCTGAG	CAGGCCCTTC	AGGACATTCT	GAGAGATGCC	CAGATTTCAG	2100
30	AAGGTGCTAG	CAGATCCCTT	GGTCTCCAGT	TGGCCAAGGT	GAGGAGCCAA	GAGAACAGCT	2160
	ACCAGAGCCG	CCTGGATGAC	CTCAAGATGA	CTGTGGAAG	AGTTCCGGCT	CTGGGAAGTC	2220
	AGTACCAGAA	CCGAGTTCCG	GATACTCACA	GGCTCATCAC	TCAGATGCAG	CTGAGCCTGG	2280
	CAGAAAGTGA	AGCTTCCTTG	GGAAACACTA	ACATTCCCTG	CTCAGACCAC	TACGTGGGGC	2340
	CAAAATGGCT	TAAAGTCTG	GCTCAGGAGG	CCACAAGATT	AGCAGAAAGT	CACGTGTGAT	2400
35	CAGCCAGTAA	CATGGAGCAA	CTGACAGGGG	AAACTGAGGA	CTATTCCAAA	CAAGCCCTCT	2460
	CACTGGTGCG	CAAGGCCCTG	CATGAAGGAG	TCGGAAGCGG	AAGCGGTAGC	CCGGACGGTG	2520
	CTGTGGTGCA	AGGGCTTGTG	GAAAAATTGG	AGAAAAACCA	GTCCCTGGCC	CAGCAGTTGA	2580
	CAAGGGAGGC	CACCTCAAGC	GAAATTGAAG	CAGATAGGTC	TTATCAGCAC	AGTCTCCGCC	2640
	TCCTGGATTG	AGTGTCTCGG	CTTCAGGGAG	TCAGTGATCA	GTCCCTTTCAG	GTGGGAAGAAG	2700
40	CAAAGAGGAT	CAACCAAAAG	GCGGATTAC	TCTCAACGCT	GGTAACCAAG	CATATGGATG	2760
	AGTTCAAGCG	TACACAAAG	AATCTGGGAA	ACTGGAAAGA	AGAAGCACAG	CAGCTCTTAC	2820
	AGAATGGAAA	AAGTGGGAGA	GAGAAATCAG	ATCAGCTGCT	TTCCCGTGCC	AATCTTGCTA	2880
	AAAGCAGAGC	ACAAGAGACA	CTGAGTATGG	GCAATGCCAC	TTTTTATGAA	GTGAGAGCA	2940
45	TCCTTAAAAA	CTCAGAGAG	TTTGACCTGC	AGGTGGACAA	CAGAAAAGCA	GAAGCTGAAG	3000
	AAGCCATGAA	GAGACTCTCC	TACATCAGCC	AGAAGGTTTC	AGATGCCAGT	GACAAGACCC	3060
	AGCAAGCAGA	AAGAGCCCTG	GGGAGCGCTG	CTGCTGATGC	ACAGAGGGCA	AAGAATGGGG	3120
	CCGGGGAGGC	CCTGGAATTC	TCCAGTGAGA	TTGAACAGGA	GATTGGGAGT	CTGAACCTGG	3180
	AAGCCAAATG	GAGAGCAGAT	GGAGCCTTGG	CCATGGAAAA	GGGACTGGCC	TCTCTGAAGA	3240
50	GTGAGATGAG	GGAAAGTGAA	GGAGAGCTGG	AAAGGAAGGA	GCTGGAGTTT	GACACGAATA	3300
	TGGATGCAGT	ACAGATGGTG	ATTACAGAAG	CCCAGAAGGT	TGATACCAGA	GCCAAAGAAC	3360
	CTGGGGTTAC	AATCAAGAGC	ACACTCAACA	CATTAGAAGG	CCTCTGCACT	CTGATGGACC	3420
	AGCCTCTCAG	TGTAGATGAA	GAGGGGCTGG	TCTTACTGGA	GCAGAAGCTT	TCCCGAGCCA	3480
	AGACCCAGAT	CAACAGCCAA	CTGGGGCCCA	TGATGTGAGA	GCTGGAAGAG	AGGGCACGTC	3540
55	AGCAGAGGGG	CCACCTCCAT	TTGCTGGAGA	CAAGCATAGA	TGGGATTCTG	GCTGATGTGA	3600
	AGAACTTGGA	GAACTATTAG	GACAACCTGC	CCCCAGGCTG	CTACAATACC	CAGGCTCTTG	3660
	AGCAACAGTG	AAGCTGCTAG	AAATATTCT	CAACTGAGGT	TCTTGGGATA	CAGATCTCAG	3720
	GGCTCGGGAG	CCATGTCATG	TGAGTGGGTG	GGATGGGGAC	ATTTGAACAT	GTTTAATGGG	3780
	TATGCTCAGG	TCACTGACC	TGACCCCAT	CCTGATCCCA	TGGCCAGGTG	GTGTCCTTAT	3840
60	TGCACCATAC	TCCTTGCTTC	CTGATGCTGG	GCAATGAGGC	AGATAGCACT	GGGTGTGAGA	3900
	ATGATCAAGG	ATCTGGAGCC	CAAAGAATAG	ACTGGATGGA	AAGACAAACT	GCACAGGCAG	3960
	ATGTTTGCTC	CATAATAGTC	GTAAGTGGAG	TCCTGGGAAT	TGGACAAGTG	CTGTTGGGAT	4020
	ATAGTCAACT	TATCTTTTGA	GTAATGTGAC	TAAAGGAAAA	AACTTTGACT	TTGCCCAGGC	4080
	ATGAAATTCT	TCCTAATGTC	AGAACAGAGT	GCAACCCAGT	CACACTGTGG	CCAGTAAAT	4140
65	ACTATTGCTC	CATATTGTCC	TCTGCAAGCT	TCTTGCTGAT	CAGAGTTCCT	CCTACTTACA	4200
	ACCCAGGGTG	TGAACATGTT	CTCCATTTC	AAGCTGGAAG	AAGTGAGCAG	TGTTGGAGTG	4260
	AGGACCTGTA	AGGCAGGCC	ATTGAGAGCT	ATGGTGCTTG	CTGGTGCTTG	CCACCTTCAA	4320
	GTCTTGAGCC	TGGGCATGAC	ATCCTTTCTT	TTAATGATGC	CATGGCAACT	TAGAGATTGC	4380
	ATTTTATTA	AAGCATTTCC	TACCAGCAAA	GCAAAATGTT	GGAAAGTATT	TACTTTTTCG	4440
70	GTTCCAAAGT	GATAGAAAAG	TGTGGCTTGG	GCATTGAAAG	AGGTAAATTT	CTCTAGATT	4500
	ATTAGTCCTA	ATTCATCTCT	ACTTTTCGAA	CACCAAAAT	GATGCGCATC	AATGTATTTT	4560
	ATCTTATTTT	CTCAATCTCC	TCTCTCTTTC	CTCCACCCAT	AATAAGAGAA	TGTTCTCTACT	4620
	CACACTTCAG	CTGGGTACCA	TCCATCCCTC	CATTCTCCT	TCCATCCATC	TTTCCATCCA	4680
	TTACTTCCAT	CCATCCTTCC	AACATATATT	TATTGAGTAC	CTACTGTGTG	CCAGGGGCTG	4740
75	GTGGGACAGT	GGTGACATAG	TCTCTGCCCT	CATAGAGTTG	ATTGTCTAGT	GAGGAAGACA	4800
	AGCATTTTGA	AAAAATAAAT	TTAAACTTAC	AAACTTTGTT	TGTCAACAAGT	GGTGTATTAT	4860
	GCAATAACCG	CTTGGTTTGC	AACCTCTTTC	CTCAACAGAA	CATATGTTGC	AAGACCTTCC	4920
	CATGGGGGCA	CTTGAGTTT	GGCAAGGCTG	ACAGAGCTCT	GGGTGTGTGA	CATTTCTTTG	4980
	CATTCCAGCT	GTCACCTCTG	GCCTTTCTAC	AACTGATTGC	AACAGACTGT	TGAGTTATGA	5040
80	TAAACCCAGT	GGGAATTGCT	GGAGGAACCA	GAGGCACCTC	CACCTTGCTT	GGGAAGACTA	5100
	TGGTGCTGCC	TGCTTCTGTT	ATTTCTCTTG	ATTTCTCTGA	AAGTGTTTTT	AAATAAGAA	5160
	CAATTGTTAG	ATGCC					

Seq ID NO: 220 Protein sequence:
Protein Accession #: NP_005553

85	1	11	21	31	41	51

WO 02/086443

PCT/US02/12476

MPALWLGCCCL CFSLLLPAAAR ATSRREVDCD NGKSRQCIFD RELHRQTGNG FRCLNCNDNT 60
 DGIHCEKCKN GYRFRERDRR CLPCNCNSKG SLARCDNSG RCSCKPGVTG ARCDRCCLPGF 120
 HMLTDAGCTQ DQRLDSDKCD CDPAGIAGPC DAGRCVCKPA VTGERCDRCR SGYNNLDGGN 180
 PEGCTQCFCY GHSASCRSSA EYSVHKITST FHQDQVWGKA VQRNGSPAKL QWSQRHQDVF 240
 SSAQRLLDPVY FVAPAKPLGN QQVSYGQSLS FDYRVDGRGR HPSAHDVILE GAGLRITAPL 300
 MPLGKTLPCG LTKTYTFFRLN EHPNNWSPQ LSYFEYRRL RNLTLALRIRA TYGEYSTGYI 360
 DNVTLISARP VSGAPAPWVE QCICPVGYKG QFCQDCASGY KRDSARLGPF GTICPCNCQG 420
 GGACDPDPTGD CYSGDENPDI ECADCPIGFY NDPHDFRSCK PCPCNNGFSC SVMPEEEVV 480
 CNMCPFGVTG ARCELADGKY FGDPFGEHGP VRCPCPCQCN MNVDFPSAGN CDRLTGRCLK 540
 CIHNTAGIYC DQCKAGYFGD PLAFNPADKC RACNCPMGS EPVGCRRDGT CVCKPFGGPG 600
 NCEHGAFSCP ACYNQVKIQM DQFMQQLQRM EALISKAQGG DGVPDTELE GRMQQAEQAL 660
 QDILRDAQIS EGASRSLGLQ LAKVRSQENS YQSRLLDCLKM TVERVRALGS QYQNRVRDTH 720
 RLITQMLSL AESEASLGNT NIPASDHYVG PNGFKSLAQE ATRLAESHVE SASNMEQLTR 780
 ETEDYSKQAL SLVRKALHEG VSGSGSPDGD AVVQGLVEKL EKTSLAQQL TREATQAEIE 840
 ADRSYQHSRL LLDVSRRLQG VSDQSFQVEE AKRIKQKADS LSTLVTRHMD EPKRTQKNLQ 900
 NWKEEAQQLL QNGKSGREKS DQLLSRANLA KSRAQEALES GNATFYEVES ILKNLREFDL 960
 QVNDNRKAEAE EAMKRLSYIS QKVSADSDKT QQAERLALSA AADAQRAKNG AGEALISSE 1020
 IEQIGSLNL EANVTADNG AMEKGLASLK SEMREVEGEL ERKELEFDN MDVQVMVITE 1080
 AQKVDTRAKN AGVTIQTDLN TLDGLLHMD QPLSVDEEGL VLEQKLSRA KTQINSQLRP 1140
 MMSELEERAR QQRGHLHLE TSIDGILADV KNLENIRDNL PFGCYNTQAL EQQ

Seq ID NO: 221 DNA sequence
 Nucleic Acid Accession #: NM_016529
 Coding sequence: 13-1854

1 11 21 31 41 51
 GTCAAGAAAA GAATGTCTGT AATTGTTCTGA ACTCCTTCAG GACGACTTCG GCTTTACTGT 60
 AAAGGGGCTG ATAATGTGAT TTTTGAGAGA CTTTCAAAAG ACTCAAAATA TATGGAGGAA 120
 ACATTATGCC ATCTGGAATA CTTTGCCACG GAAGGCTTGC GGCATCTCTG TGTGGCTTAT 180
 CCTGATCTCT CTGAGAAATGA GTATGAGGAG TGGCTGAAAG TCTATCAGGA AGCCAGCACC 240
 ATATTGAAGG ACAGAGCTCA ACGGTTGGAA GAGTGTACG AGATCATTGA GAAGAATTTG 300
 CTGCTACTCT GAGCCACAGC CATAGAAGAT CGCCTTCAAG CAGGAGTTCC AGAAACCATC 360
 GCAACACTGT TGAAGGCAGA AATTAAATA TGGGTGTTGA CAGGAGACAA ACAAGAACT 420
 CGGATTAATA TAGGCTATTC CTGCGGATTG GTATCGCAGA ATATGGCCCT TATCCTATTG 480
 AAGGAGGACT CTTTGGATGC CACAAGGSCA GCCATTACT AGCACTGCAC TGACCTTGGG 540
 AATTTGCTGG GCAAGGAAAA TGACGTGGCC CTGATCATCG ATGGCCACAC CCTGAAGTAC 600
 CGGCTCTCTT TCGAAGTCCG GAGGAGTTTC CTGGATTGG CACTCTCGTG CAAAGCGGTC 660
 ATATGCTGCA GAGTGTCTCC TCTGCAGAA TCTGAGATAG TGGATGTGGT GAAGAAGCGG 720
 GTGAAGGCCA TCACCTCGC CATCGGAGAC GCGGCCAAG ATGTCGGGAT GATCCAGACA 780
 GCCCAGCTGG GTGTGGGAAT CAGTGGGAAT GAAGGCATGC AGGCCACCAA CAACCTGGAT 840
 TACGCCATCG CACAGTTTTC CTACTTAGAG AAGCTTCTGT TGGTTTATGG AGCCTGGAGC 900
 TACAACCGGG TACCAAGTG CATCTGTATG TGCTTCTATA AGAACGTGGT CCTGTATATT 960
 ATTGAGCTTT GGTTCGCTTT TGTTAATGGA TTTTCTGGGC AGATTTTATT TGAACGTGG 1020
 TGACATCGCC TGTACATGT GATTTTCACC GCTTTCGCGC CCTTCACTCT GGAATCTTT 1080
 GAGAGGTCTT GCATCAGGA GAGCATGCTC AGGTTTCCCC AGCTCTACAA AATCACCAG 1140
 AATGGGGAAG GCTTCAACAC AAAGGTTTTC TGGGTCACCT GCATCAACGC CTTGGTCCAC 1200
 TCCTCATCTC TCTTCTGGTT TCCCATGAAA GCTCTGGAGC ATGATACTGT GTTTGACAGT 1260
 GGTATGCTA CCGACTATTT ATTGTTGGA AATATTGTTT ACACATATGT TGTGTGTTACT 1320
 GTTTGTCTGA AAGCTGGTTT GGAGACCACA GCTTGGACTA AATTCAGTCA TCTGGCTGTC 1380
 TGGGGAAGCA TGCTGACCTG GCTGGTGTTC TTTGGCATCT ACTCGACCAT CTGGCCACC 1440
 ATTCCCATTT CTCCAGATAG GAGAGGACAG GCAACTATGG TCCTGAGCTC CGCACACTTC 1500
 TGTTGGGAT TATTCTGTGT TCCTACTGCC TGTTTGATTG AAGATGTGGC ATGGAGAGCA 1560
 GCCAAGCACA CCGCAAAAA GACATTGCTG GAGGAGGTGC AGGAGCTGGA AACCAGTCT 1620
 CGAGTCTCTG GAAAGCGGT GCTGCGGAT AGCAATGGAA AGAGGCTGAA CGAGCGCGAC 1680
 CGCCTGATCA AGAGGCTGGG CCGGAAGACG CCCCAGACGC TGTTCGGGGG CAGCTCCCTG 1740
 CAGCAGGGCG TCCTCATGCG GTATGCTTTT TCTCAAGAAG AACACGGAGC TGTTAGTCAG 1800
 GAAGAAGTCA TCCGCTCTTA TGACACCACC AAAAAAGAAAT CCAGGAAGAA ATAAGACATG 1860
 AATTTTCTCT ACTGATCTTA GGAAAGAGAT TCAGTTTGTG GCACCCAGTG TTAACACATC 1920
 TTTGTGAGAG AAGACTGGCG TCCAAGGCCA AAACACCAGG AAACACATTT CTGTGGCCTT 1980
 AGTTAAGCAG TTTGTTAGTT ACATATTCCC TCGCAACCT GAGGTGCAGA CCACAGGGGA 2040
 AGCTATCTTT GCCCTCCCAA CTCGTCTGCA GTGCTTAGCC TAACTTTTGT TTATGTCGTT 2100
 ATGAAGCATT CAACGTGTCT CTGTGAGGTC TCAAAATAAA AACATTATGT TTCACCAATA 2160
 AGAAAAA AAAAAA

Seq ID NO: 222 Protein sequence:
 Protein Accession #: NP_057613

1 11 21 31 41 51
 MSVIVRTPSG RLRLYCKGAD NVIFERLSKD SKYMEETLCH LEYFATEGLR TLCVAYADLS 60
 ENEYEWLKV YQEASTILKD RAQRLEECYE IIEKNLLLLG ATAIEDRLQA GVPETIATLL 120
 KAEIKIWLVT GDKQETAINI GYSCRLVSQN MALILLKEDS LDATRAAITQ HCTDLGNLLG 180
 KENDVALIID GHTLKYALSF EVRRSFLDLA LSCKAVICCR VSPLQKSEIV DVVKKRVKAI 240
 TLAIGDGAND VGMITQAHVG VGISGNEGMQ ATNNSDYAIA QFSYLEKLLL VHGAWSYNNRV 300
 TKCILYCFYK NUVLYIIEIW FAFVNGFSQO ILFERWCIGL YNVIPTALFP FTLLGIFERS 360
 TQESMLRFPQ LYKITQNGEK FNTKVFWGHG INALVHSLIL FWFPMKALEH DTVFDSGHAT 420
 DYLFVGNIVY TYVVVTVCLK AGLETTAWTK FSHLAVNGSM LTLWVFFGIY STIWPTIPIA 480
 PDMRGQATMV LSSAHFWLGL FLVPTACLIE DVAWRAAKHT CKKTLLEEVQ ELETKSRVLG 540
 KAVLRDSNGK RLNERDLRIK RLGRKTPPTL FRGSSLLQGV PHGYAFSQEE HGAVSQEEVI 600
 RAYDTTKKKS RKK

Seq ID NO: 223 DNA sequence
 Nucleic Acid Accession #: BC017001
 Coding sequence: 1-394

1 11 21 31 41 51

5 AACGCTGGGC AGGSCCGGCG CGGCTCGGGG GCGCCCCGAG GGGCCCGGGC CGAGCGGCGG 60
CGCGCAGGGC GGCAGCATCC ACTCGGGCCG CATCGCCGCG GTGCACAAAG TGCCGCTGAG 120
CGTGCTCATC CGGCCGCTGC CGTCCGTGTT GGACCCCGCC AAGGTGCAGA GCCTCGTGA 180
CACGATCCGG GAGGACCCAG ACACGCTGCC CCCCATCGAT GTCTCTGGA TCAAGGGGCG 240
CCAGGGAGGT GACTACTTCT ACTCCTTTGG GGGCTGCCAC CGTACGCGG CCTACCAGCA 300
ACTGCAGCGA GAGACCATCC CGCCCAAGCT TGTCCAGTCC ACTCTCTCAG ACCTAAGGGT 360
GTACCTGGGA GCATCCACAC CAGACTTGCA GTAGCAGCCT CTTTGGCACC TGCTGCCACC 420
TTCAGAGGCC CAGAAGACAC ACCTGGCCTC CAGCAGGCTG GGCCATGCAG AAGGGATAGC 480
10 AGGGGTGCAT TCTCTTTGCA CCTGGCGAGA GGGTCTGACT CTGGGCACCC CTCTCACCAG 540
CTACAAGGCC TTGGAATCAC TGTACAGTGT GGGAGCCCCA GTTCCCACTT CTGTGACAAT 600
AGGATCATGG CCTTACCCTT GAAGCATTAC CGAGAAGGAG AACAGAGATG GGCTTGAAGA 660
GCCACGTGCT GCCGGCTCCA AATTCCTAAG GACAGGATC CCTCTGCATT TTTGTCTATG 720
TAACCTCTTA TATGGACTAC ATTCACTGTC AAGGAAAGGA AAACCTTGAT TGCAGTGGTT 780
15 TAAACAAACA GAAGATTGTT TTTCCACATA GCATGGATTG TGAGATGGG TGGCTAATGG 840
TATTGGTTCA ACAACTCCAC GGAGGTAGGG GTCACGTCTT GGATCCTTTT GCCTTAATCT 900
CAGTGTCTGT TACTTCATGG TCCCAAGATG GCTGCTGTAT CCCCAGAAT CATGTCTGCG 960
TTCAGGAAG GAGGGGTGGA GGAAGAGGAA GGGCCAAACT AGCTGGACCC GTCACCTTCT 1020
ATCAGAAAGT AAAACCTCGT CAGAAGTCTG TTTCTGCTC TCTCCCTCTG CATATCTTCA 1080
20 CTTAGATGCC CTTGGCCCGA GCCAGCTACC ATTGCACCTC TAGCTGCAAA CAAAGCTAAG 1140
ACAGCAGGGA ACAGAAATGT CATGGCTGAA TAGACCAATC AAGAGAGAAA TGCAGAAATG 1200
GGCACACTGC CTCTCTCAAT AAAACTGGGA TCCCATTAAC AAGAGAGAAA TGCAGAAATG 1260
TGTACCAATT AGCTTTTGTCT GTGTAACAAA CCATCCCAAA ACTTGGCAGC TAGAAACAAA 1320
CCCTGTATTT TCCACACATC CTATGGGTG GCAATTTGGG CTGGGCTCAA CAGGGCAGTT 1380
25 CTGCTGCTCA CACCTGGGAT CCTCATGGA GCTAAGGTCA GCTGTACCT CAGCTGGGCC 1440
TGGATGGTCT AGGATAGCCT TACTCACTTG CCTGGCAGGT GACAGGCTGT TGGCTGGAAT 1500
TGCTTGGTTC TCCTCCATGT GGCCTCTCCA GCAGGCTAGC TCAGGCTTAT TCACATGATG 1560
GCTTCAGATG TCCAAAGAGA GTGAGAGTAG AAGCTGAAAG ACTTCTTGAG TTCTTGGCCT 1620
GGAACCTGGA CTAGGACAGT GTCACCTCTG CTAAGTTCTT TTGGTCAGAG CAAATCACAA 1680
30 GGCTTTACCC AGATTCAAGG GATGAGAAAC AGACTACATG TCTTGATGAG GGAACCCACA 1740
AAGAGCTTGT GGCCATTTT CACCTATCAC AAATAATTTT GGATGGGTAT TTATTGGAT 1800
AAAGGTATT CTCTCTTCCC CTTTCTCTC TGTCTCATG GGCCTCACTC TGCCAAAGTTG 1860
GAAGGCACCT AGACATTGTC CTGGCCCTCA GGGTCTAGGG GAAGAGGTGT TGGGGCAGGA 1920
35 AGTGAAGTCT TCCATGGGCT GGACCCACTG TAGTAGGAGT GCCTCCTTGT CTGCACTGCT 1980
GGTATGGGTT TAGGCCAGGT AGGACATTCC AGAGGGGCTT CTGAAAACCA AGAGTCCCTG 2040
GGGAAAGGGA ACAGAGTAAG GCAGGCTTGG TTCTCACTGC CCTCTAAGGG AACTTGGTCA 2100
CTCGGCACCT TTAAGCCTCA GTTTCTCCAG TTCAATAATA AGGACAAGAG CTTTCCCAT 2160
GCATTCTCTT TCCCCGGGAA AGTTGACTGA GGTGACCAAT AATAGAATTG AAAAGGGAGA 2220
40 GTGTCTTCAG TCGAATGTGG CATCCTGGAT TGGGTCTTGG AACAAAAACA GGACATTAGT 2280
GGGAAATATG GAAATCTGAA AAAAGTCTGA ATTTTAGTTA ATATAACCAAT TTCAGTCTCT 2340
TGGTTTGTAG AGATGTACCA TGGTGATGTA AGATGTTGAC CTTGGGGTAG GCTGGGTGAA 2400
GGGTATACAG GAACCTTTTG TACTATCTCT GCAACTTCTC TGTAATCTA GTATCATTCC 2460
AAAAATAAAG TTTATTTAAT TTAATAAAAA AAAAAAATAA AA

Seq ID NO: 224 Protein sequence:
Protein Accession #: AAH17001.1

50 1 11 21 31 41 51
TLGRAGAGRG APEGPGPSGG AQGGSIHSGR IAAVHNPLS VLIRPLPSVL DPAKVQSLVD 60
TIREDPDSVP PIDVLWIKGA QGGDYFYSFG GCHRYAAYQQ LQRETIPAKL VQSTLSDLRV 120
YLGASTPDLQ

Seq ID NO: 225 DNA sequence
Nucleic Acid Accession #: NM_021048
Coding sequence: 1..1110

60 1 11 21 31 41 51
ATGCCTCGAG CTCCAAGCG TCAGCGCTGC ATGCCTGAAG AAGATCTTCA ATCCCAAAGT 60
GAGACACAGG GCCTCGAGGG TGCACAGGCT CCCCTGGCTG TGGAGGAGGA TGCTTCATCA 120
TCCACTTCCA CCAGCTCCTC TTTTCCATCC TCTTTTCCCT CCTCCTCCTC TTCTCTCTCC 180
65 TCCTCTGCT ATCCTCTAAT ACCAAGCACC CCAGAGGAGG TTTCTGCTGA TGATGAGACA 240
CCAAATCTC CCAGAGTGC TCAGATAGCC TGCTCCTCCC CTTCCGTCGT TGCTTCCCTT 300
CCATTAGATC AATCTGATGA GGGCTCCAGC AGCCAAAAGG AGGAGAGTCC AAGCACCCTA 360
CAGGTCTGTC CAGACAGTGA GTCTTTACCC AGAAGTGAGA TAGATGAAAA GGTGACTGAT 420
TTGGTGCAGT TTCTGCTCTT CAAGTATCAA ATGAAGGAGC CGATCACAAA GGCAGAAATA 480
70 CTGGAGAGTG TCATAAAAAA TTATGAAGAC CACTTCCCTT TGTGTGTTAG TGAAGCCTCC 540
GAGTGCAATG TGCTGGTCTT TGGCATTGAT GTAAAGGAAG TGGATCCAC TGGCCACTCC 600
TTTGTCTCTG TCACCTCCCT GGGCTCACC TATGATGGGA TGCTGATGA TGTCAGAGC 660
ATGCCCAAGA CTGGCATTCT CATACTTATC CTAAGCATAA TCTTCATAGA GGGCTACTGC 720
75 ACCCTGAGG AGGTCACTG GGAAGCACTG AATATGATGG GGCTGTATGA TGGGATGGAG 780
CACTCATTT ATGGGGAGCC CAGGAAGCTG CTCACCCAAG ATTGGGTGCA GGAAGACTAC 840
CTGGAGTACC CCAGAGTGCC TGGCAGTGAT CCGTGCACGT ATGAGTTTCT GTGGGGTCCA 900
AGGGCTCATG CTGAAATTAG GAAGATGAGT CTCCTGAAAT TTTTGGCCAA GGTAAATGGG 960
AGTGATCCAA GATCCTTCCC ACTGTGGTAT GAGGAGGCTT TGAAAGATGA GGAAGAGAGA 1020
80 GCCCAGGACA GAATTGCCAC CACAGATGAT ACTACTGCCA TGGCCAGTGC AAGTTCTAGC 1080
GCTACAGGTA GCTTCTCCTA CCCTGAATAA

Seq ID NO: 226 Protein sequence:
Protein Accession #: NP_066386

85 1 11 21 31 41 51
MPRAPKRQRC MPEEDLQSQS ETQGLEGAQA PLAVEEDASS STSTSSSFPS SFPSSSSSSS 60

WO 02/086443

PCT/US02/12476

SSCYPLIPST PEEVSADDET PNPQSAQIA CSSPSVVASL PLDQSDGESS SQKEESPSTL 120
QVLFDSESLP RSEIDEKVTD LVQPLLKYQ MKEPITKAEI LESVIKNYED HFPLLFSEAS 180
ECMLLVFGID VKEVDPTGHS FVLVTSGLT YDGMISDVQS MPKTGILILI LSIFIEGYC 240
TPBEVIWEAL NMMGLYDME HLIYGEPRKL LTQDWQENY LEYRQVPGSD PARYEPLWGP 300
RAHAIRKMS LLKFLAKVNG SDPRSFLWY EEALKDEBER AQDRIATDD TTAMASASSS 360
ATGSFSTPE

Seq ID NO: 227 DNA sequence

Nucleic Acid Accession #: NM_005025.1

Coding sequence: 82-1314

1 11 21 31 41 51
| | | | | |
15 GCGGAGCACA GTCCGCCGAG CACAAGCTCC AGCATCCCGT CAGGGGTTGC AGGTGTGTGG 60
GAGGCTTGAA ACTGTTACAA TATGGCTTTC CTGGAAGTCT TCTCTTTGCT GGTCTGTCAA 120
AGTATGGCTA CAGGGGCCAC TTCCCTGAG GAAGCCATTG CTGACTTGTC AGTGAATATG 180
TATAATCGTC TTAGAGCCAC TGGTGAAGAT GAAATATATC TCTTCTCTCC ATTGAGTATT 240
GCTCTTGCAA TGGGAATGAT GGAAGTGGG GCCCAAGGAT CTACCCAGAA AGAAATCCGC 300
CACTCAATGG GATATGCAG CTTAAAAAT GGTGAAGAA TTTCTTTCTT GAAGGAGTTT 360
20 TCAAAACATG TAACGTCTAA AGAGAGCCAA TATGTGATGA AAATTGCCAA TTCTTTGTTT 420
GTGCAAAATG GATTTTCATG CAATGAGGAG TTTTGTCAA TGATGAAAA ATATTTTAAT 480
GCAGCAGTAA ATCATGTGGA CTTCACTCAA AATGTAGCCG TGGCCAACTA CATCAATAAG 540
TGGGTGGAGA ATAACACAAA CAATCTGGTG AAAGATTGGG TATCCCCAAG GGATTTTGAT 600
GCTGCCACTT ATCTGGCCCT CATTAAATGCT GTCTATTTC AAGGGAACTG GAAGTCGCAG 660
25 TTAGAGCCTG AAAAATACTG AACCTTTTCT TTCACATAAG ATGATGAAA TGAGTCCAA 720
ATTCCAATG TGTATCAGCA AGGAGAATTT TATTATGGGG AATTTAGTGA TGGCTCCAAT 780
GAAGCTGGTG GTATCTACCA AGTCCTAGAA ATACCATATG AAGGAGATGA AATAAGCATG 840
ATGCTGGTGC TGTCCAGACA GGAAGTTCCT CTGCTACTC TGGAGCCATT AGTCAAAGCA 900
CAGCTGGTGG AAGAATGGGC AAACCTCTGTG AAGAAGCAA AAGTAGAAGT ATACCTGCCC 960
30 AGGTTACAGC TGAACACAGA AATTGATTGA AAAGATGTTT TGAAGGCTCT TGAATAAAT 1020
GAAATTTTCA TCAAAGATG AAATTTGACA GGCCTCTCTG ATAATAAGGA GATTTTCTT 1080
TCCAAAGCAA TTCACAAGTC CTTCTAGAG GTTAATGAAG AAGGCTCAGA AGCTGCTGCT 1140
GTCTCAGGAA TGATTGCAAT TAGTAGGATG GCTGTGCTGT ATCTCAAGT TATTGTGCAC 1200
CATCCATTTT TCTTTCTTAT CAGAAACAGG AGAAGTGGTA CAATCTTATT CATGGGACGA 1260
35 GTCATGCATC CTGAAACAAAT GAACACAAGT GGACATGATT TCGAAGAACT TTAAGTTACT 1320
TTATTTGAAT AACAAAGGAA ACAGTAACCA AGCACATTAT GTTTGCAAT GGTATATATT 1380
TAGGATTTGT GTTTTACAGT ATATCTTAAG ATAATATTTA AAATAGTTCC AGATAAAAC 1440
AATATATGTA AATTATAAGT AACCTGTCAA GGAATGTTAT CAGTATTAAAG CTAATGGTCC 1500
40 TGTATATGTA TGTGTTTGT GTGCTGTTGT TTAAATAAAA AGTACCTATT GAACATGTG

Seq ID NO: 228 Protein sequence:

Protein Accession #: NP_005016.1

1 11 21 31 41 51
| | | | | |
45 MAFLGLFSL VLQSMATGAT FPPEAIADLS VNMYNRLRAT GEDENILFSP LSIALAMGMM 60
ELGAQGSTQK EIRHSMGYDS LKNGEESFSL KEFSNMVTAK ESQVVMKIAN SLFVQNGFHV 120
NEEFLLQMKK YPNAAVNHVD FSQNVAVANY INKVENNTN NLVKDLVSPR DFDAATYLAL 180
50 INAVYFKGNW KSQRPENTR TFSPTKDES EVQIPMMYQQ GEFYGEFSD GSNEAGGIYQ 240
VLEIPYEGDE ISMMLVLSRQ BVPLATLEPL VKAQLVEEWA NSVKKQKVEV YLPRFTVEQE 300
IDLKVLKAL GITETPIKDA NLGSLDNKE IFLSKAIHKS FLEVNEEGSE AAASVGMIAI 360
SRMAVLPQV IVDHFFFLI RNRRTGTILF MGRVMHPETM NTSGHDFEEL

Seq ID NO: 229 DNA sequence

Nucleic Acid Accession #: NM_003695

Coding sequence: 12-398

1 11 21 31 41 51
| | | | | |
60 CGACATCAGA GATGAGGACA GCATTGTGTC TCCTTGACGC CCTGGCTGTG GCTACAGGGC 60
CAGCCCTTAC CTTGCGCTGC CAGTGTGCA CCAGCTCCAG CAAGTCAAG CATTTCTGTG 120
TCTGCCCGGC CAGCTCTGCG TTCTGCAAGA CCACGAACAC AGTGGAGCCT CTGAGGGGGA 180
ATCTGGTGAA GAAGGACTGT GCGGAGTCGT GCACACCCAG CTACACCTCG CAAGGCCAGG 240
65 TCAGCAGCGG CACCACTGCC ACCCAGTGCT GCCAGGAGGA CCTGTGCAAT GAGAAGCTGC 300
ACAACGCTGC ACCCACCCTGC ACCGCCCTCG CCCACAGTGC CCTCAGCCTG GGGCTGGCCC 360
TGAGCCTCCT GGCGGTATC TTAGCCCCCA GCCTGTGACC TTCCCCCAG GGAAGGCCCC 420
TCATGCCTTT CCTTCCCTTT CTCTGGGGAT TCCACACCTC TCTTCCCAG CCGGCAACGG 480
GGGTGCCAGG AGCCCCAGG TGAGGGCTTC CCCGAAAGTC TGGGACAGG TCCAGGTGGG 540
70 CATGGAATGC TGATGACTTG GAGCAGGCC CACAGACCCC ACAGAGGATG AAGCCACCCC 600
ACAGAGGATG CAGCCCCAG CTGCATGGAA GGTGGAGGAC AGAAGCCCTG TGGATCCCCG 660
GATTTACAC TCTTCTGTT TTGTTGCCGT TTATTTTGTA CTCAATCTC TACATGGAGA 720
TAAATGATT AAACC

Seq ID NO: 230 Protein sequence:

Protein Accession #: NP_003686

1 11 21 31 41 51
| | | | | |
80 MRTALLLLAA LAVATGPALT LRCHVCTSSS NCKHSVVCFA SSRFCKTTNT VEPLRGNLVK 60
KDCAESCTPS YTLGQVSSG TSSTQCCQED LCNEKLHNAA PTRTALAHS LSLGLALSLL 120
AVILAPSL

Seq ID NO: 231 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 126-752

1	11	21	31	41	51	
CGGGGCGAGGT	GGCTCATGCT	CGGGAGCGTG	GTTGAGCGGC	TGGCGCGGTT	GTCTCGGAGC	60
AGGGGCGCAG	GAATTTCTGAT	GTGAAACTAA	CAGTCTGTGA	GCCCTGGAAC	CTCCACTCAG	120
5 AGAAGATGAA	GGATATCGAC	ATAGGAAAAG	AGTATATCAT	CCCCAGTCCT	GGGTATAGAA	180
GTGTGAGGGA	GAGAACACAG	ACTTCTGGGA	CGCACAGAGA	CGGTGAAGAT	TCCAAGTTCA	240
GGAGAACTCG	ACCGTTGGAA	TGCCAAGATG	CCTTGGAAAC	AGCAGCCCGA	GCCGAGGGCC	300
TCTCTCTTGA	TGCCTCCATG	CATTCTCAGC	TCAGAACTCT	GGATGAGGAG	CATCCCAAGG	360
9 GAAAGTACCA	TCATGGCTTG	AGTGCTCTGA	AGCCCATCCG	GACTACTTCC	AAACACCAGC	420
10 ACCCAGTGGA	CAATGCTGGG	CTTTTTCTCT	GTATGACTTT	TTCGTGGCTT	TCTTCTCTGG	480
CCCGTGTGGC	CCACAAGAAG	GGGAGGCTCT	CAATGGAAGA	CGTGTGGTCT	CTGTCCAAGC	540
ACGAGTCTTC	TGACGTGAAC	TGCAGAAGAC	TAGAGAGACT	GTGGCAAGAA	GAGCTGAATG	600
AAGTTGGGCC	AGAGCTGCTC	TCCCTGCGAA	GGTTGTGTG	GATCTTCTGC	CGCACCAGGC	660
15 TCATCCTGTC	CATCGTGTGC	CTGATGATCA	CGCAGCTGGC	TGGCTTCAGT	GGACCAAAAT	720
TTCAGGATGG	CTGTATTCTG	CGGTGAGAAT	GAGAGAGTCA	AGCTGGGCGA	AATCTCTCGC	780
CAAGAGTTCA	GCCCTCCTTT	GGAGACTGCT	CCATCAGTGC	CGAGGTGTGT	GGGAACAGGC	840
TTCACTGCAC	CGCCATCTTA	CTGAGTTGCT	TCACGTGAGG	AAAAGGGGGC	TTTGGCCCTG	900
TGACTCAGTT	CCACATTTTG	GATTGCATAC	TGGAAAAGAA	GCCAACTCTC	TTGCTAGTAA	960
20 ACCAGCAACC	CGGCTGTATA	CAGTGGTGAC	CCAAGCAATG	GATATAAACC	TAAAAATCTG	1020
AGGGAGGGGA	GAGGTGGAAT	ACAGTAGTTC	TTGGAATCTG	AAGTCTCCTA	TTTGATCAGG	1080
TTATTTCCCTG	GAGCTTGGCA	AAAATCTGAT	TGGTGGGGAT	CTCCTAGGAC	CTAGTGGACA	1140
TCGTGTATTA	ATTTAATCTC	AGGAAAAACA	AGAAATTAAC	CCAGAGAGAG	TCTGGGTTTT	1200
GGAAATTCAG	GAGCTACCTC	CCAGACCGTG	GTGCTGGGCC	TCCATTTTIG	TCTGTCAATC	1260
25 AGCTCTGACT	TACAGCTGCA	GTCACCTTTG	CTATAAGGCA	CCTGGGTAGA	AGGGTGGATG	1320
GGCTTCACAT	CAATTTTTTT	CTTCCTTTAG	GGTGGGGGAT	TGGTTTGGCT	TTCTTTTGT	1380
GTGTTTTTTT	TTTATTTTTT	TGTCAAGATT	GATTTTTAGA	TGCAAGGACT	TGAAAAGACC	1440
CAGAAGGATG	CCACCAGTTT	TTCTTGGAGG	CCTAGGATTT	TTTATTTCTG	CCCGAGCAGA	1500
GGTAATTCCT	CACAATCTTG	TGCACAGTA	GCACCAGCCA	TTTTGAGCAG	AGTACTCTTT	1560
20 TGGGAGGCTT	TTCTGTTTTG	TTTGTTTTTA	ATTCTCTTTC	CTTAGCAGCA	AGGTCTTTTT	1620
30 TCCTAGAGAA	TCTACTCCGT	TGCAGAATCA	TTGCAACCTC	AGGAGCCCTC	ACTGATTGAG	1680
TGCTGTCAAG	CTGATATACT	ACTTTGGACT	CTGGAACACG	ATATGGGTTC	TATTTCTCTAT	1740
TTCTACTGTG	TGTCGTTAAA	CAACCGTCGG	AGACCAGATG	ACCTGTTAGA	TGGCTAGTCC	1800
35 TGATAAATC	GACTCTGTAT	GTTTCAATGT	ATGTTACTGC	AATGCTTCAC	CTGCTGTACA	1860
GTGTTTGTGA	GATGCTCTTT	GAAGATGGTA	CTTTTATATT	T		

Seq ID NO: 232 Protein sequence:
Protein Accession #: Eos sequence

1	11	21	31	41	51	
MKIDIDIGKEY	IIPSPGYRSV	RERTSTSGTH	RDREDSKFR	TRPLECQDAL	ETAARAEGLS	60
LDASMSHSQL	ILDEHHPGK	YHGLSALKP	IRTSKHQHP	VDNAGLFSCM	TFWLSLSLAR	120
VAHKKGELSM	EDVWLSLKH	SSDVNCRLE	RLWQEBELNE	GFDAASLRRV	VWIFCRTRLI	180
45 LSIVCLMITQ	LAGFSGPNFQ	DGCILRSE				

Seq ID NO: 233 DNA sequence
Nucleic Acid Accession #: CAT cluster

1	11	21	31	41	51	
TTTTAATGGT	GCTCATATAT	ACTGTATTTT	TTGTTGTTTA	GTTTACTTTA	TTGAGAGTGT	60
CACAACATGA	ATCACATAAT	CATGATTTTT	TTTTTTTACT	TTTACTCCCC	AAATTTATTC	120
TGTTTCTTAG	ATCGTAGTCA	TTGAGAAGTC	CCAATAACTC	TAAACTTTTG	AGTTATAACG	180
55 TAGTAACACT	CTCTTTCATC	TTTGTGTTAG	CTCTGTAGTC	TAACTCTGGA	TTTAAATTTT	240
TTTGTTCCTA	AAGTCACAT	TGAATTATTC	TTAGATACTC	TAAGCCACTG	AATTCAGTTC	300
TGTTTGACTG	AAAGCAAAAC	AACGTGACAG	TTTATTTTCA	AACACTAATC	TCTTGATATT	360
TGTTTATGCT	ATATCTTTTT	ATTAATATAT	TATTTTGACT	AAGCTTTTCA	AAAAATTTTG	420
AAGCTATTTT	AATCATCAAG	TATGGAACAC	AAATTTACTAT	TGCATTTTCC	TATATATGCA	480
60 TATATATATG	ATTAACCAAG	ATTGTATCAT	TTTGGCCTTA	ATGCTCTGGT	ATAAAAGATA	540
ATTAGCTAC	TATAGTATTA	ATAAATTTTT	CAGTTGGTTT	GGGCAAAATT	AAACCTGAAA	600
AATAGGTTAA	AAAGTAGTTA	CAAATTAAC	TTACTAATTT	ATACCTGATT	TTTTTTCTTG	660
AATTAAGATA	CATTTTAAAT	GAGCTTTATA	ATACCTTAAA	AAGTTGGTTC	TAATTTAAAA	720
TATGAAGACT	CTGGCTATCA	TCCTGGGATA	GTAATTTCTA	ATTATATAGT	ATTTCAAAC	780
65 TATATATTTT	TTAGTTCTCT	TGAGATAACT	AATTTCTAAT	TATATATGTT	TCAAAACCA	840
TATCCTGTAT	TTTTTTTAA	AATTGTTTTA	TAAATAGGTC	ATAAGATACA	AGGTCTGCAT	900
TAGAAGACCC	ACTCTTACTA	GGTTCCCTAA	GGATCTGCCA	TAGATTTTTT	TTTTTTTTTT	960
70 TTTTTTTTAG	GTAGTTTAAA	GCAAGCACTG	ATACCAGTGG	GAGTTGGTCT	TGATCTAGGA	1020
GATTCGTGTA	AGCATCCAAA	AACAATGCCT	AATTTAGATT	CTTAGGTTAT	GGCTTGTGAC	1080
TCCAGATAAA	AGATGGAGAA	TACCTCATGT	ACTGTGACTT	GAAAATGAAT	TCTTAAATTT	1140
CTTAGGCTCT	CTCCATGTAT	CTTCTTAAAG	GAAAAGTTTC	TGAGTGTGAT	CTCTCTTTTG	1200
CCATAGTATC	AAGTGGAGGG	TAGTTCAGAA	AAGTTAATAG	GAAATCTTTT	GTGACAGCAG	1260
ACTATAATAG	AAGTTTGAGT	AATATTTTAA	TAAATTTATA	TAATTCAAAT	GATAAAAAATG	1320
75 TATCAATGTT	ATCCAAATGAT	TTTTATTAAA	AAATTACCTT	ATTATTAGAA	CTGTGCCAT	1380
TACATAAAAA	GTGCTCATGT	ATTGAAATTT	TAAATAATTT	ATTTAAATCA	AGACCACCAT	1440
AAGTCATTAA	TAATTTAATA	ATTGTTTTAA	ATCAGTGGTT	TTCAACCCCTC	ACTTCATATT	1500
AGAAATCATCT	GAGGACTTTT	AATATGGAAT	CCACCTCATA	ACAATTAAGT	CTAAATTTCT	1560
GGAGATGGA	GCCATGCTTG	TTTTTCCAAA	AGCTCTTTGA	GTGATCTTAA	TTTGTAGTCA	1620
GAGTTGAAGA	CCACTGCTCT	AAATTAGTGC	AGGAAAATGC	TTTTATTCTC	CCCATGTTAA	1680
80 CTTTTAAAA	TAGTAATGTA	CCCAGTTAAG	TTTTGTATGT	TAAATTTCCA	CTAAAGAAC	1740
TATTTCTTCA	ATAACTAGCA	TTTATTACAT	GAAATTTAAG	AGTTTAAAGT	CCATCAAAT	1800
AGCCCTTGTTG	TAAATATTAT	ATTCTTCTCT	TATAACTTCA	AAATAGATAT	TTCAATCAAA	1860
CTGTTTCAGGT	GAGAAAACAT	AATGGATTTT	TTTTTTTTTC	CTCTGGAGCT	GCCGTCTCAG	1920
TGAGATGGAG	GAGGTGGGCA	CATTAAAGGT	CAGTTCACTA	ACCTATGGTT	CAGAGTTCTG	1980
ATCATATGGA	AGTTTGGAAA	AGAGAGCTTA	TCACAGGTTT	GTATGCTGGT	GAATGGATAG	2040
85 TTTTAAATCT	CACCTGTCTA	AAAGAGAAATC	AGCTCTCCAG	CAGTTCTAGA	AAAGCTTTGA	2100
CAATCCCCAA	GGGGCAGTGT	TACCTTACTC	CTTCACTGCT	TCTTAGAAGG	TAGAATTAAG	2160
TTTCTGGAAT	TGCACCTACA	TGTTTTCTTA	TTAACATTCA	GAATTGGGAA	TATTAATTTT	2220

TCCAGTGGAGT AGTTTTCTGA AATTGGTAAC TTGGAGAGTA AAATAACGTA TTTTGCTTTT 2280
 CAATTTTGTG TTTGTTTACT TTTATGTAAA AATTGTGATAT GTGAATTACA CAGTTCTAAT 2340
 AAAACCTCAT GCCTTTTTCAT TACATCTAAT TTGAACCTCTC AACTTCAGTG CCAGAAGTGC 2400
 TTTAAAGATG CTTTAATGAA AAGTATTAAG AAAATATATA GATTTGTATG TCAGTTTATA 2460
 CTTCAGAAAT CCATATATTT GTCATATTTA TTTTTTGTAGA AACCTCCTAA TTGGATAACT 2520
 AGATGGTATT TAAAATGAAT GCCCAAAAAT ATCTTGATACC TTTGTCCAAA AGTTTATCTG 2580
 TTGGAAGCCG CCAGCCATTTC ATGTAGAGAG TTTATAAGAA AATAATTTAA AATTGTATGC 2640
 ATTTTATATT ACTATGGTAT CTGTGTACCA TATTCTAAG TATTCAATTAT TAAATTGGTA 2700
 CTTCTTAAAA CCATAACCTG GCTTGCCTTT TAGTGTTAAA CACAAAATCC AACATTGTAT 2760
 ATAGAGATTTC TTCTTTTATG AAGAAGAGCT GACGTAATTT ATTACCAAGT CATCTGCACA 2820
 AAGACATTAA CATAAGTCTC TGAGCAGTGA TACATTTTCA AACATGAAGA GTGACAAACA 2880
 CCACATTAAA CAACCACGGC AACACTCAGA CTTGGCACTT TCCTACGAAT CCATCCTATA 2940
 TGTGCCTGGT ATGCGCTCTG GCATAACTTA CACGAATGCT CCTCCCTACT TGTCTACGCT 3000
 CCTTCATCAA GCACTTGCCA ACACATTAC CTCTAACTTG TACAACCTTA CCAACTCACC 3060
 ACAACATCTG CAACTCTACC CTATCAACTG CCAACCTAAA GACCCCAAC ACAACACAAC 3120
 CCCCAAACAC AAAACCACTA AATCATAACC ACCACACAG CCACACACA CACACCAACC 3180
 CACACAACCA ACACACCAGC ACCAAACACC CCACCAACAA CAAGCTAACA ACCACAAACA 3240
 GACAACACAT CACATACACT CACTACCCCC CCATACCTCC ACCCACCA

Seq ID NO: 234 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 27-281

1 11 21 31 41 51
 AGCAGGAGGA GAGCTGGCGG GAAGACATGC ACCCCTTGAA GACCCAGAGA GAGGCCGTCT 60
 GTCTACCGGG TAGCAGTTAC ATCAGACTGA GACACTTCCT GTTTACAGGA GACTATAAAA 120
 TTCCTGCCCC GTGCTCATTT GGGGCTGAGC CCATTTTAGG CCTCAGCCCA TCTGCACCCA 180
 GGGCGTCACT GAAACAGTGT GTTGCTCCAC ACCGCTTGT TTTGCTTGT GCGCGCTCT 240
 CAGGGTTCCG AACCAATCAA GAGCCTTGCA GAAAGCATTA ACGTGCTTT CTCTTTGGCA 300
 GAGTTTTTCT TTGCTCTGAT CTTGGAGACA TCCCTCTGCC TAGTGGAAC ATAAGGAATA 360
 CAGAAAGAAT GCAAGGAGAT AGACCAACGT GAGATTCTCC TTCATGCACT CAAGAGAAAG 420
 ATGTTGACAG AAGAGCTAGT CTTTCAGGCT GGGCTGGTGA CCTGAGAAAG AATGTCAGC 480
 TTTCTTCTC CACTTGGCAT ATCAAGAGCC AGGCGTGGAA GACTAAAAA GGAATGTGTT 540
 ATAAAACTG TTCAGCGGTT CGCCACAAAG AAGTGGTAAA GTAGCAAAA TGGGGATGGA 600
 GATGCCAGGA GGAAGATGC CAGGGGTAAA GTGGGAAAAT GGGAACTGA AGCCAGGAGG 660
 TCAAGCCAA GCAACAGGTG TTCTGTTTTT CATCACAGAA CTAATAAGTG GTGCTGAGGA 720
 CTCAAACCCG GGAAGGCCCA CTCTAGAACC CATGCTGGTC ATCCATATCC CCAAGGCCCT 780
 GGTGAGAA CAAGCTAAGCA GATGGCTTGG GTCATCAGGA CGTCCATTAC ATCCAAAGGA 840
 AGACAGCTG TGACGTTTCA AAAGCAAAAG TCCCTACCA GCCAGTGAAG CTACCTGATT 900
 TCTCAGTATC TTACGCCAG TGACACGATC TACCTCAAA ACTTAAAAA AAAAGGGAAA 960
 CATAAACACA TAACAGCAGC AGCAATAATT AAAGATGAGA TGAGAACAA TAAGAAAAA 1020
 GGAAGGTTCT CCTGTGACTG TTTTATTTTT AGGGAAACAG AGAGGAAGAA GAATGATTTT 1080
 TCTTTTGTG ACTCTATATC CAACTCTGAG GTTTGATTAA AGAAATGACC TTGAACCACA 1140
 CCAAGAAAAA ATAAAGACA ATTTCCAGTA AGTATGCCAG TTCGAATTA TGATTACTT 1200
 TTTATTTTA TCTGCGCAGT AGCAGAGATT TACATGCATT ACCATGATTA ACATCTGAAA 1260
 TTTGACCTTG AATAATCTT TACATTGTAA ATTCTTAATG ATCAAAACA GGTCTCTAGT 1320
 GATTAAAAA TATTAGTAAT TAATTATTAA AGGAGAATAA TTGCAATATC AACATTCTTA 1380
 AAATCTCAAG GCTTTTAAAG CATTTGTACA AATGACTGGA CATTTTTTAA ATTTGAAAAA 1440
 AAAAAAAGC CCTCCATCTG ATTCTCATTT TCATTGTGAG TGCAACAA CA AAAAAGGTAT 1500
 GCATTCTCT TCTGCGCAGT CACTGTCTCG CAAGCTAGAA ATTCTCACGA CTACCTTTGA 1560
 TCCCATCAAA GCCAAAGAAA GAAAAGAAA TTGTTCTGTA CAGATATATG ACATTAAAAA 1620
 ATAATCCC

Seq ID NO: 235 Protein sequence:
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 MHPLKTQREA VCLPRSSYIR LRHFLFTGDY KIPAPCSFGA DAILGLSPSA PRRSLKQCV 60
 PHRLVLLVGA LSGFRPIQEP CRKH

Seq ID NO: 236 DNA sequence
 Nucleic Acid Accession #: NM_002075
 Coding sequence: 406..1428

1 11 21 31 41 51
 CCACAATAGG GGCAGACCTG TCCATCCTTC TCTGTGGGTC CCCTGTACCT TTCTCCCCCA 60
 ACAGGATCAG ACCCAGAGGC AGCTGGTTGG GGTTTGTGCA GAAGAAGGAT TATCCAGATC 120
 AGTCCCTTCT AATCTCAGCT CCTGCCTGTA CCCTCCCACT CTACCCAAAC CCTCTTCCCC 180
 ACCACCTTGA GCTGAGGAGC ACAGTTTGAG GCCCCCCCAA CCCCCCGCCG GTCGGGGCCA 240
 GGCCAGGCCA GGCCAGCTCC TCTGGCAGCA GAGCCTGGGC AGGTGACGGG CGGGCGCGGG 300
 CGTCGCAGCT GAGGGAGTAA GGAGGCTCCC AGGAACCCGA GCTGGAACCC CGGCGGAGGT 360
 CCAGCCAGAG CCCAAGAGCC AGAGTGACCC CTCGACCTGT CAGCCATGGG GGAGATGGAG 420
 CAACTGCGTC AGGAAGCGGA GCAGCTCAAG AAGCAGATTG CAGATGCCAG GAAAGCCTGT 480
 GCTGACGTTA CTCTGGCAGA GCTGGTGTCT GGCCTAGAGG TGGTGGGACG AGTCCAGATG 540
 CGGACGCGGC GGACGTTAAG GGGACACCTG GCCAAGATT ACGCCATGCA CTGGGCCACT 600
 GATTCTAAGC TGCTGGTAAG TGCCCTCGCA GATGGGAAGC TGATCGTGTG GGACAGCTAC 660
 ACCACCAACA AGGTGCACGC CATCCCACTG CGCTCCTCCT GGGTCATGAC CTGTGCCTAT 720
 GCGCCATCCG GGAACCTTGT GGCATGTGGG GGGCTGGACA ACATGTGTTT CATCTACAA 780
 CTCAAATCCG GTGAGGGCAA TGTCAAGGTC AGCCGGGAGC TTTCTGCTCA CACAGGTTAT 840
 CTCTCCTGCT GCCGCTTCTT GGATGACAAC AATATTGTGA CCAGCTCGGG GGACACCAG 900
 TGTGCCTTGT GGGACATTGA GACTGGGCAG CAGAAGACTG TATTGTGGG ACACACGGGT 960
 GACTGCATGA GCCTGGCTGT GTCTCTGAC TTCAATCTCT TCATTTCGGG GGCCTGTGAT 1020
 GCCAGTGCCA AGCTCTGGGA TGTGCGAGAG GGGACCTGCC GTCAGACTTT CACTGGCCAC 1080

5
10
15

```

GAGTCGGACA TCAACGCCAT CTGTTTCTTC CCCAATGGAG AGGCCATCTG CACGGGCTCG 1140
GATGACGCTT OCTGCCGCTT GTTTGACCTG CGGGCAGACC AGGAGCTGAT CTGCTTCTCC 1200
CACGAGAGCA TCATCTGCGG CATCACGTCC GTGGCCTTCT CCCTCAGTGG CCGCTACTA 1260
TTCGTAGGCT ACGACGACTT CAACTGCAAT GTCTGGGACT CCATGAAGTC TGAGCGTGTG 1320
GGCATCCTCT CTGGCCACGA TAACAGGGTG AGCTGCCTGG GAGTCACAGC TGACGGGATG 1380
GCTGTGGCCA CAGGTTCTCT GGAACAGCTT CTCAAAAATCT GGAACAGTGG AGGCTGGAGA 1440
AAGGGAGAGTG GAAGGCAAGT AACACACTCA GCAGCCCCCT CCGCGACCCC ATCTCATTCA 1500
GGTGTCTCTT TCTATATTCG GGGTGCCATT CCCACTAAGC TTTCTCCTTT GAGGGCAGTG 1560
GGGAGCATGG GACTGTGCTT TTGGGAGGCA GCATCAGGGA CACAGGGGCA AAGAACTGCC 1620
CCATCTCCTC CCATGGCCTT CCCTCCCCAC AGTCCTCACA GCCTCTCCCT TAATGAGCAA 1680
GGACAACCTG CCCCTCCCCA GCCCTTTGCA GGCCCGACAG ACTTGAGTCT GAGGCCCCAG 1740
GCCCTAGGAT TCCTCCCCCA GAGCCACTAC CTTTGTCCAG GCCTGGGTGG TATAGGGCGT 1800
TTGGCCCTGT GACTATGGCT CTGGCACCAC TAGGGTCTCT GCCCTCTTCT TATTATGCT 1860
TTCTCCTTTT TCTACCTTTT TTTCTCTCCT AAGACACCTG CAATAAAGTG TAGCACCTCG 1920
GT

```

Seq ID NO: 237 Protein sequence:
Protein Accession #: NP_002066

20
25

```

1 11 21 31 41 51
| | | | |
MGEMEQLRQE AEQLKKQIAD ARKACADVTL AELVSGLEV V GRVQMRTRT LRHLAKIYA 60
MHWATSKLL VSASQDGLKI VWDSYITNKV HAIPLRSSWV MTCAYAPSGN FVACGGLDNM 120
CSIYNLKSRE GNVKVSRELS AHTGYLSCCR FLDDNNIVTS SGDTCALWD IETGQKTVF 180
VGHTGDCMSL AVSPDFNLFI SGACDASAKL WDVREGTCRQ TFTGHESDIN AICFPNGEA 240
ICTGSDDASC RLFDLRADQE LICFSHESII CGITSVAPSL SGRLLFAGYD DFNCONVWDSM 300
KSERVIGLSG HDNRVSCSLGV TADGMAVATG SWDSFLKIWN

```

Seq ID NO: 238 DNA sequence
Nucleic Acid Accession #: CAT cluster

30
35
40
45
50

```

1 11 21 31 41 51
| | | | |
TCCCAATGTG TNGAACCTAC CATAAATTCT TTTCTTACNG GACAATCTTA TNCTAANCAA 60
TACCATTTCG TTTTAAGGCA GATAATCCTC CAAGTTTTCT AATGATATCT GAAACTATTA 120
ACTGATTCTG TGAATTATGA AATCTGAAAA GGAATTGGAA GTTGCTAAAA ATCTATCATT 180
TGCAATGACC AGTGTGAAGC ACAGTGGAAAT GAGAATGCGT GCCCTGACAC CAAAGAAAAA 240
TAAGTGACTG GAAAGCTGAA GAATCACCCG CTTCAGTGAC ATGGAAACCCA GTGATTGTAT 300
TTTTGACGAG TATCGGGTGA CTTTGAGGTG GTCAAGAAAC CACACTTTAA GAACAATGTC 360
CAAAAAGGGG AAAAAAAGA GCAACCAAAG AAAAAAATC CATAAAATTG CACAGAAGAA 420
AAGAAAGAAA AATAAAATAC ACAATATGGA CGATGGAGAA AAACAGTTAC ATTTCTTTAT 480
GGATCAAGAA GTTTGTGTAC ACATAATCTC ATTTTGAGAT ATATAACTAT TTTTGTCTTT 540
CAGAAGTGAA TCAAAATATT TCAAAATGCT GTCTTATGAA ACTACAATAT TCTCAGAGAT 600
TAGAAAAGT TTTCTGTAAA AGTCAGATAG TAAATATTTT AGGTTTTCGA GTGTCTTTTG 660
CAACTACTCA ACTTTCCTAC TGTAGCACA GAGTAGCTGT GGTACTGTGC AAATAAATTG 720
CTTGTGTTCC AATAAAGCTT CATTTACAAA AACATGCCAT GGGCCATATT TGGCCTGTAC 780
ACTGTTGTTT GCCAAGTCTT AATATAGTTG CTTAGCAAGT ATTGTGAGCT ATTTGAGGAA 840
GACATGAAAG TTCATTGGGT TGCTAAAAAG TATGTAGAAA TTCAAAGGAA AATTAAAAAT 900
TAGGCTAAGT TATAATACAC TGTTTTAACA ATTGTAAAT GTAAAGAGAA TTTACAAATA 960
AAAAATCCAA ATAAAA

```

Seq ID NO: 239 DNA sequence
Nucleic Acid Accession #: NM_001786.1
Coding sequence: 130-1023

55
60
65
70
75
80

```

1 11 21 31 41 51
| | | | |
GGGGGGGGGG GGCACCTGGC TTCAAAGCTG GCTCTTGGA ATTGAGCGGA GAGCGACGCG 60
GTTGTTGTAG CTGCCGCTGC GGCCGCCGCG GAATAATAAG CCGGGATCTA CCATACCCAT 120
TGACTAACTA TGGAGAGATTA TACCAAAATA GAGAAAATTG GAGAAGGTAC CTATGGAGTT 180
GTGTATAAGG GTAGACACAA AACTACAGGT CAACTGGTAG CCATGAAAAA AATCAGACTA 240
GAAAGTGAAG AGGAAGGGGT TCCTAGTACT GCAATTCGGG AAATTTCTCT ATTAAAGGAA 300
CTTCGTATC CAAATATAGT CAGTCTTCAG GATGTGCTTA TGCAGGATTC CAGTTATAT 360
CTCATCTTTG AGTTTCTTTC CATGGATCTG AAGAAATACT TGGATTCTAT CCCTCCTGGT 420
CAGTACATGG ATTCTTCACT TGTAAAGAGT TATTTATACC AAATCCTACA GGGGATTGTG 480
TTTTGTCACT CTAGAAGAGT TCTTCACAGA GACTTAAAC CTCAAAATCT CTTGATTGAT 540
GACAAAGGAA CAATTAACT GGCTGATTTT GGCCTTGCCA GAGCTTTTGG AATACCTATC 600
AGAGTATATA CACATGAGGT AGTAACACTC TGGTACAGAT CTCCAGAAGT ATTGCTGGGG 660
TCAGCTCGTT ACTCAACTCC AGTTGACATT TGGAGTATAG GCACCATATT TGCTGAACTA 720
GCAACTAAGA AACCACTTTT CCATGGGGAT TCAGAAATTG ATCAACTCTT CAGGATTTC 780
AGAGCTTTGG GCACTCCCAA TAATGAAGTG TGGCCAGAAG TGGAACTCTT ACAGGACTAT 840
AAGAATACAT TTCCCAAATG GAAACCAGGA AGCCTAGCAT CCCATGTCAA AAACCTGGAT 900
GAAAATGGCT TGGATTGTCT CTCGAAAATG TTAATCTATG ATCCAGCCAA ACGAATTCT 960
GGCAAAATGG CACTGAATCA TCCATATTTT AATGATTGAG ACAATCAGAT TAAGAAGATG 1020
TAGCTTTCTG ACAAAGAGTT TCCATATGTT ATGTCAACAG ATAGTTGTGT TTTTATTTGT 1080
AACTCTTGTC TATTTTGTG TATATATAT TTTCTTGTGA TCAAACTTCA GCTGTACTTC 1140
GTCTTCTAAT TTCAAATAA TAACTTAAAA ATGTAAATAT TCTATATGAA TTTAAATATA 1200
ATTCTGTAAA TGTGAAAAA AAAAAAATA AAAAA

```

Seq ID NO: 240 Protein sequence:
Protein Accession #: NP_001777.1

85

```

1 11 21 31 41 51
| | | | |
MEDYTKIEKI GEGTVGVVY GRHKTTGQVV AMKKIRLESE EEGVPSTAIR EISLLKELRH 60
PNIVSLQDVL MQDSRLYLIF EFLSMDLKKY LDSIPPQYIM DSSLVKSYLY QILQGIVFCH 120

```

SRRVLHRDLK PQNLLIDDKG TIKLADFLA RAFGIPIRVY THEVVTWLYR SPEVLLGSAR 180
 YSTPVDIWSI GTIFAEALATK KPLPHGDSEI DQLFRIFRAL GTPMNEVWPE VESLQDYKNT 240
 FPKWKPGSLA SHVKNLDENG LDLLSKMLIY DPAKRISGKM ALNHPYFNDL DNQIKKM

5

Seq ID NO: 241 DNA sequence
 Nucleic Acid Accession #: NM_033379.1
 Coding sequence: 132-854

10 1 11 21 31 41 51
 CGCCGCGCGG CGGGCTCAAC TTTGTAGAGC GAGGGGCCAA CTTGGCAGAG CGCGCGGCCA 60
 GCTTTGCAGA GAGCGCCCTC CAGGGACTAT GCGTGCGGGG ACACGGGATC TACCCATACC 120
 ATTGACTAAC TAGGGAAGAT TATACCAAAA TAGAGAAAAA TGGAGAAGGT ACCTATGGAG 180
 15 TTGTGTATAA GGGTAGACAC AAAACTACAG GTCAAGTGGT AGCCATGAAA AAAATCAGAC 240
 TAGAAAGTGA AGAGGAAGGG GTTCCCTAGTA CTGCAATTCT GGAAATTTCT CTATTAAAGG 300
 AACTTCGTCA TCCAAATATA GTCAGTCTTC AGGATGTGCT TATGCAGGAT TCCAGGTTAT 360
 ATCTCATCTT TGAGTTTCTT TCCATGGATC TGAAGAAATA CTGGATTCT ATCCCTCCTG 420
 GTCAGTACAT GGAATCTTCA CTGTTAAGG TAGTAACACT CTGGTACAGA TCTCCAGAAG 480
 20 TATTGCTGGG GTCAGCTCGT TACTCAACTC CAGTTGACAT TTGGAGTATA GGCACCATAT 540
 TTGCTGAATC AGCAACTAAG AAACCACTTT TCCATGGGGA TTCAGAAATT GATCAACTCT 600
 TCAGGATTTT CAGAGCTTTG GGCACCTCCA ATAATGAAGT GTGGCCAGAA GTGGAATCTT 660
 TACAGGACTA TAGAATATCA TTTCCCAAT GGAACACAGG AAGCCTAGCA TCCCATGTCA 720
 AAAACTTGGG TAAGAAATGGC TTGGATTTGC TCTCGAAAAT GTTAATCTAT GATCCAGCCA 780
 25 AACGAATTC TGCAAAATG GCACTGAATC ATCCATATTT TAATGATTTG GACAAATCAG 840
 TTAAGAAGAT AGAAGTTTCT GACAAAAGT TTCCATATGT TATGTCAACA GATAGTTGTG 900
 TTTTATTGT TAACCTCTGT CTATTTTGT CTTATATATA TTTCTTGTG ATCAAACTTC 960
 AGCTGTACTT CGTCTCTTAA TTTCAAAAT ATAACCTAAA AATGTAAATA TTCTATATGA 1020
 ATTTAAATAT AATTCTGTAA ATGTGAAAAA AAAAAA AAAAAA

30

Seq ID NO: 242 Protein sequence:
 Protein Accession #: NP_203698.1

35 1 11 21 31 41 51
 MEDYTKIEKI GEGTYGVVYK GRHKTGQVV AMKKIRLESE EEGVPSTAIR EISLLKELRH 60
 PNIVSLQDVL MQDSRLYLIF EPLSMDLKKY LDSIPPGQYM DSSLVKVVT L WYRSPEVLLG 120
 SARYSTPVDI WSIGTIFAEL ATKKPLPHGD SEIDQLFRIP RALGTPNNEV WPEVESLQDY 180
 40 KNTFFKWKPG SLASHVKNLD ENGLDLSKM LIYDPAKRIS GKMALNHPYF NDLDNQIKKM

40

Seq ID NO: 243 DNA sequence
 Nucleic Acid Accession #: AF101051.1
 Coding sequence: 221-856

45 1 11 21 31 41 51
 GAGCAACCTC AGCTTCTAGT ATCCAGACTC CAGCGCGGCC CGGGGCGCGG ACCCCAACCC 60
 CGACCCAGAG CTCTCTCCAG GCGCGCGCAG CGAGCAGGGC TCCCGCGCTT AACTTCCTCC 120
 50 GCGGGGCCCC GGCACCTTCG GGAGTCCGGG TTGCCCACTC GCAAACTCTC CGCCTCTGTC 180
 ACCTGCCACC CCTAGGCCAG CGCGGGCGCC CGAGCGAGTC ATGGCCAAAG CGGGGCTGCA 240
 GCTGTGTGGG TCCATTCTCG CTCTCTGGG ATGGATCGGC GCCATCGTCA GCAGTGCCTC 300
 GCCCCAGTGG AGGATTTACT CCTATGCCGG CGACAACATC GTGACCGCCC AGGCCATGTA 360
 CGAGGGGCTG TGGATGTCTT CGGTGTGCGA GAGCACCGGG CAGATCCAGT GCAAGTCTT 420
 55 TGACTCTCTG CTGAATCTGA GCAGCACATT GCAAGCAACC CGTGCCTTGA TGGTGGTTGG 480
 CATCTCTCTG GAGTGAATAG CAATCTTTGT GGCCACCGTT GGCATGAAGT GTATGAAGTG 540
 CTTGGAAGAG GATGAGGTGC AGAAGATGAG GATGGCTGTC ATTGGGGGTG CGATATTTCT 600
 TCTTGCAAGT CTGGCTATTT TAGTTGCCAC AGCATGGTAT GGCAATAGAA TCGTTCAGAA 660
 ATTCTATGAC CCTATGACCC CAGTCAATGC CAGGTACGAA TTTGGTCAGG CTCCTCTCAC 720
 60 TGGCTGGGCT GCTGCTTCTC TCTGCTTCT GGGAGGTGCC CTACTTTGCT GTTCTGTGCC 780
 CCGAAAAACA ACCTCTTACC CAACACCAAG GCCCTATCCA AAACCTGCAC CTTCAGCGG 840
 GAAAGACTAC GTGTGACACA GAGGCAAAAG GAGAAAAACA TGTGAAACA AACCGAAAAT 900
 GGACATTGAG ATACTATCAT TAACATTAGG ACCTTAGAAT TTTGGGTATT GTAATCTGAA 960
 GTATGGTATT ACAAAACAAA CAAACAAACA AAAAACCCAT GTGTTAAAT ACTCAGTGCT 1020
 65 AAACATGGCT TAATCTTATT TTATCTTCTT TCCTCAATAT AGGAGGGAAG ATTTTACCAT 1080
 TTGTATTACT GCTTCCCAT TTAGTAACTAT ACTCAATGG GGGAGGGGTG GCTCCTTAAA 1140
 TATATATAGA TATGTATATA TACATGTTTT TCTATTAAAA ATAGACAGTA AAATACTATT 1200
 CTCATTATGT TGATACTAGC ATACTTAAAA TATCTCTAAA ATAGGTAAAT GTATTTAATT 1260
 CCATATTGAT GAAGATGTTT ATTGGTATAT TTTCTTTTTC GTCCTTATAT ACATATGTAA 1320
 70 CAGTCAATAA TCATTTACTC TTCTTCATTA GCTTTGGGTG CCTTGCCAC AAGACCTAGC 1380
 CTAATTTACC AAGGATGAAT TCTTTCAATT CTTCATGCGT GCCCTTTTCA TATACTTATT 1440
 TTATTTTTTA CCATAATCTT ATAGCACTTG CATGTTATT AAGCCCTTAT TTGTTTGTG 1500
 TTTCAATTGG CTCTATCTCC TGAATCTAAC ACATTTCTAT GCCTACATTT TAGTTCTTAA 1560
 75 AGCCAAGAAG AATTTATTAC AAATCAGAAC TTTGGAGGCA AATCTTTCTG CATGACCAAA 1620
 GTGATAAATT CCTGTTGACC TTCCACACA ATCCCTGTAC TCTGACCCAT AGCACTCTTG 1680
 TTTGCTTTGA AAATATTTGT CCAATTGAGT AGCTGCATGC TGTCCCCCA GGTGTTGTAA 1740
 CACAACTTTA TTGATTTGAT TTTTAAGCTA CTTATTCTAT GTTTTATATC CCCCTAACT 1800
 ACCTTTTTGT TCCCCATTCC TTAATTGTAT TGTTTTCCCA AGTGTAAATTA TCATGCGTTT 1860
 TATATCTTCC TAATAAGGTG TGGTCTGTTT GTCTGAACAA AGTGCTAGAC TTTCTGGAGT 1920
 80 GATAATCTGG TGACAAATAT TCTCTCTGTA GCTGTAAGCA AGTCACTTAA TCTTTCTACC 1980
 TCTTTTTTCT ATCTGCCAAA TTGAGATAAT GATACTTAAC CAGTTAGAAG AGSTAGTGTG 2040
 AATATTAATT AGTTTATATT ACTCTCATTC TTTGAACATG AACTATGCCT ATGTAGTGTG 2100
 TTTATTTGCT CAGCTGGCTG AGACACTGAA GAAGTCACTG AACAAAACCT ACACACGTAC 2160
 CTTCACTGTA TTCACTGCCT TCTCTCTCT ACCAGTCTAT TTCCACTGAA CAAAACCTAC 2220
 85 ACACATACCT TCATGTGGTT CAGTGCCTTC CTCTCTCTAC CAGTCTATTT CCAGTGAACA 2280
 AAACCTACGC ACATACCTTC ATGTGGCTCA GTGCCTTCCT CTCTCTACCA GTCTATTTCC 2340
 ATCTTTTCAG CTGTGTCGTA CATGTTTGTG CTCTGTTCCT TTTTAAACAC TGCTCTTACT 2400
 TTTCCAGTCT GTACAGAAATG CTATTTCTACT TGAGCAAGAT GATGTATGGA AAGGGTGTG 2460

GCACTGGTGT CTGGAGACCT GGATTGAGT CTTGGTGCTA TCAATCACCG TCTGTGTTTG 2520
 AGCAAGGCAT TTGGCTGCTG TAAGCTTATT GCTTCATCTG TAAGCGGTGG TTTGTAATTC 2580
 CTGATCTTCC CACCTCACAG TGATGTTGTG GGGATCCAGT GAGATAGAAT ACATGTAAGT 2640
 GTGGTTTTGT AATTGAAAAA GTGCTATACT AAGGGAAGA ATTGAGGAAT TAACTGCATA 2700
 CGTTTTGGTG TTGCTTTTCA AATGTTTGAA AATAAAAAAA TGTTAAGAAA TGGGTTTCTT 2760
 GCCTTAACCA GTCTCTCAAG TGATGAGACA GTGAAGTAAA ATTGAGTGCA CTAACGAAT 2820
 AAGATTCTGA GGAAGTCTTA TCTTCTGCAG TGAGTATGGC CCAATGCTTT CTGTGGCTAA 2880
 ACAGATGTAA TGGGAAGAAA TAAAGCCTA CGTGTTGGTA AATCCACAG CAAGGGAGAT 2940
 TTTTGAATCA TAATACTCA TAAGGTGCTA TCTGTTTCAAT GATGCCCTCA GAGCTCTTGC 3000
 TGTTAGCTGG CAGCTGACGC TGCTAGGATA GTTAGTTTGG AAATGGTACT TCATAATAAA 3060
 CTACACAAGG AAAGTCAGCC ACCGTGCTCT ATGAGGAATT GGACCTAATA AATTTTAGTG 3120
 TGCTTCCAA ACCTGAGAAT ATATGCTTTT GGAAGTTAAA ATTTAARTGG CTTTGGCCAC 3180
 ATACATAGAT CTTTCATGATG TGTGAGTGTA ATTCATGTG GATATCAGT ACCAAACATT 3240
 ACAAATAAAT TTTATGGCCC AAAATGACCA ACGAAATGT TACAATAGAA TTTATCCAAT 3300
 TTTGATCTTT TTATATTCTT CTACCACACC TGGAAACAGA CCAATAGACA TTTTGGGGTT 3360
 TTATAATGGG AATTTGTATA AAGCATTACT CTTTTCAT AAATTGTTTT TTAATTTAAA 3420
 AAAAGGAAAA AAAAAAAAAA AAA

Seq ID NO: 244 Protein sequence:
 Protein Accession #: AAD16433.1

1 11 21 31 41 51
 | | | | |
 MANAGLQLLG FILAFLGWIG AIVSTALPQW RIYSYAGDNI VTAQAMYEGL WMSCVSQSTG 60
 QIQCKVFDL LNLSSLTQAT RALMVVGILL GVIAIFVATV GMKCMKLED DEVQKMRMAV 120
 IGGAIPLLAG LAILVATAWY GNRIVQEFYD PMTPVNARYE FGQALPTGWA AASLCLLGGA 180
 LLCSCPRKT TSYPTPRYP KPAPSSGKDY V

Seq ID NO: 245 DNA sequence
 Nucleic Acid Accession #: CAT cluster

1 11 21 31 41 51
 | | | | |
 TTTTFTTTT TTTTFTTTT TTTTCAAGG AGAGCACAAG GAACTTTATT AATGACTTTC 60
 TTAATGGTTA AATGCTGTTT ACCAAGTGAC CCAGAGGCAG CGTGGTTTAG TGGTTTCAAC 120
 AGCATGGTCC CGAGAGTCTG ACAAACCTCA GTTCAAATCC TTCTTTGTGC TTCACTTAGT 180
 TTTTCTTCTT GAGATTAGT TTCTTCATCG TTAACAATGA GGATATTAAAT ATGTTTCACA 240
 CAGTTGTTAT GAAGAATGCA TATATTAGAA TGCCTGTAGT CTCAGCTACT CAGGAGGCTA 300
 AGGTGGGGAG GTGCTCAAG CCCAGGAAT CAAAGCTGCA ATGCATTATG ATTACAGCTG 360
 TTAATAGGCA CTGCACCTCA GCCTGGGCAA TGTAGTAAGA TCCCATCTCT GGCTCGGAGG 420
 GTCCTACGCC CACGGAGTCT CGCTGATTGC TAGCACAGCA GTCTGAGATC AAACCTGCA

Seq ID NO: 246 DNA sequence
 Nucleic Acid Accession #: XM_058553.2
 Coding sequence: 897-1400

1 11 21 31 41 51
 | | | | |
 AATTTTCAGA AGTTTCGTAT GGGGATGGTT TTATATAAAT TCAGGTTTTT CCCACAATAA 60
 TAAATGTATT TAGTCTCAGT GCTCAATAGA AGAGATTCTT AATAGAAAAG GATTCAAAC 120
 GTGAAACCAT TTCTCTTTTA ATGTTTCACA TTCTGTGTAC AGATTGTGTC TCTTGTGACT 180
 CTGTTATCCA TAATATGGAC AGTTCCTGAG TCCTAACATT GAGAGGTTTT CCCTTAGTGC 240
 ATAGAGGGAA TGAGTATTAA TTGGAGAAGC TTAAGTATT GCCACTTTAG CACTGAAGAT 300
 TGGGATGAGA GGAGGTGAAA CCTCACTAGA AAAAGGGACA ATGTTAGTGT GGCCCTTCTT 360
 GATCATGTTT AAGAAAAGTC ATGAAAATGG TGAACCTAGT TTTCCAAGCA TATTGGAAGG 420
 GTTGAGTGTA TACTGTCTGT CAAAGACTTC CAGCATTTCC AGGTCCCTAGA GAGGAACAAG 480
 ACTGTAAAC TGCTATCTG TATTTTAAAG AACCCAGGAG GAAAGCTTTA TAATAGAAC 540
 TTATTTCTGT GTTTATGTAT AAGGGGTTTT TTGTTTTTTT AAAGACAGGA TCTCACTCCA 600
 TTGTCAGGCC CAAGTGCAAT GGCACGAACC TCATAGCTCC TGGACTTAAG TGATCTGCCT 660
 GCCTTTTGCTT CCTGAGTAGC TGGGACTACA GGCATGAGCC CCATGCTCTG GCTAAGTTTG 720
 TTTTFTTGT TGTGTTGTTT TTTGTTTTTG GGGGGGGTTG TTTTGTTTTT TGTAGAGACG 780
 TAGTCTTGCT TTGTTGCCAG GCTAGTCTCA AACTCCTGGC TTCAAGTGAT CCTCCTGCCT 840
 CAGCTCCCA GAGTGCTAGG ATTACAGCAC TTGGATTGAG CTCTTCTTAT TCCAACATGG 900
 AAGAACTTA CACCGACTCC CTGGACCCCTG AGAAGCTATT GCAATGCCCT TATGACAAA 960
 ACCATCAAAT CAGGGCTTGC AGGTTTCCTT ATCATCTTAT CAAGTGACAGA AAGAAATCATC 1020
 CTGATGTTGC AAGCAAATTG GCTACTTGTG CCTTCAATGC TCGCCACCAG GTTCTCTGAG 1080
 CTGAAATTAG TCATCATATC TCAAGCTGTG ATGACAGAAG TTGTATTGAG CAAGATGTTG 1140
 TCAACCAAAC CAGGAGCCTT AGACAAGAGA CTCTGGCTGA GAGCACTTGG CAGTCCCTC 1200
 CTTGCGATGA AGACTGGGAT AAAGATTGTG GGGAGCAGAC CAGCACCCCA TTTGTCTGGG 1260
 GCACAACCTCA CTACTCTGAC AACAACAGCC CTGCGAGCAA CATAGTTACA GAACATAAGA 1320
 ATAACCTGGC TTCAGGCATG CGAGTTCCCA AATCTCTGCC GTATGTTCTG CCATGGAAAA 1380
 ACAATGGAAA TTCAAGATAA CTGAATACCT ATCTCATCAA ATGCCAGACC CTAGAAGACT 1440
 GTTGCTTCTT CTCTACACAG TGGGTTCTCA TTTTCTCTCT AATCTAATA TAGAATGGTA 1500
 AACTCCCTGT GACTTTCCAA ACTGACAAGC ACACTTTTTT CCTCCCCCTT TGAATCCTCA 1560
 TTTAATGCAA GAACCTCAT ACTCAGAAGC TTCCAATAA ACCTTTGATA CAGATTG

Seq ID NO: 247 Protein sequence:
 Protein Accession #: XP_058553.1

1 11 21 31 41 51
 | | | | |
 MEETYDSDLD PEKLLQCPYD KNHQIRACRF PYHLIKCRKN HPDVASKLAT CPFNARHQVP 60
 RABISHHSS CDDRSCIEQ VVNQTRSLRQ ETLARSTWQC PPCDEDDWDK LWEQTSTPFV 120
 WGTTHYSNN SPASNIVTEH KVNLAGSMRV PKSLPYVLPW KNNGNAQ

WO 02/086443

Seq ID NO: 248 DNA sequence
Nucleic Acid Accession #: NM_003392
Coding sequence: 758..1855

PCT/US02/12476

5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85

1	11	21	31	41	51	
TTAAGGAAAT	CCGGGCTGCT	CTTCCCCATC	TGGAAGTGGC	TTTCCCCACA	TCGGCTCGTA	60
AACTGATTAT	GAAACATACG	ATGTTAATTC	GGAGCTGCAT	TTCACAGCTG	GGCACTCTCG	120
CGCGCTGGTC	CCCCGGGCGT	CGCCCCCCAC	CCCTGCCCCT	TCCCTCCCGC	GTCTTCCCCC	180
CATCCTCCAC	CCCCCGCGCT	GGCCACCCCG	CCTCCTTGGC	AGCCTCTGGC	GGCAGCGCGC	240
TCCACTCGCC	TCCCGTGCTC	CTCTCGCCCA	TGGAATTAAT	TCTGGCTCCA	CTTGTGTCTC	300
GGCCAGGTT	GGGAGAGGGA	CGGAGGGTGG	CCGCAGCGGG	TTCTGTAGTG	AATTACCCAG	360
GAGGGACTGA	GCACAGCACC	AACATAGAGG	GGTTCAGGGG	GTGCGGGAAT	CGAGCGAGCA	420
GGAAGGAGGC	AGCGCTGGC	ACCAAGGGCTT	TGACTCAACA	GAATTGAGAC	ACGTTTGTAA	480
TCGCTGGCGT	GGCCCGCGCA	CAGGATCCCA	GCGAAAATCA	GATTTCCTGG	TGAGGTTGCG	540
TGGGTGGATT	AATTGGGAAA	AAGAACTGCG	CTATATCTTG	CCATCAAAAA	ACTCACGGAG	600
GAGAAGCGCA	GTCAATCAAC	AGTAACTTA	AGAGACCCCC	GATGCTCCCC	TGGTTAACT	660
TGTATGCTTG	AAAATTATCT	GAGAGGGAAT	AAACATCTTT	TCCTTCTTCC	CTCTCCAGAA	720
GTCCATTGGA	ATATTAAGCC	CAGGAGTTGC	TTTGGGGATG	GCTGGAGTGG	CAATGTCTTC	780
CAAGTTCTTC	TGGTCTGCTT	TGGCCATATT	TTTCTCTTTC	GCCCAGGTTG	TAATTGAAGC	840
CAATTCTTGG	TGGTCTGCTAG	GTATGAATAA	CCCTGTTCAG	ATGTCAGAA	TATATATTAT	900
AGGAGCACAG	CCTCTCTGCA	GCCAACTGGC	AGGACTTTCT	CAAGGACAGA	AGAACTCTGT	960
CCACTTGTAT	CAGGACCAAC	TGCAGTACAT	CGGAGAAGGC	GCGAAGACAG	GCATCRAAGA	1020
ATGCGCAGTAT	CAATTCCGAC	ATCGACGGTG	GAACTGCAGC	ACTGTGGATA	ACACCTCTGT	1080
TTTTGGCAGG	GTGATGCGCA	TAGGCAGCCG	CGAGACGGCC	TTACATACAG	CCGTGAGCGC	1140
AGCAGGGGTG	GTGAACGCCA	TGAGCCGGGC	GTGCCGCGAG	GGCGAGCTGT	CCACTGCGCG	1200
CTGCAGCCGC	GGCCGCGCGC	CCAAGGACCT	GCCGCGGGAC	TGGCTCTGGG	GCGGCTGCGG	1260
CGACCAACATC	GACTATGGCT	ACCGCTTTTG	CAAGGAGTTC	GTGGACGCCC	GCGAGCGGGA	1320
GCGCATCCAC	GCCAGGGGCT	CCTACGAGAG	TGCTCGCATC	CTCATGAACC	TGCACAAACA	1380
CGAGGCGCGC	CGCAGGACGG	TGTACAACCT	GGCTGATGTG	GCCTGCAAGT	GCCATGGGGT	1440
GTCCGGCTCA	TGTAGCCTGA	AGACATGCTG	GCTCGAGCTG	GCAGACTTCC	GCAAGGTGGG	1500
TGATGCGCTG	AAGGAGAAGT	ACGACAGCGC	GGCGGCCATG	CGGCTCAACA	GCCGGGGCAA	1560
GTTGGTACAG	GTCAACAGCC	GCTTCAACTC	GCCCACCACA	CAAGACCTGG	TCTACATCGA	1620
CCCCAGCCCT	GACTACTGCG	TGCGCAATGA	GAGCACCAGC	TGCTGGGCA	CGCAGGGCCG	1680
CCTGTGCACT	AGACGTCCG	AGGGCATGGA	TGGCTGCGAG	CTCATGTGCT	GCGCCCGTGG	1740
GTACGACCAG	TTCAAGACCG	TGCAGACGGA	GCGCTGCCAC	TGCAAGTTCC	ACTGGTGCTG	1800
CTACGTCAAG	TGCAAGAAGT	GCACGGAGAT	CGTGGACCAG	TTTGTGTGCA	AGTAGTGGGT	1860
GCCACCCAGC	ACTCAGCCCC	GCTCCCAGGA	CCGCTTATT	TATAGAAAGT	ACAGTGATTC	1920
TGGTTTTTGG	TTTTTAGAAA	TATTTTTTAT	TTTTCCCCAA	GAATTGCAAC	CGGAACCAAT	1980
TTTTTTCTCT	TACCATCTA	AGAACTCTGT	GGTTATTAT	TAATATTATA	ATTATTATTT	2040
GGCAATAATG	GGGGTGGGAA	CCACGAAAAA	TATTTATTTT	GTGGATCTTT	GAAAAGGTAA	2100
TACAAGACTT	CTTTTGATA	GTATAGAATG	AAGGGGGAAA	TAACACATAC	CCTAATCTAG	2160
CTGTGTGGGA	CATGGTACAC	ATCCAGAAGG	TAAAGAAATA	CATTTTCTTT	TTCTCAAATA	2220
TGCCATCATTA	TGGGATGGGT	AGGTTCCAGT	TGAAAGAGGG	TGGTAGAAT	CTATTCAACA	2280
TTCACTTCT	TACACCAAAA	TAGATTGTAA	ATTCTCTGGT	GCAAGATAAA	AGGCTCTGGG	2340
AAAACAAAAC	AAAACAAAAC	AAACCTCCCT	TCCCAGCAG	GGCTGCTAGC	TTGCTTCTG	2400
CATTTTCAAA	ATGATAATTT	ACAATGGAAG	GACAAGAATG	TCATATTCTC	AAGGAAAAAA	2460
GGTATATCAC	ATGCTCAATT	CTCCTCAAT	ATTCCATTG	CAGACAGACC	GTCAATTCT	2520
AATAGCTCAT	GAAATTTGGG	CAGCAGGGAG	GAAAGTCCCC	AGAAATTAAA	AAATTTAAAA	2580
CTCTTATGTC	AAGATCTTGA	TTTGAAGCTG	TTATAAGAA	TGGGATTCCA	GATTTGTAAA	2640
AAGACCCCCA	ATGATCTCTG	ACACTAGATT	TTTTGTTTGG	GGAGGTTGGC	TGAAACATAA	2700
ATGAATATAT	CTGTATTTTC	TAGGGATAC	TTGGTTAGTA	AATTATAATA	GTAGAAATAA	2760
TACATGAATC	CCATTCACAG	GTTTCTCAGC	CCAAAGCAAC	AGGTAATTGC	GTGCCATTCA	2820
GCACGTGACC	AGAGCAGACA	ACCTATTTGA	GGAAAAACAG	TGAAATCCAC	CTTCTCTTTC	2880
ACACTGAGCC	CTCTCTGATT	CCTCCGTGTT	GTGATGTGAT	GCTGGCCACG	TTTCCAAACG	2940
GCAGCTCCAC	TGGGTCCCCT	TTGGTTGTAG	GACAGGAAAT	GAAACATTAG	GAGCTCTGCT	3000
TGGAACACAG	TTCACTACTT	AGGGAATTTT	GTTTCTTAAA	ACTTTTATTT	TGAGGAGCAG	3060
TAGTTTTCTA	TGTTTTAATG	ACAGAACTTG	GCTAATGGAA	TTACACAGAG	TGTTGCAGCG	3120
TATCACTGTT	ATGATCCTGT	GTTTAGATT	TCCACTCATG	CTTCTCTTAT	TGTACTGCAG	3180
GTGTACCTTA	AAACTGTGCC	CAGTGTACTT	GAACAGTTGC	ATTATAAAGG	GGGGAAATGT	3240
GGTTTAATGG	TGCTGATAT	CTCAAAGTCT	TTGTACATA	ACATATATAT	ATATATACAT	3300
ATATATAAAT	ATAAATATAA	ATATATCTCA	TGCGAGCCAG	TGATTTAGAT	TTACAGCTTA	3360
CTCTGGGGTT	ATCTCTCTGT	CTAGAGCATT	GTTGTCTTTC	ACTGCAGTCC	AGTTGGGATT	3420
ATTCCAAAAG	TTTTTTGAGT	CTTGAGCTTG	GGCTGTGGCC	CCGCTGTGAT	CATACCCTGA	3480
GCACGACGAA	GCAACCTCGT	TTCTGAGGAA	GAAGCTTGAG	TTCTGACTCA	CTGAAATGCG	3540
TGTTGGGGTTG	AAGATATCTT	TTTTTCTTTT	CTGCCCTACC	CCTTTGTCTC	CAACCTCCAT	3600
TTCTGTTTAC	TTTGTGGAGA	GGGCATTACT	TGTTGTTTAT	AGACATGGAC	GTTAAGAGAT	3660
ATTCAAACT	CAGAAGCATC	AGCAATGTTT	CTCTTTTCTT	AGTTCAATCT	GCAGAATGGA	3720
AACCCATGCC	TATTAGAAAT	GACAGTACTT	ATTAAATTGAG	TCCCTAAGGA	ATATTACAGC	3780
CACATACATG	ATAGCTTTTT	TTTTTTTTTT	TTTTTTTTTA	TAAGGACACC	TCTTTCCAAA	3840
CAGGCCATCA	AATATGTTCT	TATCTCAGAC	TTACGTTGTT	TTAAAAGTTT	GGAAAGATAC	3900
ACATCTTTCT	ATACCCCCCC	TTAGGAGGTT	GGGCTTTTAT	ATCACCTCAG	CCAACCTGGG	3960
CTCTTAATTT	ATTGCATAAT	GATATCCACA	TCAGCCAACT	GTGGCTCTTT	AATTTATTGC	4020
ATAATGATAT	TCACATCCCC	TCAGTTGCCAG	TGAATTGTGA	GCAAAAGATC	TTGAAAGCAA	4080
AAAGCACTAA	TTAGTTTAAA	ATGTCACCTT	TTTGGTTTTT	ATTATACAAA	AACCATGAAG	4140
TACTTTTTTT	ATTTGCTAAA	TCAGATTGTT	CCTTTTTAGT	GACTCATGTT	TATGAAGAGA	4200
GTTGAGTTTA	ACAATCCTAG	CTTTTAAAAG	AAACTATTTA	ATGTAAAATA	TTCTACATGT	4260
CATTGAGATA	TTATGTATAT	CTTCTAGCCT	TTATTCTGTA	CTTTTAATGT	ACATATTTCT	4320
GTCTTGGCGT	ATTGTATAT	TTCACTGGTT	TAAAAACAA	ACATCGAAAG	GCTTATTCCA	4380
AATGGAAGAT	AGAAATATAA	ATAAAACGTT	ACTTGTAAAA	AAAAAAA		

Seq ID NO: 249 Protein sequence:
Protein Accession #: NP_003383

1 11 21 31 41 51

MAGSAMSSEK FLVALAIFFS FAQVVIEANS WWSLGMNPNV QMSEVYIIGA QPLCSQLAGL 60
 SQGQKMLCHL YQDHMQYIGE GAKTGIKECQ YQFRHRRWNC STVDNTSVFG RVMQIGSRET 120
 AFTYAVSAAG VVNAMSACRAC EGELSTCCGS RAARPKDLPR DMLWGGCGDN IDYGYRFAKE 180
 FVDARERERI HAKGSYESAR ILMNLHNNEA GRRTVYNLAD VACKCHGVSG SCSLKTCWLQ 240
 LADFRKVGDA LKEKYDSAAA MRLNSRGKLV QVNSRFNSPT TQDLVYIDPS PDYCVRNEST 300
 GSLGTQGRCL NKTSEGMDCG ELMCCGRGYD QFKTVQTERC HCKFHWCCYV KCKKCTEIVD 360
 QFVCK

Seq ID NO: 250 DNA sequence
 Nucleic Acid Accession #: NM_014058
 Coding sequence: 56..1324

1 11 21 31 41 51
 TGACTTGGAT GTAGACCTCG ACCTTCACAG GACTCTTCAT TGCTGGTTGG CAATGATGTA 60
 TCGGCCAGAT GTGGTGAGGG CTAGGAAAAG AGTTTGTGG GAACCTCGGG TTATCGGCC 120
 CGTCATCTTC ATATCCCTGA TTGTCTGGC AGTGTGCATT GGACTCACTG TTCATTATGT 180
 GAGATATAAT CAAAAGAAGA CCTACAATTA CTATAGCACA TTGTCATTTA CAACCTGACAA 240
 ACTATATGCT GAGTTTGGCA GAGAGGCTTC TAACAATTTT ACAGAAATGA GCCAGAGACT 300
 TGAATCAATG GTGAAAATG CATTTTATAA ATCTCCATTA AGGGAAGAAAT TTGTCAAGTC 360
 TCAGGTTATC AAGTTCAGTC AACAGAAGCA TGGAGTGTG GCTCATATGC TGTGATTGT 420
 TAGATTTTAC TCTACTGAGG ATCCTGAAAC TGTAGATAAA ATTGTTCAAC TTGTTTACA 480
 TGAAAAGCTG CAAGATGCTG TAGGACCCCT TAAAGTAGAT CCTCACTCAG TTAATAATTA 540
 AAAAATCAAC AAGACAGAAA CAGACAGCTA TCTAAACCAT TGCTGCGGAA CACGAAGAAG 600
 TAAACTCTA GTTCAGAGTC TCAGGATCGT TGGTGGGACA GAAGTAGAAG AGGGTGAATG 660
 GCCCTGGCAG GCTAGCTGCG AGTGGGATGG GAGTCATCGC TGTGGAGCAA CCTTAATTAA 720
 TGCCACATGG CTTGTGAGTG CTGCTCACTG TTTTACAACA TATAAGAAC CTGCCAGATG 780
 GACTGCTTCC TTTGGAGTAA CAATAAAACC TTCGAAAATG AAACGGGGTC TCCGAGAAT 840
 AATTGTCCAT GAAAAATACA AACACCCATC ACATGACTAT GATATTCTC TTGCAGAGCT 900
 TTCTAGCCCT GTTCCCTACA CAAATGCAGT ACATAGAGTT TGTCTCCCTG ATGCATCTTA 960
 TGAGTTTCAA CCAGGTGATG TGATGTTTGT GACAGGATTT GGAGCACTGA AAAATGATGG 1020
 TTACAGTCAA AATCATCTTC GACAAGCACA GGTGACTCTC ATAGACGCTA CAACTTGCAA 1080
 TGAACCTCAA GCTTACAATG ACGCCATAAC TCCTAGAATG TTATGTGCTG GCTCCTAGA 1140
 AGGAAAAACA GATGCATGCC AGGGTGACTC TGGAGGACCA CTGGTTAGTT CAGATGCTAG 1200
 AGATATCTGG TACCTTGCTG GAATAGTGAG CTGGGGAGAT GAATGTGCGA AACCACACAA 1260
 GCCTGTGTTT TATACTAGAG TTACGGCCTT GCGGGACTGG ATTACTTCAA AAACCTGGTAT 1320
 CTAAGAGAGA AAAGCCTCAT GGAACAGATA ACATTTTTTT TTGTTTTTTG GGTGTGGAGG 1380
 CCATTTTATG AGATACAGAA TTGGAGAAGA CTTCGAAAAC AGCTAGATTT GACTGATCTC 1440
 AATAAACTGT TTGCTTGATG CAAAAAATAA A

Seq ID NO: 251 Protein sequence:
 Protein Accession #: NP_054777

1 11 21 31 41 51
 MYRPDVVRAR KRVCWEPWVI GLVIFISLIV LAVCIGLTVH YVRYNQKTTY NYYSTLSFTT 60
 DKLYAEPGRE ASNMFTEMSQ RLESWVQNAF YKSPRLREFV KSOVIKFSQQ KHGVLAMHLL 120
 ICRFHSTEDP ETVDKIVQLV LHEKLQDAVG PPKVDPHSVK IKKINKTETD SYLNHCCGTR 180
 RSKTLGQSLR IVGGTEVEEG EWPWQASLQW DGSHRGATL INATWLVSAA HCFTTYKNPA 240
 RWTASFGVTI KPSKMKRGLR RIIVHEKYKH PSHDYDISLA ELSSPPVPTN AVHRVCLPDA 300
 SYEFQPGDVM FVTGFGALKV DGYSQNHRLQ AQVTLIDATT CNEPQAYNDA ITPRMLCAGS 360
 LEGKTDACQG DSGGPLVSSD ARDIWYLAGI VSWGDECAKP NKPGVYTRVT ALRDWITSKT 420
 GI

Seq ID NO: 252 DNA sequence
 Nucleic Acid Accession #: NM_003504.2
 Coding sequence: 71-1771

1 11 21 31 41 51
 GGCACGAGGC CTGCTGCCGC CGGGCTCTTG GTACCTCAGC GCGAGCGCCA GGCCTCCGGC 60
 TCCGCTGGCT ATGTTCTGTG CCGATTTCOG CAAAGAGTTC TACGAGGTGG TCCAGAGCCA 120
 GAGGGTCTTT CTCTCTGTGG CCTCGGACGT GGATGCTCTG TGTGCGTGCA AGATCCTTCA 180
 GGCCTTGTTT CAGTGTGACC ACGTGCAATA TACGCTGGTT CCAGTTTCTG GGTGGCAAGA 240
 ACTTGAAACT GCATTTCTTG AGCATAAAGA ACAGTTTCAT TATTTTATTC TCATAAACTG 300
 TGGAGCTAAT GTAGACCTAT TGGATATTCT TCAACCTGAT GAAGACACTA TATTCTTTGT 360
 GTGTGACACC CATAGGCCAG TCAATGTCGT CAATGTATAC AACGATACCC AGATCAAATT 420
 ACTCATTAAA CAAGATGATG ACCTTGAAGT TCCCGCCTAT GAAGACATCT TCAGGGATGA 480
 AGAGGAGGAT GAAGAGCATT CAGGAAATGA CAGTGATGGG TCAGAGCCTT CTGAGAAGCG 540
 CACACGGTTA GAAGAGGAGA TAGTGGAGCA AACCATGCGG AGGAGGCRGC GGCAGAGATG 600
 GGAGGCCCGG AGAAGAGACA TCCTCTTTGA CTACGAGCAG TATGAATATC ATGGGACATC 660
 GTCAGCCATG GTGATGTTTG AGCTGGCTTG GATGCTGTCC AAGGACCTGA ATGACATGCT 720
 GTGTTGGGCC ATCGTTGGAC TAACAGACCA GTGGGTGCAA GACAAGATCA CTCAAATGAA 780
 ATACGTGACT GATGTTGGTG TCCTGCAGCG CCACGTTTCC CGCCACAACC ACCGGAACGA 840
 GGATGAGGAG AACACACTCT CCGTGGACTG CACACGGATC TCCTTTGAGT ATGACCTCG 900
 CCTGGTGCTC TACCAGCACT GGTCCCTCCA TGACAGCCTG TGCAACACCA GCTATACGCG 960
 AGCCAGGTTT AAGCTMTGGT CTGTGCATGG ACAGAAGCGG CTCAGGAGT TCCTTGAGA 1020
 CATGGGTCTT CCCTGAAGC AGGTGAAGCA GAAATTCCAG GCCATGGACA TCTCCTTGAA 1080
 GGAGAATTTG CGGGAATGA TTGAAGAGTC TGCAAAATAA TTTGGGATGA AGGACATGCG 1140
 CGTGACAGCT TTCAGCATTC ATTTTGGGTT CAAGCACAAG TTTCTGCGCA GCGACGTGGT 1200
 CTTTGCCACC ATGTCTTTGA TGGAGAGCCC CGAGAAGGAT GGCTCAGGGA CAGATCACTT 1260
 CATCCAGGCT CTGGAAGGAG TCTCCAGGAG TAACCTGGAC AAGCTGTACC ATGGCCTGGA 1320
 ACTGCCAAG AAGCAGCTGC GAGCCACCCA GCAGACCATT GCCAGCTGCC TTTGCACCAA 1380
 CCTCGTCATC TCCAGGGGCT CTTCCTGTA CTGCTCTCTC ATGGAGGGCA CTCAGATGT 1440
 CATGCTGTTT TCTAGGCCGG CATCCCTAAG CCTGCTCAGC AAACACCTGC TCAAGTCTCT 1500
 TGTGTGTTCC ACAAGAACC GCGCTGCAA ACTGCTGCCC CTGGTGATGG CTGCCCCCT 1560

GAGCATGGAG CATGGCACAG TGACCGTGGT GGGCATCCCC CCAGAGACCG ACAGCTCGGA 1620
 CAGGAAGAAC TTTTGGGA GGGCGTTTGA GAAGGCAGCG GAAAGCACC GCTCCCGGAT 1680
 GCTGCACAAC CATTTTGACC TCTCAGTAAT TGAGCTGAAA GCTGAGGATC GGAGCAAGTT 1740
 TCTGGACGCA CTATTTCCTC TCTGTCTCTA GGAATTTGAT TCTTCCAGAA TGACCTTCTT 1800
 ATTTATGTAA CTGGCTTTCA TTTAGATTGT AAGTTATGGA CATGATTTGA GATGTAGAAG 1860
 CCATTTTSTA TTAATAAAA TGCTTATTTT AGGCTCCGTC CCCAAAAAA AAAAAAAA 1920
 AAAAAAAA AA

Seq ID NO: 253 Protein sequence:
 Protein Accession #: NP_003495.1

1 11 21 31 41 51
 MFVSDFRKEF YEYVQSQRVL LFVADVDAL CACKILQALF QCDHVQYTLV PVSGWQBLET 60
 AFLEHKEQFH YFILINGAN VLLDLILQPD EDTIPFVCDT HRPVNVVNVY NDTQIKLLIK 120
 QDDLEVPAY EDIPEDEED EEHSGNDSG SEPSEKTRRL EEEIVEQTM RQRREWEAR 180
 RRDILFDYEQ YEYHGTSSAM VMFELAWMLS KDLDNMLWNA IVGLTDQWVQ DKITQMKYVT 240
 DVGVLQRHVS RHNHRNDEDE NTLSDVCTRI SFYEDLRLVL YQHWSLEDSL CNTSYTAARF 300
 KLVSVHGGKR LQEFLLAMGL PLKQVKQKQFQ AMDISLKENL REMIEESANK FGMKDMRVQT 360
 FSIHFGPKHK FLASDVVFAT MSLMESPEKD GSGTDHFIQA LDSLSRSNLD KLYHGLELAK 420
 KQLRATQOTI ASCLCTNLVI SQGPFYLCSL MEGTDPVMLF SRPASLSLLS KHLKSFVCS 480
 TKNRRCKLLP LVMAAPLSME HGTVTVVGIP PETDSSDRKN FFGRAFEKAA ESTSSRMLHN 540
 HPDLSVIELK AEDRSKFLDA LISLLS

Seq ID NO: 254 DNA sequence
 Nucleic Acid Accession #: NM_022337
 Coding sequence: 48..683

1 11 21 31 41 51
 GGCTGCGCTT CCCTGGTCAG GCACGGCAGC TCTGGCCGGC CGCCAGGATG CAGGCCCGCG 60
 ACAAGGAGCA CCTGTACAAG TTGCTGGTGA TTGGCGACCT GGGCGTGGG AAGACCACTA 120
 TCATCAAGCG CTACGTGCAC CAGAACTTCT CCTCGCACTA CCGGGCCACA ATCGGCGTGG 180
 ACTTCGCGCT CAAGGTGCTC CACTGGGACC CGGAGACTGT GGTGCGCCTG CAGCTCTGGG 240
 ATATGCGAGK TCAAGAAAGA TTTGAAACA TGACGAGGGT CTATTACCGA GAAGCTATGG 300
 GTGCATTAT TGTCTTCGAT GTCAACAGGC CAGCCACATT TGAAGCAGTG GCAAAGTGGA 360
 AAAATGATT GGAATCCAAG TTAAGTCTCC CTAATGGCAA ACCGCTTCA GTGTTTGT 420
 TGGCCAAACA ATGTGACCAG GGAAGGATG TGCTCATGAA CAATGGCCTC AAGATGGACC 480
 AGTTCTGCAA GGAGCAGCGT TTCGTAGGAT GGTTTGAAAC ATCAGCAAAG GAAATATATA 540
 ACATTGATGA AGCCTCCAGA TGCTGTGTA AACACATACT TGCAATGAG TGTGACCTAA 600
 TGGAGTCTAT TGAGCCGGAC GTCGTGAAGC CCCATCTCAC ATCAACCAAG GTTGCCAGCT 660
 GCTCTGGCTG TGCCAAATCC TAGTAGGCAC CTTTGTCTGT GTCTGGTAGG AATGACCTCA 720
 TTGTTCCACA AATTGTGCCT CTATTTTAC CATTTTGGGT AAACGTCAGG ATAGATATAC 780
 CACATGTGGC AAGCCAAAGA TCTATGCCTC TGTTTTTCAT ATGAGAGAGA AATAGCAAT 840
 GTTCTTCTTA TGCTTTCTC ACCATCATCA CAGTGTTCAC AAACCTTTGA AAATATTTAG 900
 TCTGTACAA ACTTCTGTCA TGTAGCTGAC CAAATCTCTG CAGGGCCACA GTCGGCACTG 960
 TTATTTGCTT CTTTAAATCA GCAAAGGCT CAAGTCTTAA AATAAAGGG GAGAAGAA 1020
 AACTAGCTGT CAAGTCAAGG ACTGGCTTTC ACCTTGCCCT GGTGTCTTTT TCCAGATTTC 1080
 AATATATTCT CTGATGGCCT GACAGGCCTA TTAAGTAGAT GTGATATTTT CTTCACAGAT 1140
 GACCTCCATT CTCGGCGACT CTAAGAGTTG CCTCTGAGT AGCTCTTTGG AATCGTGAAC 1200
 ACAGGTGTGC TATATTGCC TTGTCTTAAC TGTCACTTGC CATGGCCTGA ATGTTGGCTT 1260
 AACTGAATAT TGTATGAAA GACATGCCTC CATATGTGCC TTTCTGTTAG CTCTCTTTGA 1320
 CTCAGCTGT GGGGCTCCTC TATACATGCT ATACATGTAA TATATATTAT ATATATTTT 1380
 GCAAGTGAAAC AATAAACAT TAAAGATAA AA

Seq ID NO: 255 Protein sequence:
 Protein Accession #: NP_071732

1 11 21 31 41 51
 MQAPHKEHLY KLVIGDLGV GKTSIIKRYV HQNFSSHRYA TIGVDFALKV LHWDPETVVR 60
 LQLWDIAGQE RFGNMTRVYV REAMGAFIVF DVTRPATFEA VAKWKNLDS KLSLPLNGKPV 120
 SVVLLANKCD QGKDVLMNNG LKMDQFCKEH GPVGFETSA KENINIDEAS RCLVKHILAN 180
 ECDLMESIEP DVVKPHLTST KVASCSGCAK S

Seq ID NO: 256 DNA sequence
 Nucleic Acid Accession #: NM_016321
 Coding sequence: 25..1464

1 11 21 31 41 51
 GGAACCGCCC GCTGCCAGCC CGGCCAGGCA CCCCTGCAGC ATGGCCTGGA ACACCAACCT 60
 CCGCTGGCGG CTGCGGCTCA CCTGCCTGCT CCGTCAGGTG ATTATGGTGA TTCTCTTCGG 120
 GGTGTTCTGT GCTACGACT TCGAGGCCGA CGCCCACTGG TTGTCAGAGA GGACGCACAA 180
 GAACTTGAGC GACATGGAGA ACGAATTTCTA CTATCGCTAC CCAAGCTTCC AGGACGTGCA 240
 CGTGAATGCT TCGTGGGCTC TCGGCTTCTC CATGACTTTC CTGACGCGCT ACGGCTTCAG 300
 CGCCGTGGGC TTCAACTTCC TGTGGCAGC CTTCCGCATC CAGTGGGCGC TGCTCATGCA 360
 GGGCTGGTTC CACTTCTTAC AAGACCGCTA CATCGTGTG GGCCTGGAGA ACCTCATCAA 420
 TGCCTGACTT TCGGTGGCCT CTGTCTGCGT GGCCTTTGGG GCAGTCTCGG GTAAAGTCAG 480
 CCCCATTACC CTGCTCATCA TGACTTTCTT CCAAGTGACC CTCTTCGCTG TGAATGAGTT 540
 CATCTCCTT AAGCTGCTAA AGGTGAAGGA TGCAGGAGGC TCCATGACCA TCCACACATT 600
 TGGGCGCTAC TTTGGGCTCA CAGTGACCGG GATCCTCTAC CGACGCAACC TAGAGCAGAG 660
 CAAGGAGAGA CAGAAATCTG TGTACCACTG GGACCTCTTT GCCATGATTG GCACCTCTT 720
 CCTGTGGATG TACTGGCCCA GCTTCAACTC AGCCATATCC TACCATGGGG ACAGCCAGCA 780
 CCGAGCGGCC ATCAACACCT ACTGCTCCTT GGCAGCCTGC GTGCTTACCT CGGTGGCAAT 840

ATCCAGTGCC CTGCACAAGA AGGGCAAGCT GGACATGGTG CACATCCAGA ATGCCACGCT 900
 CGCAGGAGGG GTGGCCGTGG GTACCGCTGC TGAGATGATG CTCATGCCTT ACGGTGCCCT 960
 CATCATCGGC TTCGTCTGGG GCATCATCTC CACCTGGGT TTTGTATACC TGACCCCAT 1020
 CCTGGAGTCC CGGCTGCACA TCCAGGACAC ATGTGGCATT AACATCTGAC ATGGCATTCC 1080
 TGGCATCATA GCGGCGATCG TGGGTGCTGT GACAGCGGCC TCGGCCAGCC TTGAAGTCTA 1140
 TGGAAAAGAA GGGCTTGTCC ATTCCTTTGA CTTCCTTGA ACCCTGGCCA TGGCCCTGAT 1260
 AAGAACACAG GGAAGTTTCC AGATTATGG TCTCTTGGT ACCCTGGCCA TGGCCCTGAT 1260
 GGGTGGCATC ATTGTGGGCG TCACTTTGAG ATTACCATC TGGGGACAA CTTCAGATGA 1320
 GAACGTCTTT GAGGATGCGG TCTACTGGGA GATGCCTGAA GGAACAGCA CTGTCTACAT 1380
 CCCTGAGGAC CCCACCTTCA AGCCCTCAGG ACCCTCAGTA CCCTCAGTAC CCATGGTGTG 1440
 CCCACTACCC ATGGCTTCTT CGGTACCCCTT GGTACCCCTAG GCTCCAGGG CAGGTGAGGA 1500
 GCAGGCTCCA CAGACTSTCC TGGGGCCAG AGGAGCTGGT GCTGACCTAG CTAGGGATGC 1560
 AAGAGTGAGC AAGCAGCACC CCCACCTGCT GGCTTGGCCT CAAGGTGCTC CCACCCCTGC 1620
 CCTCCCTCTT ATCCAGGGGG GTCTGMCTGA GAATGGAGAA GGAGAAGCTA CAAAGTGGGC 1680
 ATCCAAGCCG GGTCTCTGGT GCAGAACTC TGCTCTGCTC TGGGGTCTTG GCCACATTGG 1740
 AGAAAAACAG GCTCAAAGTG GGGCTGGGAC CTGGTGGGTG AACCTGAGCT CTCCAGGAG 1800
 ACAACTTAGC TGCCAGTCAC CACCTATGAG GCTCTTCTAC CCCGTGCTG CACCTCGGCC 1860
 AGCATCTCCT ATGCTCCCTG GGTCCCTCAG ACCTCTCTGT GTTGTGTGCG TGGCAGCCTC 1920
 CAGGAATAAA CATTCTTGTG TCCCTTTGTA AAAAAAAAAA AAAAAAAAAA

Seq ID NO: 257 Protein sequence:
 Protein Accession #: NP_057405

1 11 21 31 41 51
 MAWNTNLRWR LPLTCLLLQV IMVILEGVFV RYDFEADAHW WSEKTHKNLS DMENEFYRY 60
 PSFQDVHVMV FVGFGLMTF LQRYGPSAVG FNFLAAPGI QWALLMQGW FHLQDRYIVV 120
 GVENLINADF CVASVCVAFG AVLKGVSPQI LLIMTFQVIT LFAVNEFILL NLLKVKDAGG 180
 SMTIHTFGAY FGLTVTRILY RNLBQSKER QNSVYQSDLF AMIGTLFLWM YWPSFNSAIS 240
 YHGDQSHRAA INTCYSLAAC VLTSVAISSA LHKXKGLDMV HIQNTATLAG VAVGTAAEMM 300
 LMPYGLIIG FVCGIISTLG FVYLTFFLES RLHIQDTGCI NNHIGIPGII GGIVGAVTAA 360
 SASLEVYKKE GLVHSPDFQG FNGDWTARTQ GKFIQYGLLV TLAALMGGI IVGLILRLPF 420
 WQPSDENCF EDVAVWEMPE GNSTVYIPED PTFKPSGSPV PSVPMVSPLP MASSVPLVP

Seq ID NO: 258 DNA sequence
 Nucleic Acid Accession #: NM_002358.2
 Coding sequence: 75..692

1 11 21 31 41 51
 GGGAAAGTGCT GTTGGAGCCG CTGTGGTTGC TGTCCGCGGA GTGGAAGCGC GTGCTTTTGT 60
 TTGTGTCCCT GGCATGCGCG CTGCAGCTCT CCCGGGAGCA GGAATCACC CTGCGCGGGA 120
 GCGCCGAAAT CGTGGCCGAG TTCTTCTCAT TCGGCATCAA CAGCATTTTA TATCAGCGTG 180
 GCATATATCC ATCTGAAACC TTTACTCGAG TGCAGAAATA CGGACTCACC TTGCTTGTAA 240
 CTACTGATCT TGAGCTCATA AAATACTTAA ATAAATGTGT GGAACAACTG AAAGATTGGT 300
 TATACAAGTG TTCACTTCAG AAATCGTTG TAGTTATCTC AAATATTGAA AGTGGTGAGG 360
 TCCTGGAAG ATGGCAGTTT GATATTGAGT GTGACAAGAC TGCAAAAGAT GACAGTGAC 420
 CCAGAGAAAA GTCTCAGAAA GCTATCCAGG ATGAAATCCG TTCAGTGATC AGACAGATCA 480
 CAGCTACGGT GACATTCTG CCACTGTGGG AAGTTTCTTG TTCAATTGAT CTGCTGATTT 540
 ATACAGACAA AGATTGTGTT GTACCTGAAA AATGGGAAGA GTCGGGACCA CAGTTTATTA 600
 CCAATCTGTA GGAAGTCCCG CTTCGTTTAT TTAATCTTAC AATCCACAAA GTAAATAGCA 660
 TGGTGGCCTA CAAATCTCTT GTCAATGACT GAGGATGACA TGAGGAAAAT AATGTAATTG 720
 TAATTTGAAA ATGTGGTTTT CCGTAAATCA GGTCTATCTA AGTTGATATG TTTTATTCTA 780
 TTGGTTAATT TTTACATGGA GAAACCAAAA ATGATACTTA CTGAAGTG TGTAATTGTT 840
 CCTTTATTTT TTTGGTACCT ATTGACTTA CCATGGAGTT AACATCATGA ATTTATTGCA 900
 CATTGTTCAA AAGGAACCGG GAGGTTTTTT TGTCAACATT GTGATGTATA TTCCTTTGAA 960
 GATAGTAATC GTAGATGAAA AACTTGTGCT TATAAGCTA GATGCTTTCC TAAATCAGAT 1020
 GTTTTGGTCA AGTAGTTTGA CTCAGTATAG GTAGGGAGAT ATTTAAGTAT AAAATACAAC 1080
 AAAGGAAGTC TAAATATTCA GAATCTTTGT TAAGGTCCTG AAAGTAACTC ATAATCTATA 1140
 AACAAAGAAA TATTGCTGTA TAGCTCCTTT TGACCTTCAT TTCATGTATA GTTTTCCCTA 1200
 TTGAATCAGT TTCAATTTAT TTGACTTTAA TTTATGTAAC TTGAACCTAT GAAGCAATGG 1260
 ATATTGTGAC TGTTTAATGT TCTGTGATAC AGAACTCTTA AAAATGTTTT TTCATGTGTT 1320
 TTATAAAATC AAGTTTTAAG TGAAAGTGAG GAAATAAAGT TAAGTTTGT TTAATAAAAA 1380
 AAAAAAAAAA

Seq ID NO: 259 Protein sequence:
 Protein Accession #: NP_002349.1

1 11 21 31 41 51
 MALQLSREQG ITRLSAEIV AEFFSFGINS ILYQRGIYPS EFTFRVQKYG LTLVTTDLE 60
 LKYLNNVVE QKDWLYKCS VQKLVVVISN IESGEVLERW QFDIECDKTA KDDSAPEKRS 120
 QRAIQDEIRS VIRQITATVT FLPLLEVSCS FDLIYTDKD LVVPEKWEES GPQFITNSEE 180
 VRLRSFTTTI HKVNSMVAYK IPVND

Seq ID NO: 260 DNA sequence
 Nucleic Acid Accession #: NM_001211
 Coding sequence: 43..3195

1 11 21 31 41 51
 AAAGGCCGTC AGCAGGACGA GGACCTGAGC CAGGAATGCA GGATGGCGGC GGTGAAGAAG 60
 GAAGGGGGTG CTTGAGTGA AGCCATGTCC CTGGAGGGAG ATGAATGGGA ACTGAGTAAA 120
 GAAAATGTAC AACCTTTAAG GCAAGGGCGG ATCATGTCCA CGCTTCAGGG AGCACTGGCA 180
 CAAGAATCTG CCTGTAACAA TACTCTTCAG CAGCAGAAAC GGSCATTGTA ATATGAAATT 240

CGATTTTACA CTGGAATGA CCCTCTGGAT GTTTGGGATA GGTATATCAG CTGGACAGAG 300
 CAGAACTATC CTCAAGGTGG GAAAGAGAGT AATATGTCAA CGTTATTAGA AAGAGCTGTA 360
 GAAGCACTAC AAGGAGAAAA ACATATATTAT AGTGATCCTC GATTTCTCAA TCTCTGGCTT 420
 AAATTAGGGC GTTTATGCAA TGAGCCTTTG GATATGTACA GTTACTTGCA CAACCAAGGG 480
 ATTGGTGTTC CACTTGCTCA GTTCTATATC TCATGGGCAG AAGAATATGA AGCTAGAGAA 540
 AACTTTAGGA AAGCAGATGC GATATTTTCA GAAGGGATTC AACAGAAGGC TGAACCACTA 600
 GAAAGACTAC AGTCCCAGCA CCGACAATTC CAAGCTCGAG TGTCTCGGCA AACTCTGTTC 660
 GCACCTTGAGA AAGAAGAAGA GGAGGAAAGT TTTGAGTCTT CTGTACCACA ACGAAGCACA 720
 CTAGCTGAAC TAAAGAGCAA AGGGAAAAAG ACAGCAAGAG CTCCAATCAT CCGTGTAGGA 780
 GGTGCTCTCA AGGCTCCAAG CCAGAACAGA GGACTCCAAA ATCCATTTCC TCAACAGATG 840
 CAAAATAATA GTAGAATTAC TGTTTTGTAT GAAAATGCTG ATGAGGCTTC TACAGCAGAG 900
 TTGTCTAAGC CTACAGTCCA GCCATGGATA GCACCCCCCA TGCCAGGGC CAAAGAGAAT 960
 GAGCTGCAAG CAGGCCCTTG GAACACAGGC AGGTCTCTGG AACACAGGGC TCGTGGCAAT 1020
 ACAGCTTCAC TGATAGCTGT ACCCGCTGTG CTTCCCAAGT TCACTCCATA TGTGGAAGAG 1080
 ACTGCACAAC AGGCAGTTAT GACACCATGT AAAATTGAAC CTAGTATAAA CCACATCCTA 1140
 AGCACCAGAA AGCCTGGAAA GGAAGAAGGA GATCCTCTAC AAAGGGTTCA GAGCCATCAG 1200
 CAAGCGTCTG AGGAGAAGAA AGAGAAGATG ATGTATTGTA AGGAGAAGAT TTAGCAGGA 1260
 GTAGGGGAAT TCTCCTTTGA AGAAATTCGG GCTGAAGTTT TCCGGAAGAA ATTAAGAGAG 1320
 TAAAGGGAAG CCGAGCTATT GACCAAGTGA GAGAAGAGAG CAGAATGCA GAAACAGATT 1380
 GAAGAGATGG AGAAGAGCTT AAAAGAAATC CAAACTACTC AGCAAGAAAG AACAGGTGAT 1440
 CAGCAAGAAG AGACGATGCC TCAAAAGGAG ACAACTAAAC TGCAATTGTC TTCCGAGTCT 1500
 CAGAAAATAC TTGCGGAGAA CATTTGGCAG GAACAACCTC ATTCTAAAGG TCCCAAGTGA 1560
 GAAACTTCAC TTTTCTGATG GTTTCTTCTT TCAGAAAAGA AGAATAAAG TCCTCTGCA 1620
 CCTTTCTCCA TTTTCTGATG GTTTCTTCTT TCAGAAAAGA AGAATAAAG TCCTCTGCA 1680
 GATCCCCCAG GAGTTTATAG TCAACGAAGA CCCCTTGCAG TTCTCAAAAC CTCAGAAAGC 1740
 ATCACTTCAA ATGAAGATGT GTCTCCAGAT GTTTGTGATG AATTTACAGG AATTGAACCC 1800
 TTGAGCGAGG ATGCCATTAT CACAGGCTTC AGAAATGTAA CAATTGTGTC TAACCCAGAA 1860
 GACACTTTGT GACTTTGCCAG AGCAGCTCGT TTTGTATCCA CTCCTTTTCA TGAGATAATG 1920
 TCCTTTGAAG ATCTCGCTTC TGATCCTGAG AGACTGTTAC CGGAAGAAGA TCTAGATGTA 1980
 AAGACCTCTG AGGACAGCA GACAGCTTGT GGCATCTACT ACAGTCAGAC TCTCAGCATC 2040
 AAGAGCTGTA GCGCAATTAT TGAAGACAGT CGTGAAGCCA CACACTCCTC TGGCTTCTCT 2100
 GGTTCCTCTG CCTCGGTTGC AAGCACCTCC TCCATCAAAT GTCTTCAAAT TCCTGAGAAA 2160
 CTAGAACTTA CTAAATGAGAC TTCAGAAAAC CCTACTCAGT CACCATGGTG TTCACAGTAT 2220
 CGCAGACAGC TACTGGAAGT TACTACCAGAG TTAAGTGCCCT CTGAGAGATT GTGTATAGAA 2280
 GACAGACCAA TGCTTAAGTT GGAATTTGAG AAGGAAATTG AATTAGGTAA TGAGGATTAC 2340
 TGCAATTAAC GAGATACCT AATATGTGAA GATTACAAGT TATTCTGGGT GGCAGCAAGA 2400
 AACTCTGCAG AATTACAGT AATAAGGTA TCTTCTCAAC CTGTCCCATG GGACTTTTAT 2460
 ATCAACCTCA AGTTAAAGGA ACGTTTAAAT GAAGATTTTG ATCATTTTTC CAGCTGTTAT 2520
 CAATATCAAG ATCGCTGTAT TGTTTGGCAC CAATATATAA ACTGCTTCAC CCTTCAGGAT 2580
 CTTCTCCAAC ACAGTGAATA TATTACCCAT GAAATAACAG TGTGTATTAT TTATAACCTT 2640
 TTGCAATAGT TGGAGATGCT GACAAAAGCA GAAATAGTCC ATGGTGACTT GAGTCCAAAG 2700
 TGTCTGATTC TCAGAAACAG AATCCACGAT CCCTATGATT GTAACAAGAA CAATCAAGCT 2760
 TTGAAGATAG TGGACTTTTC CTACAGTGTG GACCTTAGGG TGCAGCTGGA TGTTTTACC 2820
 CTCAGCGGCT TCGGACTGT ACAGATCCTG GAAGGACAAA AGATCCTGGC TAACTGTTCT 2880
 TCTCCCTACC AGGTGACCT GTTTGGTATA GCAGATTAG CACATTACT ATTGTTCAAG 2940
 GAACACCTAC AGGTCTTCTG GATGGGTCC TTCTGGAAC TTAGCCAAA TATTCTGAG 3000
 CTAAAGATG GTGAATTGTG GAATAAATTC TTTGTGCGGA TTCTGAATGC CAATGATGAG 3060
 GCCACAGTGT CTGTTCTTGG GGAGCTTGCA GCAGAAATGA ATGGGGTTTT TGCACTACA 3120
 TTCCAAAGTC ACCTGAACAA AGCCTTATGG AAGGTAGGGA AGTTAACTAG TCCTGGGGCT 3180
 TTGCTCTTTC AGTGAGCTAG GCAATCAAGT CTCACAGATT GCTGCTCAG AGCAATGGTT 3240
 GTATTGTGGA ACTACTAACC TGTATGTGCT GTAATTTAAT TTAGGACACA TTTAGATGCA 3300
 CTACCATGTC TGTCTACTT TTTGTTACAG GTATATTTTG ACGTCACTGA TATTTTATAT 3360
 ACAGTGATAT ACTTACTCAT GGCCTTGTCT AACTTTTGTG AAGAACTATT TTATCTAATA 3420
 CAGACTCATT ACAAATGGTT ACCTTGTAT TTAACCCATT TGTCTCTACT TTTCCCTGTA 3480
 CTTTCCCAT TTGTAATTTG TAAATGTTC TCTTATGATC ACCATGTATT TTGTAATAA 3540
 TAAATAGTA TCTGTTAAAA AAAAAA AAAA AAAA AAAA AAAA AAAA AAAA AAAA AAAA

Seq ID NO: 261 Protein sequence:
 Protein Accession #: NP_001202

1 11 21 31 41 51
 MAAVKKEGGA LSEAMSLGEG EWELSKENVO PLRQGRIMST LQALAQESSA CNNTLOQQR 60
 APEYEIRPYT GNDPLDVWDR YISWTEQNYF QGGKESNMST LLERAVEALQ GEKRYYS DPR 120
 FLNLWLKLR LCNPLDMYS YLHNQIGIV LAQFYISWAE EYEARENFRK ADAIFQEGIO 180
 QKAEPFLERLQ SQHRQPQARV SRQTLLELEK EEEEEVFESS VPQRSTLAL KSKGKKTARA 240
 PIIRVGALK APSQNRGLQN PFPQMQNNS RITVFDENAD EASTAELSKP TVQPWIAPP 300
 PRAKENELQA GPWNTGRSLE HRPRGNTASL IAVPAVLPSF TPYVEETAQQ PVMTPCKIEP 360
 SINHLSTRK PGKEEGDPLQ RVQSHQQAEE EKKEKMYCK EKIYAGVGEF SFEEIRAEVF 420
 RKKLKEQREA ELLTSAEKRA EMQKQIEEMB KKLKEIQTQ QERTGDQEE TMPTKETTCL 480
 QIASSEKQIP GMTLSSSVQC VNCCARETSL AENINQEQPH SKGPSVPFPI FDEPLLSEKK 540
 NKSPPADPPR VLAQRRLPLV LKTSSESITN EDVSPDVCE FTGIEPLSED AIITGFRNVT 600
 ICFNPEDTCD FARAARFVST PFHEIMSLKD LPSDPERLLP EEDLDVKTSE DQQTACGTIY 660
 SQTLSIKKLS PIIEDSREAT HSGGFSGSSA SVASTSSIKC LQIEKLELT NETSENPTQS 720
 FWCSQYRRQL LKSLPELSAS AELCIEDREP PKLEIEKEIE LGNEDYCIKR EYLICEDYKL 780
 FWVAPRNSAE LTVIKVSSQP VFWDFYINLK LKERLNEFD HFCSCYQYQD GCIVWHQYIN 840
 CFTLQDLQH SEYITHEITV LIIYNLLTIV EMLHKAIEVH GDLSPRLCIL RNRHDPYDC 900
 NKNQALQIV DPFYSVDLRV GLDVFTLSGF RTVQILEGQK ILANCSPPYQ VDLFGIADLA 960
 HLLLFKEHLQ VFWDGSEWKL SQNISLKDGL ELWNKFPVRI LNADEATVS VLGELAAEMN 1020
 GVFDTPQSH LNKALWKVVK LTPGALLFQ

Seq ID NO: 262 DNA sequence
 Nucleic Acid Accession #: NM_003784
 Coding sequence: 365..1507

1 11 21 31 41 51

5
10
15
20
25
30
35
40

GTCTACTTAT	CAATAAGCAG	CTGCCTGTGC	AGAGTGCAGG	CTGCACCTTT	GGACAGCCTT	60
TAAAACTGAA	TTCTCAGAAT	TTTAGAACAA	ATTTTGTGCT	AGAAATGCTG	ACTTTGGTTC	120
ATTAGGTAGT	GGTAAACACG	GCTCCCTTCG	AAGCTCTCCT	TCATCACCTT	CCTAAGTGCA	180
TGTACAGGGA	AGCTCTCCTT	CATCACCTTC	CTAAGTGCAT	GGGGGAAAT	ACCTAGGGCT	240
CAACAGTCTT	GAGAAGTGTG	GAAACATTTT	CTTTGTGAGT	GAGAACAGAT	CACCTAGAGA	300
AAGGAAACCA	GATTCCCATC	ACTGCTTCTG	GGTATCAGAT	GCTAGCGCTG	CACTCCATTT	360
TGCAATGGCC	TCCTTGCTG	CAGCAAATGC	AGAGTTTTCG	TTCAACCTGT	TCAGAGAGAT	420
GGATGACAA	CAAGGAAATG	GAAATGTGTT	CTTTTCTCTT	CTGAGCCTCT	TCGCTGCCTT	480
GGCCCTGGTC	CGCTTGGGCG	CTCAAGATGA	CTCCCTCTCT	CAGATTGATA	AGTTGCTTCA	540
TGTTAACACT	GCCTCAGGAT	ATGGAACTC	TTCTAATAGT	CAGTCAGGGC	TCCAGTCTCA	600
ACTGAAAAGA	GTTTTTCTG	ATATAAATGC	ATCCACAAG	GATTATGATC	TCAGCATTGT	660
GAATGGGCTT	TTTGCTGAAA	AAGTGTATGG	CTTTCATAAG	GACTACATTG	AGTGTGCCGA	720
AAAATTATAC	GATGCCAAAAG	TGGAGCGAGT	TGACTTTACG	AATCATTTAG	AAGACACTAG	780
ACGTAATATT	ATAAAGTGGG	TTGAAAATGA	AACACATGGC	AAAATCAAGA	ACGTGATTGG	840
TGAAGGTGGC	ATAAGCTCAT	CTGCTGTAAT	GGTGTGGTGG	AATGCTGTGT	ACTTCAAAGG	900
CAAGTGGCAA	TCAGCCTTCA	CCAAGAGCGA	AACCATAAAT	TGCCATTTC	AATCTCCCAA	960
GTGCTCTGGG	AAGGCAGTCG	CCATGATGCA	TCAGGAACGG	AAGTTCAATT	TGCTGTGTAT	1020
TGAGGACCCA	TCAATGAAGA	TTCTTGAGCT	CAGATACAA	GGTGGCATAA	ACATGTACGT	1080
TCTGTGCTCT	GAGAAATGACC	TCTCTGAAAT	TGAAAACAAA	CTGACCTTTC	AGAATCTAAT	1140
GGAAATGGAC	AATCCAAGGC	GAATGACCTC	TAAGTATGTT	GAGGTATTTT	TTCTCAGTTT	1200
CAAGATAGAG	AAGAATTATG	AAATGAAACA	ATATTGAGA	GCCTAGGGC	TGAAAGATAT	1260
CTTTGATGAA	TCCAAAGCAG	ATCTCTCTGG	GATTGCTTCG	GGGGGTCGTC	TGTATATATC	1320
AAGGATGATG	GACAAAATCTT	ACATAGAGGT	CACGTAGGAG	GGCACCGAGG	CTACTGCTGC	1380
CACAGGAAGT	TAATTTGTAG	AAAAGCAACT	CCCTCAGTCC	ACGCTGTTTA	GAGCTGACCA	1440
CCCATTCCTA	TTTTTTATCA	GGAAGGATGA	CATCATCTTA	TTCAAGTGGA	AAGTTTCTTG	1500
CCCTTGAAAA	TCCAAATGGT	TTCTGTATTA	GCAGTCCCCA	CAACATCAAA	GRACCACCAC	1560
AAGTCAATAG	ATYTGRGTTT	AATTGGAAAA	ATGTGGTGT	TCCTTTGAGT	TTATTTCTTC	1620
CTAAGCATGG	TCAGCAGATG	ACACTGGTGA	CTTGACCTTT	CCTAGACACC	TGGTTGATTG	1680
TCCTGATCCC	TGCTCTTAGC	ATTCTACCAC	CATGTGTCTC	ACCCATTCTT	AATTTTCATTG	1740
TCCTTTCTTC	CACGCTCATT	TCTATCATT	TCCCCCATGA	CCCGTCTGGA	AATTATGGAG	1800
RGTGCTCAAC	TGGTAAGGAG	AACGTAGAAG	TAGCCCTAGG	GATCCTTTTT	GAAACTCTAC	1860
AGTTATCGCA	GATATTCTAG	CTTCATTGTA	AGCAATCTAG	GAAATAAGCC	CTGCTGCTTT	1920
CTAGAAATAA	GTGTGAAGGA	TAAATTTTCT	TGTTTGACCT	ATGAAAGATT	TAGAGTTTAC	1980
CTTCATATGT	TTGATTTTAA	ATCAGTGTAT	AATCTAGATG	GTAAGAAATG	TGAAATTTGGG	2040
ATTAGGGACA	NTTCAATAAT	GCTTTCAATT	GACAAATTTT	GGCCTTTCTT	GGCCTTTCTT	2100
TGATAAGACA	ATATGTACAT	GTTTTTTCAT	ATATTAAAGA	TCTTTTAACT	GTTGGCAGTT	2160
GTTATCTACA	GAATCATATT	TCATATGCTG	TGTAGTTTAT	AAGTTTTTCC	TCTATTTATC	2220
AGAAATAAGA	AATACAACAT	ACCTGTAA				

Seq ID NO: 263 Protein sequence:
Protein Accession #: NP_003775

45
50
55

1	11	21	31	41	51	
MASLAAANAE	FCFNLFREMD	DNQNGNVFF	SSLSLFAALA	LVRLGAQDD	LSQIDKLLHV	60
NTASGYGNSS	NSQSQLSQL	KRVFSDINAS	HKOYDLSIVN	GLFAEKVYGF	HKDYIECAEK	120
LYDAKVERVD	FTNHLEDTRR	NINKWVENET	HGKIKNVIGE	GGISSAVMV	LVNAVYFKGK	180
WQSAFTKSET	INCHFKSPKC	SGKAVAMMHQ	ERKFNLSVIE	DPSMKILELR	YNGGINMYVL	240
LPENDLSEIE	NKLTFFQNLK	WTNPRRMTSK	VVEVFPPQFK	IEKNYEMKQY	LRALGLKIDF	300
DESKADLSGI	ASGRLYISR	MMHKSIVIEV	EEGTATAAT	GSNIVEKQLP	QSTLFRADHP	360
FLFVIRKDDI	ILPSGKVSCP					

Seq ID NO: 264 DNA sequence
Nucleic Acid Accession #: AB052906
Coding sequence: 74-814

60
65
70
75
80
85

1	11	21	31	41	51	
AAAACCTTGA	GGTGATTCAT	CTTCCAGGCT	CTCCTTCCAT	CAAGTCTCTC	CTCCCTAGCG	60
CTCTGGGTCC	TTAATGGCAG	CAGCCGCCGC	TACCAAGATC	CTTCTGTGCC	TCCCGCTTCT	120
GCTCCTGCTG	TCCGGCTGGT	CCCGGCTGG	GCGAGCCGAC	CCTCACTCTC	TTTGCTATGA	180
CATCACCGTC	ATCCCTAAGT	TCAGACCTGG	ACCACGGTGG	TGTGCGGTTC	AAGGCCAGGT	240
GGATGAAAG	ACTTTTCTTC	ACTATGACTG	TGGCAACAAG	ACAGTCAAC	CTGTCACTCC	300
CCTGGGGAAG	AACTAAATG	TCACAACGGC	CTGGAAGCA	CAGAACCAG	TACTGAGAGA	360
GGTGGTGGAC	ATACTTACAG	AGCAACTGCG	TGACATTGAG	CTGGAGAATT	ACACACCCAA	420
GGAACCCCTC	ACCCTGCAGG	CCAGGATGTC	TTGTGAGCAG	AAAGCTGAAG	GACACAGCAG	480
TGGATCTTGG	CAGTTCAGTT	TCGATGGGCA	GATCTTCTCT	CTCTTTGACT	CAGAGAAGAG	540
AATGTGGACA	ACGTTTCATC	CTGGAGCCAG	AAAGATGAAA	GAAAAGTGGG	AGAATGACAA	600
GGTTGTGGCC	ATGTCCTTCC	ATTACTTCTC	AATGGGAGAC	TGTATAGGAT	GGCTTGAGGA	660
CTTCTTGATG	GGCATGGACA	GCACCCCTGA	GCCAAGTGCA	GGAGCACCAC	TGCCCATGTC	720
CTCAGGCACA	ACCAACTCA	GGGCCACAGC	CACCACCTTC	ATCCTTTGCT	GCCTCCTCAT	780
CATCCTCCCC	TGCTTTCATC	TCCTTGGCAT	CTGAGGAGAG	TCCTTTAGAG	TGACAGGTTA	840
AAGCTGATAC	CAAAAGGCTC	CTGTGAGCAC	GGTCTTGATC	AAACTCGCCC	TTCTGTCTGG	900
CCAGCTGCCC	ACGACCTACG	GTGTATGTCC	AGTGGCCTCC	AGCAGATCAT	GATGACATCA	960
TGGACCAAT	AGCTCATTC	CTGCCCTGAT	TCCTTTTGCC	AACAATTTTA	CCAGCAGTTA	1020
TACCTAACAT	ATTATGCAAT	TTTCTCTTGG	TGCTACCTGA	TGGAATTCCT	GCACCTAAAG	1080
TTCTGGCTGA	CTAACAAAGA	TATATCATTT	TCTTTCTTCT	CTTTTGTGTT	GGAAAATCAA	1140
GTACTTCTTT	GAATGATGAT	CTCTTTCTTG	CAAATGATAT	TGTCAGTAAA	ATAATCACGT	1200
TAGACTTCAG	ACCTCTGGGG	ATTCTTTCCG	TGTCCTGAAA	GAGAATTTT	AAATTATTTA	1260
ATAAGAAAAA	ATTATATATTA	ATGATTGTTT	CCTTTAGTAA	TTTATTGTTC	TGTACTGATA	1320
TTTAAATAAA	GAGTTCTATT	TCCAAAAAAA	AAAAAAA			

Seq ID NO: 265 Protein sequence:
Protein Accession #: BAB61048.1

1 11 21 31 41 51
 5 | MAAAAATKIL LCLPLLLLLS GWSRAGRADP HSLCYDITVI PKFRPGPRWC AVQGGVDEKT 60
 | FLHYDCGNKT VTPVSPGLKK LNVTTAWKAQ NPVLREVVDI LTEQLRDIQL ENYTPKEPLT 120
 | LQARMSCEBQK AEGHSSGSQW FSPDGQIFLL FDSEKRMWTT VHPGARKMKE KWENDKVVM 180
 | SFHYFSMGDC IGWLEDFLMG MDSTLEPSAG APLAMSSGTT QLRATATTLL LCCLLIILPC 240
 | FILPGI

Seq ID NO: 266 DNA sequence
 Nucleic Acid Accession #: XM_084853.1
 Coding sequence: 127-444

1 11 21 31 41 51
 15 | ATTGATGATA TATTTAACGA AATCAAATTT GGTGAATATG TGGACACTGG AAAGCTAATC 60
 | GACAAGATCA ACTTACCAGA TTCTCTAAAA GTGTACCTTA ACCACAAGCC ACCTTTTGGT 120
 | AACACCATGA GTGGCATCCA CAAGAGCTTT GAGGTGCTCG GTTATACCAA CTCCAAGGG 180
 | AAAAAGGCCA TTGGAAGAGA GGACTTCTCG AGACTGCTCG TTTACTAAAG TGAGCATATG 240
 20 | ACGGAGGAGG AGATGTTGGA TTGCTTTGCT TCACTGTTTG GCCTGAATCC CGAGGGATGG 300
 | AAATCCGAGC CTGCAACCTG CTCCGTCAAA GGTTCAAGAA TTGCTCTGA AGAAGAACTT 360
 | CCAGACGAAA TCACTGCAGA AATATTGCGG ACTGAAATTC TTGGCTTAAC CATTTCAGAA 420
 | GATTCCGGCC AGGATGGTCA GTGAAGTTAC CAGGAATGTT TAAAGCACA AGGACTTTGG 480
 | GTGTGTGTGC ATGCACATGT GTGTGTTTTC CATGAGGCAC TGCTTTTAT GCATTTCCCT 540
 25 | CCCCCTCTC ATCTTTAGAA CATTTAGACA TTAAAGCAAG TTTCTGGTGA GCAATG

Seq ID NO: 267 Protein sequence:
 Protein Accession #: XP_084853.1

1 11 21 31 41 51
 30 | MSGIHKSEFV LGYTNSKGGK AIRREDFLRL LVTKGEHMT EEMLDCAFSL FGLNPEGWKS 60
 | EPATCSVKGS EICLEEELPD EITAEIPATE ILGLTISED GQDQG

Seq ID NO: 268 DNA sequence
 Nucleic Acid Accession #: NM_001898
 Coding sequence: 57-482

1 11 21 31 41 51
 40 | GGCTCTCACC CTCCTCTCCT GCAGCTCCAG CTTTGTGCTC TGCTCTGAG GAGACCATGG 60
 | CCCAGTATCT GAGTACCCTG CTGCTCCTGC TGGCCACCCT AGCTGTGGCC CTGGCCTGGA 120
 | GCCCCAAGGA GGAGGATAGG ATAATCCCGG GTGGCATCTA TAACGCAGAC CTCAATGATG 180
 45 | AGTGGGTACA GCGTGCCCTT CACTTCGCCA TCAGCGAGTA TAACAAGGCC ACCAAAGATG 240
 | ACTACTACAG ACGTCCGCTG CCGGTACTAA GAGCCAGGCA ACAGACCGTT GGGGGGGTGA 300
 | ATTACTTCTT CGAGCTAGAG GTGGGCGCGA CCATATGTAC CAAGTCCCGA CCCAATCTGG 360
 | ACACCTGTGC CTTCCATGAA CAGCCAGAAC TGCAGAAGAA ACAGTGTGTC TCTTTCGAGA 420
 | TCTACGAAGT TCCTTGGGAG AACAGAAGGT CCCTGGTGAA ATCCAGTGT CAAGAATCCT 480
 50 | AGGGATCTGT GCCAGGCCAT TCGCACCAGC CACCACCACC TCCCACCCCT TGTAGTGCTC 540
 | CCACCCCTGG ACTGGTGGCC CCCACCCTGC GGGAGGCCCT CCCATGTGCC TGCGCCAAGA 600
 | GACAGACAGA GAAGGCTGCA GGAGTCTTT GTTGCTCAGC AGGGCGCTCT GCCCTCCCTC 660
 | CTTCTCTCTT GCTTCTAATA GCCCTGGTAC ATGTATACACA CCCCCCACC TCCTGCAATT 720
 | AAACAGTAGC ATCGCC

Seq ID NO: 269 Protein sequence:
 Protein Accession #: NP_001889.1

1 11 21 31 41 51
 60 | MAQYLSTLLL LLATLAVALA WSPKEEDRII FGGIYNADLN DEWVQRALHF AISEYNKATK 60
 | DDYRRPLRV LRARQQTVGG VNYFFDVEVG RTICTKSQPN LDTCAFHEQ ELQKKQLCSF 120
 | EIVEVPWENR RSLVKSRQSS S

Seq ID NO: 270 DNA sequence
 Nucleic Acid Accession #: XM_093210
 Coding sequence: 13-1854

1 11 21 31 41 51
 70 | ATGGCAAGCG CCGGAATCTC CTCAGCTGCC GTTTCACAAA AGAGGTACCA GGTCCGCACC 60
 | AAACGAGCAC ACAAGCAGCA CCAGGAGCTG CAGAAGAAGG AGGCGGCAGC GATGGACCAG 120
 | GGCAGAGGGA ATGGGGAGGG GGCATCTTAC CCCATATCTG AGGTGCGACT GCGGGACGTA 180
 | GAGCGGACTG GGCCTTTCCC GTTGGCGCGT GGCCTCAATC AGGACTTCTT GCCCACGTGC 240
 75 | GCCTTCAAAA CGGTAAAGAG TGCAACTGAA CGTGTGAGAC ATGGTGCAGA TAGGCTGAGA 300
 | GGCGGCGGGA GAGATGCCCA TGAACCTAAG TACCCGGACA CGCCCTCCAC TTCTACCACC 360
 | ACGAGTAACA CCGCCCCCAC GGGACCGCTC TCGAGGTCCC CCAAGCCCAAG GACGCAAGGA 420
 | GGAACGCCCC GGGCGCGCGC CAGCAGCGGC GGGCACCAGC CCAATGGCCA CGGAACCTAG 480
 | CACTGGCAGT CCGGCTCTCT CACACCGCAG CGGTGCAGTG TGGCCGACGG AGCCTCCCGG 540
 80 | GCGGAGGACC CAGCTAGGCC GTCAACCCCG TTGCTCCCA GGAAGGGGG ACCAGGCAAA 600
 | CTGCCCAAGG CCCCGAGCCC AGGCTCCCTG GCGGAGGCCT CCGCTGGTCC CGCCAGATC 660
 | ATGGCGGCCA CCAGGCTCCC GAGCCATGGC TTCTGTCTCC GGAACGGCCC GCGCTCCTGG 720
 | CTGTCCAGCT AG

Seq ID NO: 271 Protein sequence:
 Protein Accession #: XP_093210

1 11 21 31 41 51

MLRHGEQKRRK RARKKWDFLP TCAFKTVRAA TERVRHGADR LRGGGRDAHE LKYPDTPSTS 60
 TTTSTNTAPTG PLSRSPKPRP QGGTPRRRPA AAGTRANGHG TQHWQSALLT PQACSVADGA 120
 SRAEDPARPS PRLLPREGAP GKLPKAPSPG SLAEASAGLL AHVRLQNADA QRVSSISQALP 180
 PNSSVGRKEE RFGAGQQRRA PAFMATELST GSRPSSHRRR AVWPEPPGP RTQLEPSPRL 240
 LPREGAPGKL FKAPSPGSLA EASAGPAQIM AATRLPSRGP LSGNGPASWL SS

Seq ID NO: 272 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1..732

1 11 21 31 41 51
 GGATACTGTG TCACTCAAAG TAATGGGAGG GAGAGAGAAC AGGGAGGGTA GGGATGCTTT 60
 TGAAAAAGCT TTTTTCCTCA CTTTAACTT GCTTTAGCGT TAAGAGTACT TACCAGCTAA 120
 TAATGTGGAG GAAATTATTC TTCTCATTC GAGATTACAG AATATATCTA TTCATCTTGA 180
 ATACCCACTT GAAGCCTCTG TAGAAATGTC TCGTCCTCCG GTTGATTTTC TAAACCTTAC 240
 ATGATTTTGT CTGTGTTCTG CAGTGAGAAA TTACATCCAT AGCAAAGACA AAAGTCTTTT 300
 TAAATTATTT TTATTTATCT TCCATATAGT TCTTACAATT TCTAAAAAAT TAACACTCAT 360
 TTAGTATCAC AATTATATGG AGAGGGTTTT TTGTATTTT AAGCATATGT GGCTTATATA 420
 AAAATTGCAG AAGTCATAGG ACTGTCATGT ATTGCAGCTC TGAGAACCAA TGCCCTGAAC 480
 TTAAGCC

Seq ID NO: 273 Protein sequence:
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 MGGRENREGR DAFKKAFFPT FNLL

Seq ID NO: 274 DNA sequence
 Nucleic Acid Accession #: NM_003976.2
 Coding sequence: 299-961

1 11 21 31 41 51
 CTCTGAGCTT CTCTGAGCCT TGTTTGCTCA TCTGGAAAAA GGGGATTAAA CCATTACCT 60
 CATGGAGTTG TGAAGAATA GCTGCAAAGC ACCTAACACA TAGTAAGGTT CCCAGTGCAG 120
 CTACTTCTGC TGGTTGAGT CTAGCTGTGT AGGCCCCCTG TTCCTCACCT GGAGAAACTG 180
 GGGTGGCAGG CCGGTCCCCC ACAAAGATA ACTCATCTCT TAATTTGCAA GCTGCCTCAA 240
 CAGGAGGCTG GGGGAACAGC TCAACAATGG CTGATGGGCG CTCTCTGGTG TGATAGAGAT 300
 GGAACCTTGA CTGTGAGGCC TCTCCACGCT GTCCCACTGC CCTTGGCCTA GCGCGCAGCC 360
 TGCCCTGTGG CCCACCTTGG CCGCTCTGGC TCTGCTGAGC AGCGTCGCAG AGGCTCCTCT 420
 GGGCTCCGCG CCCCGCAGCC CTGCCCCCGG CGAAGGCCCC CCGCTGTGCC TGGCGTCCCC 480
 CGCCGGCCAC CTGCGGGGGG GACGACGCG CCGCTGGTGC AGTGGAAGAG CCGCGCGGCC 540
 GCGCGCGCAG CCTTCTCGGC CCGCGCCCCC GCGCGCTGCA CCCCCTCTCT CTCTTCCCCG 600
 CCGGGGCGCG CCGCGCGCGG CTGGGGGCCG GGGCAGCGCG GCTCGGGCAG CCGGGGCGCG 660
 GGGCTGCCGC CTGCGCTCGC AGTGTGTGCC GGTGCGCGCG CTCGCGCTGG GCCACGCTC 720
 CGACGAGCTG GTGCGTTTCC GCTTCTGCGC CGGCTCTGCG CGCGCGCGCG GCTCTCCACA 780
 CGACCTCAGC CTGGCCAGCC TACTGGGCGC CGGGGCCCTG CGACCGCCCC CGGGCTCCCG 840
 GCCCGTCAAG CAGCCCTGCT GCCGACCCAC GCGCTACGAA CGGCTCTCCT TCATGGACGT 900
 CAACAGCAC CTGGAAGACG TGGACCGCCT CTCCGCCACC GCCTGCGGCT GCCTGGGCTG 960
 AGGGCTCGCT CAGGGGCTTT GCAGACTGGA CCTTACCCGG TGGCTCTTCC TGCTGGGAC 1020
 CCTCCCGCAG AGTCCCACTA GCCAGCGGCC TCAGCCAGGG ACGAAGGCCCT CAAAGCTGAG 1080
 AGGCCCTTAC CGGTGGGTGA TGGATATCAT CCCCAGACAG GTGAAGGGAC AACTGACTAG 1140
 CAGCCCCAGA GCCCTCACCC TGCGGATCCC AGCCTAAAG ACACCAAGAGA CCTCAGCTAT 1200
 GGAGCCCTTC GCGCTCCAG CTGACAGACT CTGGCACTGG CCAGGCCCTG AACCTGGGAG 1260
 CCCTCCTCTG ATGAACACTA CAGTGGCTGA GGCATCAGCC CCGCCCCAGG CCCTGTAGGG 1320
 ACAGCATTTG AAGGACACAT ATTGCAGTTG CTGTGTTGAA AGTGCCCTGT CTGGAACCTG 1380
 CCTGTACTCA CTCATGGGAG CTGGCCCC

Seq ID NO: 275 Protein sequence:
 Protein Accession #: NP_003967.1

1 11 21 31 41 51
 MELGLGGLST LSHCPWPRRQ PALWPTLAAL ALLSSVAEAS LGSAPRSPAP REGPPPVLAS 60
 PAGHLPGGRT ARWCGRARR PFPQPSRPAP PFPAPPSALP RGGRAARAGG PGSRARAGA 120
 RGCRLRSQLV PVRALGLGHR SDELVRFRFC SGSCRRARSP HDLSLASLLG AGALRPFPFS 180
 RVPVQPCCRP TRYEAVSFMD VNSTWRTVDR LSATACGCLG

Seq ID NO: 276 DNA sequence
 Nucleic Acid Accession #: NM_057091.1
 Coding sequence: 783-1445

1 11 21 31 41 51
 ACTGGCCGCT GAGAGAAGAA TCGGGTGGAG CAGAGAGCAG CTGCTGCAGG GCAGACAGCC 60
 GGACCCCAAA ATCTGCACGT ACCAGCAGTC AGCCGCCCCA CGCAGGGACC GGCTTACCCC 120
 TCGCTCCCGG CCTCACTCA CTTTCTCCCG CCTCGGCCG GGCTCCCGAG CTCTCTACTT 180
 CGCGTGTCTA CAAACTCAAC TCCTGGTTTC CGTGCTCTC CACCGCTCGA GTTCTCTACT 240
 CTCCATATCC GAGGGGCCCC TCCAGCATC TACCCCTCTG CCAACCTCGG GGGACCTAGC 300
 CAAGCTAGGG GGAAGTGGAT CCGACGGGTG GAGCAGCCAG GTGAGCCCCG AAAGGTGGGG 360
 CGGGGCGGGG GCGCTCCAG CCCACCCCGG GGATCTGGTG ACGCTGGGGG TGGAAATTTGA 420
 CACCGGACGG CTGCGGGCGG GGCAGGAGG CTGCTGAGGG ATGGAGTTGG GCCCGGCCCC 480
 CAGACAAGGC CCGGGGCGTC CGCCAGCAGC AGGTCCCTCG GCGCCAGACC CTCGCTGCCA 540

CCGGGGCTG GAGCCCCACA CCGGAGGCTG CAGACTGGCT GCCAAGGCCA CACTTTTGGC 600
 TAAAAAGAGC ACTGCCAGGT GTACAGTCCT GGGCATGCGC TGTTTGAGCT TCGGGGGAGA 660
 GCGCCAGCACT GGTCCCCGGA AAGGTGCCTA GAAGAACAAG GTGCAGGACC CCGTCTGCC 720
 TCAACAGGAG GGTGGGGGAA CAGCTCAACA ATGGCTGATG GGGCTCCTG GTGTTGATAG 780
 AGATGGAAT TGGAATTTGA GGCCTCTCCA CGCTGTCCCA CTGCCCTGG CCTAGGCGGC 840
 AGCTTGCCCT GTGGCCCAAC CTGGCCGCTC TGGCTCTGCT GAGCAGCGTC GCAGAGGCCT 900
 CCTTGGGCTC CGCGCCCCGC AGCCCTGCCC CCGCGGAAGG CCCCCCGCT GTCTGGCGT 960
 CCCCCCGCGG CCACCTGCGG GGGGGACGCA CGGCCGCTG GTGCAGTGA AGAGCCCGGC 1020
 GGCGCCGCGC CGAGCCTTCT CGGCCGCGC CCGCCGCGC TGCAACCCCA TCTGCTCTC 1080
 CCGCGGGGGG CCGCGCGGCG CGGGCTGGGG CCGCGGGCAG CCGCGCTCGG GCAGCGGGGG 1140
 CGCGGGGCTG CGCCTGCGC TCGCAGCTGG TGGCGGTGCG CGCGCTCGGC CTGGGCCACC 1200
 GCTCOGACGA GCTGGTGCCT TTCCGCTTCT GCAGCGGCTC CTGCGCGC GCAGCTCTC 1260
 CACACGACCT CAGCCTGCGC AGCCTACTGG GCGCGGGGGC CCTGCGACCG CCCCCGGGCT 1320
 CCGCGCCGCT CAGCCAGCCC TGCTGCCGAC CCACGCGCTA CGAAGCGGTC TCCTTCATGG 1380
 AGCTCAACAG CACTTGAGGA ACCGTGGACC GCCTCTCCGC CACCGCTGCG GGCTGCCTGG 1440
 GCTGAGGCTC CGTCCAGGG CTTTGACAGC TGGACCTTA CCGTGGCTC TTCTGCTCTG 1500
 GGACCCCTCC GCAGAGTCCC ACTAGCCAGC GGCCTCAGCC AGGACGAAG GCCTCAAAGC 1560
 TGAGAGGCCC CTACCGGTGG GTGATGGATA TCATCCCGA ACAGGTGAAG GGACAACTGA 1620
 CTAGCAGCCC CAGAGCCCTC ACCCTGCCGA TCCAGCCCTA AAGACACCA GAGACCTCAG 1680
 CTATGAGGCC CTTGGAGCCC ACTTCTCACA GACTCTGGCA CTGGCCAGGC CTCGAACCTG 1740
 GGACCCCTCC TCTGATGAC ACTACAGTGG CTGAGGCATC AGCCCCCGC CAGGCCCTGT 1800
 AGGGACAGCA TTTGAAGGAC ACATATTGCA GTTGCTTGGT TGAAGTGCC TGTGCTGGAA 1860
 CTGGCTGTA CTCATCATG GGAGCTGGCC CC

Seq ID NO: 277 Protein sequence:

Protein Accession #: NP_003967.1

1 11 21 31 41 51
 MELGLGLST LSHCPWPRRQ PALWPTLAAL ALLSSVAEAS LGSAPRSPAP REGPPPVLAS 60
 PAGHLPGGRT ARWCSGRARR PFPQPSRPAP PFPAPPSALP RGGRAARAGG PGSRAARAAGA 120
 RGRRLRSQLV PVRALGLGHR SDELVRFRFC SGSCRRARSP HDLSLASLLG AGALRPFPFGS 180
 RPSVQPCCRP TRYEAVSFMD VNSTWRTVDR LSATACGCLG

Seq ID NO: 278 DNA sequence

Nucleic Acid Accession #: NM_057160.1

Coding sequence: 1-714

1 11 21 31 41 51
 ATGCCCGGCC TGATCTCAGC CCGAGGACAG CCCCTCCTTG AGGTCTCTCC TCCCCAAGCC 60
 CACCTGGGTG CCCTCTTTCT CCCTGAGGCT CCACTTGGTC TCTCCGCGCA GCCTGCCCTG 120
 TGGCCACACC TGGCCGCTCT GGCTCTGCTG AGCAGCGTCG CAGAGGCCCTC CCTGGGCTCC 180
 GCGCCCGCCA GCCCTGCCCC CCGCGAAGGC CCGCCGCTG TCCTGGCGTC CCGCCGCGGC 240
 CACCTGCGGG GGGGACGCAC GGGCCGCTGG TGCACTGGAA GAGCCCGCGG GCCCGCGCGG 300
 CAGCCTTCTC GGGCCGCGCC CCGCCGCGCT GCACCCCAT CTGCTCTTCC CCGCGGGGGG 360
 CGCGCGGGCG GGGCTGGGGG CCGGGGACAG CGCGCTCGGG CAGCGGGGGG GCGGGGCTGC 420
 CGCCTGCGCT CGCAGCTGGT GCGGTGCGC GCGCTCGGCC TGGGCCACCG CTCGACGAG 480
 CTGGTGGGTT TCCGCTTCTG CAGCGGCTCC TGCCGCGCGC CGCGCTCTCC ACACGACCTC 540
 AGCCTGGCCA GCCTACTGGG CGCCGGGGCC CTGCGACCGC CCGCGGGGTC CCGCCCGGTC 600
 AGCCAGCCCT GCTGCCGACC CACGCGCTAC GAAGCGGTCT CCTTCATGGA CGTCAACAGC 660
 ACCTGGAGAA CGTGGACACT CCTCTCCGCC ACCGCTTGGG GCTGCTGGG CTGAGGGCTC 720
 GCTCCAGGGC TTTGACAGCT GGACCCCTAC CGTGGCTCT TCCTGCCTGG GACCCCTCCG 780
 CAGAGTCCCA TAGCCAGGCG GCCTCAGCCA GGGACGAAGG CCTCAAAGCT GAGAGGCCCC 840
 TACCGGTGGG TGATGGATAT CATCCCCGAA CAGGTGAAGG GACAACCTGAC TAGCAGCCCC 900
 AGAGCCCTCA CCCTGCGGAT CCCAGCCTAA AAGACACCAG AGACCTCAGC TATGGAGCCC 960
 TTTGGACCCA CTTCTCACAG ACTCTGGCAC TGGCCAGGCC TCGAACCTGG GACCCCTCCT 1020
 CTGATGAACA CTACAGTGGC TGAGGCATCA GCCCCGCGCC AGGCCCTGTA GGGACAGCAT 1080
 TTGAAGGACA CATATTGCAG TTGCTTGGTT GAAAGTGCTT GTGCTGGAAC TGGCCTGTAT 1140
 TCACTCATGG GAGCTGGCCC C

Seq ID NO: 279 Protein sequence:

Protein Accession #: NP_476501.1

1 11 21 31 41 51
 MPGLISARQ FLLEVLPQA HLGALFLPEA PLGLSAQPAL WPTLAALALL SSVAEASLGS 60
 APRSPAPREG PFPVLASPAH HLPGRRTARW CSGRARRPPP QPSRPAPPPP APPSALPRGG 120
 RAARAGPGS RARAAGARG RLRSQVLPVR ALGLGHRSDS LVRFRFCSSG CRRARSPHDL 180
 SLASLLGAGA LRPPPGSRPV SQPCCRPTRY EAVSFMDVNS TWRTVDRLSA TACGCLG

Seq ID NO: 280 DNA sequence

Nucleic Acid Accession #: NM_057090.1

Coding sequence: 29-715

1 11 21 31 41 51
 CTGATGGGCG CTCCTGGTGT TGATAGAGAT GGAACCTGGA CTTGGAGGCC TCTCCACGCT 60
 GTCCCACTGC CCCTGGCTTA GCGCGCAGGC TCCACTTGGT CTCTCCGCGC AGCCTGCCCT 120
 GTGGCCCAACC CTGGCCGCTC TGGCTCTGCT GAGCAGCGTC GCAGAGGCCCT CCCTGGGCTC 180
 CGCGCCCGCG AGCCCTGCCC CCGCGAAGG CCGCCGCGCT GTCTGGCGT CCGCCGCGG 240
 CCACCTGCGG GGGGACGCA CCGCCGCTG GTGCAGTGA AGAGCCCGCG GCGCGCGGCC 300
 GCAGCCTTCT CGGCCGCGC CCGCCGCGCC TGCAACCCCA TCTGCTCTTC CCGCGGGGGG 360
 CCGCGCGGGG GGGCTGGGG GCGCGGGCAG CGCGCTCGGG GCAGCGGGGG CGCGGGGCTG 420
 CGGCTGCGC TCGCAGCTGG TGGCGGTGCG CGCGCTCGGC CTGGGCCACC GCTCCGACGA 480
 GCTGGTGCCT TTCCGCTTCT GCAGCGGCTC CTGCGCGCGC GCGCGCTCTC CACACGACCT 540
 CAGCCTGGCC AGCCTACTGG GCGCGGGGCG CCTGCGACCG CCGCCGGGCT CCGCGCGGCT 600
 CAGCCAGCCC TGCTGCCGAC CCACGCGCTA CGAAGCGGTC TCCTTCATGG ACCTCAACAG 660

CACCTGGAGA ACCGTGGACC GCCTCTCCGC CACCGCCTGC GGCTGCCTGG GCTGAGGGCT 720
 CGCTCCAGGG CTTTGCAGAC TGGACCCTTA CCGGTGGCTC TTCTGCCTGG GGACCCTCCC 780
 GCAGAGTCCC ACTAGCCAGC GGCTCAGCC AGGGACGAAG GCCTCAAAGC TGAGAGGGCC 840
 CTACCGGTGG GTGATGATA TCATCCCGCA ACAGGTGAAG GGACAACTGA CTAGCAGCCC 900
 CAGAGCCCTC ACCCTGGCGA TCCAGCCTA AAAGACACCA GAGACCTCAG CTATGGAGCC 960
 CTTGGAGCCC ACTTCTCACA GACTCTGGCA CTGGCCAGGC CTCGAAACCTG GGACCCTTCC 1020
 TCTGATGAAC ACTACAGTGG CTGAGGCATC AGCCCCGCC CAGGCCCTGT AGGGACAGCA 1080
 TTTGAAGGAC ACATATTGCA GTTGTCTGGT TGAAGTGCC TGTGCTGGAA CTGGCCTGTA 1140
 CTCATCATG GGAGCTGGCC CC

Seq ID NO: 281 Protein sequence:
 Protein Accession #: NP_476431.1

1 11 21 31 41 51
 MELGLGLST LSHCPWPRRQ APLGLSAQPA LWPTLAALAL LSSVAEASLG SAPRSPAPRE 60
 GPPPVLASPA GHLEGGGTAR WSGRRARRPP PQPSRPAPPP PAPPSALPRG GRAARAGGPG 120
 SRARAAGARG CRLRSQLVFV RALGLGHRSD ELVRFRFCSG SCRARSPPHD LSLASLLGAG 180
 ALRPPPGSRP VSQPCCRPTR YEAVSEMDVN STWRTVDRLS ATACGCLG

Seq ID NO: 282 DNA sequence
 Nucleic Acid Accession #: Eos sequence

1 11 21 31 41 51
 CTACTGCACC TGCCCTCTGT TTCCTTTGGA AATCTCTTAC CTTTCATTAG GGTTCCTTTC 60
 ATAGCAATTT CCTTTGGTTT TTAAGACTTC TACATTGCTT TTTCTTTTAT TATCTGTGCT 120
 CCGTGAACCT TATGAATGCT GCTTAAATAT AATGTCAAAT TATGTTTATG CTGCCTACTC 180
 AGGTAACGTT TTTCTTTGCT CTCATCTTGG TTTCCATATA CTATTTTGGG TTTTGTGTA 240
 GATCTAATCA ATGATCTAGT CAGAAGCTAC TTCACTGGCT AACAGTATC ATGTTCATGT 300
 GCTAAAAATG AACTTGAATC ACGGAAGTAG TGGTTGGTCC AGTTTGAAGG CTCCTATTAG 360
 TATCTTTCAT CTTGGCTGTA ATAATAGCCA TTATTTGTTA TGCCTTTGTT ATGTAGCAGA 420
 CACTCTAAGC GATTTTATGT GTATTATTCA AATTGCTATT ACTGTTCTTT TTATAGTTGA 480
 GAATCTCAGG ATACCTACAT TTATCACTTT TTCAATATAT ATGTATTTCT TATT

Seq ID NO: 283 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 564-1481

1 11 21 31 41 51
 GAGACTTTTA ATCATCTATC CCTTGTGCTT TACGCAGACC CTACAATACA CTAGAGGCTT 60
 CAAAGAGGTC AAAAATTCAC ATGTGTAGAC AAATTAGGTC CCTTAAGATG CCAGGCAAACT 120
 GAAGTGCTAC CAAACACAGC AATGACTGTC CTAAAGTGC GTTCTGGGAT ACACCTGTAA 180
 ACTTGGATCA AGTTCCCTCC CCTCTCCTCA AAATATATCG ACTTGTGCTG AAAGAAATCA 240
 CGACCGATGC TCACAATCTC GACCTCGTAA TTATATAGGG GGTGGTTTGG GTTCTGCGGT 300
 CTTTCCCTGA TTCACTGGCA GGTAAACATAT TTCACTGTACA AAATGAACAG CAACACCAGC 360
 GCAAAACAGG GACAGGCCCT CAAAGTTGTC GGTAGGGAGC CAGGACCCCG CCAAGTGGCGT 420
 GGGGAGACAC CGTACTAAAC AAGCTTGCAA ACAGCAGGCA CCTTCTCTGC ACTGAGGAGG 480
 AAGGGCTGSC TAAAGGAGGC CGGGGCGGAG GAAGCCAAGC TCTGCAGGCC CTGACAAAGT 540
 CCTCCCGGCC TACCAGCGTC GCCATGGCAA CGCGGGGTCT GTGCTGCGCC GGATTGGCCG 600
 GCCTGGCGCG CGCAGGGCGG GCTGGGAAAG CGCGTCCCGC CCGCGGCTCC GCCAGTTTGA 660
 ACTTGGCGGG CAGATGTGCG CGCGCGGGCC GCTGGGGGCC TACTTTTCCC TCTTCTACG 720
 CCGGTTTCTC TGCTGACTGC AGACCCAGGT CTCGGCCCTC CTCGACTCC TGCTCAGTCC 780
 CTATGACGGG CGCACGTGGG CAGGGGCTGG AGGTGGTGGC CTCGCGTCC CCGCGCTGC 840
 CGCTGAGCTG CAGCAATTC ACCAGGTGCG TGTGTCTCTC CCTTGGCCAC CAGAGCTTCC 900
 AGTTTGACGA GGACGACGGT GACGGGGAGG ATGAGGAAGA CGTGGATGAT GAGGAAGAGC 960
 TGGATGAAGA TGCCCATGAT TCAGAGGCCA AAGTGGCGAG CCTGAGAGGA ATGGAGTTAC 1020
 AGGGGTGGCG CAGCACTCAG GTTGAATCAG AAAATAACCA AGAAGAACAG AAACAGGTGC 1080
 GCTTACCGA AAGCCGCTCG ACACCATGGG AGGTGTGTTT TATTGGCAAA GAAAAAGAA 1140
 AACGTGACCG GCTGCAACTG AAAGCTCTAG AGGAATTAAT TCAACAATA GAAAAAGAA 1200
 AAGAAATGGA AGAAGCTGAA AAAAGAAAGA TAATTGCTGA AGAAAAGCAC AAGGAATGGG 1260
 TTCAGAAAAA GAATGAGCAA AAAAGAAAG AAAGAGAACA AAAAATTAAT AAAGAAATGG 1320
 AGGAAAAAGC AGCAAGAGAA CTGGAGAAAG AATACTTGCA AGAAAAGCA AAAGAAAAAT 1380
 ATCAAGATG GTTAAAGAAA AAAATGCTG AAGAATGTGA GAGGAAGAG AAAGAAAAAG 1440
 AAAACAACAG CAAGCTGAAA TACAGGAGAA AAAGGAAATA GCAGAAAAA AGTTTCAAGA 1500
 ATGGTTGGAA AATGCGAAAC ATAAACCTCG TCCAGCTGCA AAGAGCTATG GTTATGCCAA 1560
 TGGAAAACTT ACAGGTTTTT ACAGTGGAAA TTCCTATCCA GAACCGAGCT TTTATAATCC 1620
 AATTCCGTGG AAACCAATTC ATATGCCACC TCCCAAGAA GCTAAGGATC TATCAGGAAG 1680
 GAAGAGTAAA AGACCTGTGA TAAGTCAGCC ACACAAGTCA TCATCTCTGG TAATTCATAA 1740
 AGCCAGGAGC AATCTTTGCC TTGAACTCT GTGCAGAATA CAAAGATAGC GTATGTGGAA 1800
 AATAACATGC TTTTATCTGG AGCTATTTAA TTTAAAAATC AGAAATTTGT TTTTACTGCT 1860
 CAGTCAATAA CTCACACTT AATGTGATTA TTGACAAATA GCAATTTTGG CATTTGTATA 1920
 TGGAGTCTCT AGAGTTGAGG AAGATATTTT CTGGATTTTG GTTTTATAA ACTTTTAAAG 1980
 GTTGATCTTG GCATGTTGTT TTGCAGAATA AGTGGCTGAA TATGTAAGAA TTGTTGTTGT 2040
 ATTTAGCTTG TATTAAGAGT ACACGTGAAT ACCAATAAAA CTACAAATT TTCTTG

Seq ID NO: 284 Protein sequence:
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 MATRGLCPWG LAGLARAGPA GKARPRRGS SLNLAGQMW AGRWGPTFPF SYAGFSADCR 60
 PRSRPSSDSC SVPMTGARGQ GLEVVRSPPF PLPLSCSNST RSLLSPLGHQ SFQFDEDDGD 120
 GEDEEDVDDE EDVDEDAHDS EAKVASLRGM ELQGCSTQV ESENNQSEKQ QVRLPESRLT 180
 PWEVWFQKKE KEEDRLQLK ALEELNQOLE KRKEMEEREK RKI IAEKHK EKVQKQNEKQ 240
 RKEREQKINK EMEKAALKE EKEYLQEKAK EKYQEWLKKK NABECERKKK EKQNSKLKY 300

RRKRR

Seq ID NO: 285 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 1-1746

5

10

15

20

25

30

35

40

45

50

55

60

65

70

75

80

85

1

11

21

31

41

51

60

120

180

240

300

360

420

480

540

600

660

720

780

840

900

960

1020

1080

1140

1200

1260

1320

1380

1440

1500

1560

1620

1680

1740

1800

1860

1920

1980

2040

2100

2160

2220

2280

2340

2400

2460

2520

2580

2640

2700

2760

2820

2880

2940

3000

3060

3120

3180

3240

3300

3360

3420

3480

3540

3600

3660

3720

3780

3840

3900

3960

4020

4080

4140

4200

4260

4320

4380

4440

4500

4560

4620

4680

4740

ATGCCACTGA AGCATTATCT CCTTTTGCTG GTGGGCTGCC AAGCCTGGGG TGCAGGGTTG

GCCTACCATG GCTGCCCTAG CGAGTGTACC TGCTCCAGGG CCTCCCAGGT GGAGTGCACC

GGGGCAGCGA TTGTGGCGGT GCCCACCCTT CTGCCCTGGA ACGCCATGAG CCTGCAGATC

CTCAACACGC ACATCACTGA ACTCAATGAG TCCCGTTCC TCAATATCTC AGCCCTCATC

GCCCTGAGGA TTGAGAAGAA TGAGCTGTCT CGCATCACGC CTGGGGCCTT CCGAAACCTG

GGCTCGCTGC GCTATCTCAG CCTCGCCAAC AACAAAGCTGC AGGTTCCTGCC CATCGGCCTC

TTCCAGGGCC TGGACAGCCT TGAGTCTCTC CTCTGTCCA GTAAACAGCT GTTGCAGATC

CAGCGGGCCC ACTTCTCCCA CTGCAGCAAC CTCAGGAGC TGCAGTTGCA CGGCAACCAC

CTGGAATACA TCCCTGACGG AGCCTTCGAC CACCTGGTAG GACTCACGAA GCTCAATCTG

GGCAAGAATA GCCTCACCCA CATCTCACCC AGGGTCTTCC AGCACCTGGG CAATCTCCAG

GTCTCCGGCG TGATAGAGAA CAGGCTCACG GATATCCCCA TGGGCACCTT TGATGGGCTT

GTAAACCTGC AGGAACCTGG TCTACAGCAG AACCAAGATT GACTGTCTCT CCCTGGTCTC

TTCCACAACA ACCACAACCT CCAGAGACTC TACCTGTCCA ACAACCAT CTCCAGCTG

CCACCCAGCA TCTTCATGCA GCTGCCCCAG CTCACCCGTC TTAATCTCTT TGGGAATTCC

CTGAAGGAGC TCTCTCTGGG GATCTTCGGG CCGATGCCCA ACCTGCGGGA GCTTTGGCTC

TATGACAACC ACATCTCTTC TCTACCCGAC AATGTCTTCA GCAACCTCCG CCAATTGCTG

GTCTGTGATT TTAGCGCGCA TCAGATCAGC TTCTCTCCCT CGGGTGCCCT CAACGGGCTA

ACGAGCTTTC GGGAGCTGCT CCGCACAC AAGCACTGC AGGACCTGGA CGGGAATGTC

TTCCGCATGT TGGCCAACCT GCAGAACATC TCCCTGCAGA ACAATCGCCT CAGACAGCTC

CCAGGGAATA TCTTCGCGCA CGTCAATGGC CTCTAGGCCA TCCAGCTGCA GAACAACCTG

CTGGAGAATC TGCCCTCTCG CATCTTCGAT CACCTGGGGA AACTGTGTGA GCTGCGGCTC

TATGACAATC CCGTGGAGGT TGACTCAGAC ATCTTCTCCG TCCGCAACTG GCTCTGTCTC

AACCAAGCTA GGTAGGGGAC GGACACTGTA CCGTGTGTTT TCAGCCAGC CAATGTCCGA

GGCAGTCCC TCATTATCAT CAATGTCAAC GTTGTGTGTT CAAGCTTCCA TGTCCCTGAG

GTGCTAGATT ACCCAGAAAC ACCATGGTAC CCAGACACAC CCAATTACCC TGACACCACA

TCCTCTCTCT TCACTCATGA GCTAACACAG CCGTGGGAAG ACTACACTGA TCTGACTACC

ATTGAGTCTA CTGATGACCG CAGCGTTTGG GGCATGACCC AGGCCAGAG CGGGCTGGCC

ATTGCCGACG TTGTAATTGG CATGTGCGCC CTGGCTGCTC CCCTGGCTGC CTGCGTCCGC

TGTTGCTGCT GCAAGAAGAG GAGCCAAGCT GTCCGTGATG AGATGAAGGC ACCCAATGAG

TGTTAAAGAG CAGGCTGGA GCAGGGCTGG GGAATGATGG GACTGGAGGA CTTGGGAATT

TCATCTTCTT GCCTCCACCC CTGGGTCCAT GGAGCTTTCC CGTGATTGCT CTTTCTGGCC

TAGATAAAG GTGTGCTTAC CTCTCTCTGA CTGCTCTGAT TCTCCCTAG AGAAGCAGGT

CGTGCGGAC GTCTCTACAA TCAGGAAGAT AGATCCAAC TGGCCATGGCA AAAGCCCTGG

GGATTTCGGA TTCATACCCC TGGGCTTCCT TCGAGAGGGC TCTTCTCTCA AATCCTCCCC

ACCTGTCTCT CAAGAACAGC CTTCCTGCGG CCCAGGCCCC CTCGGGCTCT CTGTAGACTC

AGTTAGTCCA CAGCTGTCTC ACTTCGTGGG AATAGTTCTC CGCTGAGATA GCCCTCTCG

CCTAAGTATT ATGAAGTTG ATTTCCCTTC TTTTGTCTCT CTTGTTGTGT CTATGCTTGG

ACCCAGTATG TCCCTCTTAA TGAAAGTTCT CCCCTTGATT TTCTGCTCCT GAAGGAGGCG

TGAGTTCTCT CCTCAAAGAA GACTTCAAAC CATTTAACCTG GTTTCTTAAG AGCCGTCAAT

CAGCCTGGTT TTGGGGATGC TATGAAAGAG AGAAGGAAAA TCATGCCGCT CAGTTCTCTG

AGACAGAAGA GCCGTCTACA GTGTCTCACT TGTGATTTT ATCTGGAATA GGAAGAAACA

CCCCAGCACA GCAAGCTCAG CCTTTTAGAG AAGGATATTT CCAAACTGCA AACTTTGCTT

TGAAAGTTT TGCACTTTAA GGAATGAAAT CATGTAGAAT TTTGGACTTC TAAAAACAT

AAAATCAGCT TATTAATACG GGATAGAGAA AGAAATCTGG TGCCCTGGGG TCCCTGTGTT

CACCCCTAGA GTTTGTTTAA AAATTTTAA TTGAAGCATG TGAAGTGTAC STGCAGAAAA

GTGGGAACAT GATAGTGTAT GGCTTGGTGG ATTTTCACAA ACTGAACATA CCTGTGTAAT

CAGCATCTAG ACCCAGACCC AGAGCATCAC AAATATCCCC CATCTGGGC TTTTCCGAGA

GGAGATGGGG GCTTCTGAAG ATGGACTTAC CTGGGACCTG CCCCCATGA GCCAGGACGG

TCCCCCACA GTACGCTGTG GCAAGGCCCC CGTGGCCAGG GGTGGAGGAG AATATGTGGG

TGTGGACAGG ATGGGAGACT GTGGCTGAA CAGGAGATT TATTATATCT GGAGACCTG

AGAGACCTG AGACCTGGGG CACCATGGCT GGCCAGGTCA GAAGCATCCT GACTGCAGAG

GTCCGTGACG CCACACCTCT TCCCTGCCA GCAAGTTGTC TGCGGCTCAT CGGAGGCCCC

TCGCTCTGGA GCCTCTATG GAGTGATAT GCCTGTATCT GTTTTAAAT TTCAATCTTC

ACTTAGGGGA AGTGAAATCG CTCAGAGATG AGATCCTTTA ATTGAAAACG AAGTGTAAAG

GAACTAGTGT TCTTTCTAAT GTGGTAAAA TCTCCATCAA CATCACAGTC AGCTGGCAGC

TGAATCTCAG AATCTCACTT ACAGCAGGCG ACACGGGGGT ACACCGATGG GTCACTGGS

GTCTGGGGGG TCCCTGGAGC TCCTCTGCG TGTGGTCTGG TTAGAGATTG AGTTGTTTGC

TCCAGGGTTA TTCTCTCTCT CGAGTCACAG TCACACGAAT ACCTGCGCTT TCTGGCTTTC

CTGCTATACA CATATTACA TGGCGCTCAA GAAGTTAGGC TCATGGCAAC GTGTGCTTT

CTCTGGACCA CTGGCCCACT TTACAGTGAA ATGGAGAATT TCAGTCTCC ACGTCTGCCC

AGGAAGAAG TTCAGCTGAC TCCACGGGGA TCTGGAATC CACGACCAAT CCGATCGGC

TCTTATTAGC TCCCGCTCC ACAAGACACC TGTGCTTGG AAATCCACCA CCAATCCGA

TCGGCTCTTA TTAGCTCCCC GCTCCACAAG ACACCTGTGA TCTGGAATC TACCACCAAT

CCGATCGGC TCTTATTAGC TCCCGCTCC ACAAGACACC TGTGACATCC TCCAGGGCCA

CAGGAGCAGG TGCTGACCAG TTTTCCCTTC CAGTTCTGTC ACAAAGATG TCCAGAGGGC

TGTTTGCAA CACTAGTGCA CTTTGTAGCT TTTCAACCTC TGTCCAGGG AATCTAGGAG

AGATGAGGCC CGTCAGAGTC AAGAGATGTC ATCCCCCAG GGTCTCCAAG GCATTTCCAC

ACTATTGGTG GCACCTGGAG GACATGCACC AAGGCTTGCC AGAGCCAAAC GGAAGTGAGC

CCAGAGCATG GCACATGAGC ATCAACCCCT GATGGTGGCC TGCTGTGCTT GGTGCCAACA

GGGGCATCCC GGCCCGTACC CCTCCAGACA GGAAGCATGG GTTTGCCAC AGACCTGTCT

GGTGCTCCTG TGAGTGGCCT CCAGATGTCT TTGTGCATAG GCACAAGTGG GCCAGGCTG

GAGGGAGGTT GGAACCTCA TCATCCGGTG GGCCCTGCCA ATCTTAACCC AGAACCTCTA

GTATTCTCTG GCAGTAGCCA TGACATTGGA GCACCTTCTC CTCAGCCAG AGGCTGACCT

GAGGGCCACT GTCTCTCAGT GACACCAACC AGGAGCACCC TAGGTGAGGG GTGAGGGCCC

CCTTATGTGA ACCTCTGCTC TCTTCTTTC TCCCATCAGA GTGGTTGGAT GGAGCCATTG

GCCTCCTTTT CTTCAAGCGG CCCTTCAACC TCTCTGCACC ATGTTGTCTG GCTGAGGAGC

TACTAGAAAA GCTGAGTGGG GTCTCCTTTC CAACAGGATG ATGCATTTCG TCAATCTCA

GGGCTGGAAT GAGCCGGCTG GTCCCCAGA AAGCTGGAGT GGGGTACAGA GTTCAGTTT

CCTCTCTGTT TACAGCTCCT TGACAGTCCC ACGCCCATCT GGAGTGGGAG CTGGAGTTA

GTGTTGGAGA AGAAACAACA AAAGCCAATT AGAACCCTA TTTTAAAAA GTGCTTACTG 4800
 TGCACAGATA CTCTTCAAGC ACTGGACGTG GATTCTCTCT CTAGCCCTCA GCACCCCTGC 4860
 GGTAGGAGTG CCGCCTCTAC CCACTTGTGA TGGGGTACAG AGGCACTTGC TCTTCTGCAT 4920
 GGTGTTCAAT AGGCTGGGAG TTTTATTTAT CTCTTCAAAC TTTGTACAAG AGCTCATGGC 4980
 TTGTCTTGGG CTCTTCTCAT TAAACCAAAG GAAATGGAAG CCATTCCCTC GTTGTCTCTC 5040
 TTAGTCTTGG TCATCAGAAC CTCACCTGGT ACCATATAGA TCAAAAGCTT TGTAAACCACA 5100
 GGAATAAATA AACTCTTCCA TCCCTTAAAG AATAGAATAG TTTGTCCCTC TCATGGGAAT 5160
 TGGGCTGTAT GTATATTGTT CTCTCTCTCT AGAATTTAGA GATACAAGAG TTCTACTTAG 5220
 AACTTTTCAT GGACACAATT TCCACAACCT TTCAGATGCT GATGTAGAGC TATTGGGAAA 5280
 GAACCTCCAA ACTCAGGAAG TTTGCAGAGA GCAGACAGCT AGAGATAACT CGGGACCCAG 5340
 AGTTGGTCGA CAGATGTAG ATGTATCCTA GCTTTTAGCC ATAAACCACT CAAAGATTCA 5400
 GCCCCAGAT CCCACAGTCA GAACTGAATC TGCCTTGTG GGAAGCCAGC AGTGGCCTTG 5460
 GGAAGGAAGC CATGGCTGTG GTTCAGAGAG GGTGGGCTGG CAAGCCACTT CCGGGGAAAA 5520
 CTCCTTCCGC CCCAGCTTTC TTCTTCTCTT AAGGAGAGAT TGTCTCACC AACCCGCTGC 5580
 CTTATGCTG CTTCAAAGC TAGATCATGT TTGCTTGTCT TAGAGAAATTA CTGCAAAATCA 5640
 GCCCCAGTGC TTGCGCATGC ATTTACAGAT TTCTAGGCC TCAGGGTTT GTAGAGTGTG 5700
 AGCCCTGGTG GGCAGGGTGG GGGGGTCTGT CTTCTGCTGG ATGCTGCTTG TAATCCATT 5760
 GGTGTACAGA ATCAACAATA AATAATATAC ATGTAT

Seq ID NO: 286 Protein sequence:
 Protein Accession #: NP_570843.1

1 11 21 31 41 51
 MPLKHYLLLL VGCQAWGAGL AYHGPCSECT CSRASQVECT GARIVAVFTP LPWNAMSLQI 60
 LNTHTLENE SPFLNISALI ALRIEKNELS RITPGAFRNL GSLRYLSLAN NKLOVLPIGL 120
 PQGLDSLES LLSSNQLLQI QPAHFSQCSN LKELQLHGNH LEYIPDGAFL HLVLTKLNL 180
 GGNLSLTHSP RVFQHLGNLQ VLRLYENRLT DIPMGTFDGL VNLQELALQQ NQIGLLSPGL 240
 FHNHNLQRL YLSNNHLSQL PPSIPMQLPQ LNRLTLFGNS LKELSLGIFG PMPNLRLEWL 300
 YDNHISLEPD NVFSNLRQLQ PLLLSRNQIS FISPAGFNGL TELRELSHT NALQDLQDNV 360
 FRMLANLQNI SLQNNRRLQL PGNIPANVNG LMAIQLQNNQ LENLPLGIFD HLKLCLELRL 420
 YDNFWRCDSD ILPLRNWLLL NQPRLGTDV PVCFSANVR QSLIIINVN VAVPSVHVPE 480
 VPSYPETPWY PDTSPYDPT SVSSTELTS PVEDYDLTT IQVTDDRSVW GMTQAQSGLA 540
 IAAIVIGIVA LACSLAACVG CCCCCKRSQA VLMQMKAPNE C

Seq ID NO: 287 DNA sequence
 Nucleic Acid Accession #: NM_002362
 Coding sequence: 1..954

1 11 21 31 41 51
 ATGTCTTCTG AGCAGAAGAG TCAGCACTGC AAGCCTGAGG AAGGCGTTGA GGCCCAAGAA 60
 GAGGCCCTGG GCCTGGTGGG TGCACAGGCT CCTACTACTG AGGAGCAGGA GGCTGCTGTC 120
 TCCTCTCTCT CTCTCTTGGT CCTGGCACC CTGGAGGAAG TGCCTGCTGC TGAGTCAGCA 180
 GGTCTCTCCC AGAGTCTCTA GGGAGCCTCT GCCTTACCCT CTACCATCAG CTCTACTTGC 240
 TGGAGGCAAC CCAATGAGGG TTCCAGCAGC CAAGAAGAGG AGGGGCCAAG CACCTGCGCT 300
 GACGCAGAGT CCTTGTTCGG AGAAGCACTC AGTAACAAGG TGGATGAGTT GGCTCATTTT 360
 CTGCTCCGCA AGTATCGAGC CAAGGAGCTG GTCACAAAGG CAGAAATGCT GGAGAGAGTC 420
 ATCAAAAATT ACAAGCGCTG CTCTCTGTG ATCTTCGGCA AAGCCTCCGA GTCCCTGAAG 480
 ATGATCTTTG GCATTGACGT GAAGGAAAGT GACCCCGCCA GCAACACCTA CACCTTGTG 540
 ACCTGCGCTG GCCTTTCTTA TGATGGCCTG CTGGGTAATA ATCAGATCTT TCCCAAGACA 600
 GGCCTTCTGA TAATCGTCTT GGGCACAATT GCAATGGAGG GCGACAGCGC CTCTGAGGAG 660
 GAAATCTGGG AGGAGCTGGG TGTGATGGGG GTGTATGATG GGAGGGAGCA CACTGTCTAT 720
 GGGGAGCCCA GGAACACTGT CACCCAAAGT TGGGTGCAGG AAAACTACCT GGAGTACCGG 780
 CAGGTACCCG GCAGTAATCC TGCAGCGCTAT GAGTTCCTGT GGGGTCCAAG GGCTCTGGCT 840
 GAAACCAAGT ATGTGAAAGT CCTGGAGCAT GTGGTCAGGG TCAATGCAAG AGTTGCGCAT 900
 GCCTACCCAT CCCTGCGTGA AGCAGCTTTG TTAGAGGAGG AAGAGGGAGT CTGA

Seq ID NO: 288 Protein sequence:
 Protein Accession #: NP_002353.1

1 11 21 31 41 51
 MSSEQKSQHC KPEEGVEAQE EALGLVGAQA PTTEEQEAUV SSSSPLVPFT LEEVPAEESA 60
 GPPQSPQAS ALPTTISFTC WRQPNQSSSS QEEEGPSTSP DAESLFREAL SNKVDELAFH 120
 LLRKYRAKEL VTKAEMLEVR IKNYKRCPPV IFGKASESLK MIFGIDVKEV DPASNTYTLV 180
 TCLGLSYDEL LGNNQIPFKT GLLIIVLGTI AMEGDSASEE EIWEELGVMG VYDGREHTVY 240
 GEPRKLLTD WVQENYLEYR QVPGSNPARY EFLWGPRLA ETSYVKVLEH VVRVNAVRI 300
 AYPRLREAL LEEBEGV

Seq ID NO: 289 DNA sequence
 Nucleic Acid Accession #: NM_002362
 Coding sequence: 46..1344

1 11 21 31 41 51
 CGGCGGCCGC GCCCTGGTTG GGTCCCACT GCTCTCGGGG GCGCCATGGA CGAGGCCGTG 60
 GGCAGCTTGA AGCAGGCGCT TCCTCTGTG GCGGAGTCCG CAACGGTCCA CGTGGAGGTG 120
 CATCAGCGCG GCACAGCAC TGCAAGAAA GAAGACATAA ACCTGAGTGT TAGAAAGCTA 180
 CTCACACAGC ATAATATGT GTTGTGTGAT TACACATGGA CTGAGTTTGA TGAACCTTTT 240
 TTGACCAAGC ATGTGCAATC TTGTCTATT ATTGACACAG AATTAAAGGT TAAAGACTCA 300
 CAGCCCATCG ATTTGAGTGC ATGCACTGTT GCACTTCACA TTTTCCAGCT GAATGAAGAT 360
 GGCCCCAGCA GTGAAATCT GGAGGAAGAG ACAGAAAACA TAATTGCAGC AAATCACTGG 420
 GTTCTACCTG CAGCTGAATT CCATGGGCTT TGGGACAGCT TGGTATACGA TGTGGAAGTC 480
 AAATCCCATC TCCTCGATTA TGTGATGACA ACTTTACTGT TTTGAGACAA GAACGTCAAC 540

AGCAACCTCA TCACCTGGAA CCGGCTGGTG CTGCTCCACG GTCCTCCTGG CACTGGAAAA 600
 ACATCCCTGT GTAAAGCGTT AGCCACAGAA TTGACAATTA GACTTTCAG CAGGTACCGA 660
 TATGGCCAAAT TAAATGAAAT AAACAGCCAC AGCCTCTTTT CTAAAGTGGT TTCGGAAGT 720
 GGCAAGCTGG TAACCAAGAT GTTTCAGAGG ATTCAAGATT TGATTGATGA TAAAGACGCC 780
 CTGGTGTTCG TGCTGATTGA TGAGGTGGAG AGTCTCACAG CCGCCCCGAA TGCCCTGCAGG 840
 GCGGGCACCG AGCCATCAGA TGCCATCCGC GTGGTCAATG CTGTCTTGAC CCAAATTGAT 900
 CAGATTAAAA GGCATTCCAA TGTGTGATT CTGACCACTT CTAACATCAC CGAGAAGATC 960
 GACGTGGCCT TCGTGGACAG GGTGACATC AAGCAGTACA TTGGGCCACC CTCTGCAGCA 1020
 GCCATCTTCA AAATCTACCT CTCTTGTGTT GAAGAACTGA TGAAGTGTCA GATCATATAC 1080
 CCTCGCCAGC AGCTGCTGAG CCTCCGAGAG CTAGAGATGA TTGGCTTCAT TGAACAACAC 1140
 GTGTCAAAAT TGAGCCTTCT TTTGAATGAC ATTTCAAGGA AGAGCGAGGG CCTCAGCGGC 1200
 CCGGTCTCTGA GAAAACTCCC CTTTCTGGCT CATGCGCTGT ATGTCCAGGC CCCCACCGTC 1260
 ACCATAGAGG GGTTCCTCCA GGCCTGTCT CTGGCAGTGG ACAAGCAGTT TGAAGAGAGA 1320
 AAGAAGCTTG CAGCTTACAT CTGATCCTGG GCTTCCCAT CTGGTGTCTT TCCCATGGAG 1380
 AACACACAAC CAGTAAGTGA GGTGCCCCA CACAGCCGTC TCCAGGGAA TCCCTTCTGC 1440
 AAACCAACG TACTTACAT CTGATCCTGG GCTTCCCAT CTGGTGTCTT TCCCATGGAG 1500
 AAGTGTATTC TATTTATGTT GTTTTAAAT GCATCTGAG AGACAACAT CTGTGCTATT 1560
 TCACTGTTTG TAAAGATAA TTCAGATTGT TTGTCTCCTT GTGAAGAAC ATCGAAACCT 1620
 GTTGTGTTCC AGCCACACCC CAGTGGATGG GATGCATAAT GCCAGCAAGT TTTGTTTAA 1680
 AGCAAAAAAG GAAGATTAT GCAGGTGTTA TAGAAGCCAG AAGAGAACT GTGTCAACCT 1740
 AAAGAAGCAT ATAATCATAG CATTAAAAAT GCACACATTA CTCCAGGTGG AAGGTGGCAA 1800
 TTGCTTCTG ATATCAGCTC GTTTGATTTA GTGCAAAAA GTTTTCAAGA CTATTTAATG 1860
 GATGTAAAAA AGCCTATTTC TACATTATAC CAACAGTAAA AAAAATGGTC GGTAAAGTGT 1920
 TCTTTCATAA TAAATAATCA AGACATGGTC CCATTGTCAG GAAAAGTGCA GACTCTGAGT 1980
 GTTCCAGGGA AACACATGCT GGACATCCCT TGTAACCCGG TATGGGCGCC CCTGCATTGC 2040
 TGGGATGTTT CTGCCACCGG TTTTGTGTTG GCAATAACGT TATCACATTT CTAATGAGGA 2100
 TTCACATTAA TATAATATAA AATAAATAGG TCAGTTACTG GTCTCTTCTC GCCGAATGTT 2160
 ATGTTTTGCT TTTATCTCAC AGTAAATAA ATATAATTAA AAA

Seq ID NO: 290 Protein sequence:
 Protein Accession #: NP_004228

1 11 21 31 41 51
 MDEAVGLDLK ALPCVAESPT VHVVEVHQRGS STAKKEDINL SVRKLNRHN IVFGDYTWTE 60
 FDEPFLTRNV QSVSIIDTEL VKVDSQPIDL SACTVALHIF QLNEDGPSSE NLEETENII 120
 AANHWWLPAA EPHGLWDSLV YDVEVKSHLL DVVMTLLFS DKNVNSNLIT WNRVVLHGP 180
 PGTKTSLCK ALAQKLTIRL SSRYRYQLI EINSLSLPSK WFSBSGKLV KMFQKIQDLI 240
 DDKDALVFLV IDEVESLTAA RNACRAGTEP SDAIRVNVAV LTQIDQIKRH SNVILTTSN 300
 ITEKIDVAFV DRADLKQYIG PPSAAAIKFI YLSCLLELMK CQIYPRQQL LTLRELEMIG 360
 FIENNVSKLS LLLNDISRKS EGLSGRVLRL LPFLAHLAYV QAPTVTIEGF LQALSIAVDK 420
 QPERKKLAA YI

Seq ID NO: 291 DNA sequence
 Nucleic Acid Accession #: NM_002658.1
 Coding sequence: 77-1372

1 11 21 31 41 51
 GTCCCCGCGC GCGCGTCGCG CCCTCCTGCC GCAGGCCACC GAGGCGCGCG CCGTCTAGCG 60
 CCCCACCTTC GCCACATGA GAGCCCTGCT GCGCGCGCTG CTTCTCTGCG TCCTGGTCGT 120
 GAGCGACTCC AAAGCGAGCA ATGAACCTCA TCAAGTTCCA TCGAACTGTG ACTGTCTAAA 180
 TGGAGGAACA TGTGTGTCCA ACAAGTACTT CTCCAACATT CACTGGTGCA ACTGCCCAA 240
 GAAATTGCGA GGGCAGCACT GTGAATAGA TAAGTCAAAA ACCTGCTATG AGGGAATGG 300
 TCACTTTTAC CGAGGAAAGG CCAGCACTGA CACCATGGGC CCGCCCTGCC TGCCCTGGAA 360
 CTCCTGCCAT CTCTTCCAG AAGCGTACCA TGCCCCAGA TCTGATGCTC TTCAGCTGGG 420
 CCTGGGGAAA CATAATTACT GCAGGAACCC AGACAACCGG AGGCGACCTT GGTGCTATGT 480
 GCAGGTGGGC CTAAGCCGCG TTGTCCAAGA GTGCATGGTG CATGACTGCG CAGATGGAAA 540
 AAAGCCCTCC TCTCTCCAG AAGAATTAAA ATTTCACTGT GGGCAAAA CTCTGAGGCC 600
 CCGCTTTAAG ATTATTGGGG GAGAATTAC CACCATCGAG AACAGCCCTT GGTTCGCGC 660
 CATCTACAGG AGGCACCGGG GGGGCTCTGT CACCTACGTG TGTGGAGGCA GCCTCATCAG 720
 CCCTTGCTGG GTGATCAGCG CCACACACTG CTTCAATTGAT TACCCAAAGA AGGAGGACTA 780
 CATCGTCTAC CTGGGTGCTC CAAGGCTTAA CTCCAACAG CAAGGGGAGA TGAAGTTTGA 840
 GGTGGAAAC CTATCTCTAC ACAAGGACTA CAGCGCTGAC ACGCTTGCTC ACCACAACGA 900
 CATTGCTCTG CTGAAGATCC GTTCCAAGGA GGGCAGGTGT GCGCAGCCAT CCCGACTAT 960
 ACAGACCATC TGCCCTGCCCT CGATGTATAA CGATCCCCAG TTTGGCACAA GCTGTGAGAT 1020
 CACTGGCTTT GGAAGAGAGA ATTCTACCGA CTATCTCTAT CCGGAGCAGC TGAAGATGAC 1080
 TGTGTGAAG CTGATTTCCC ACCGGGAGTG TCAGCAGCCC CACTACTACG GCTCTGAAAT 1140
 CACCACCAA ATGCTATGTG CTGCTGACCC CCAATGGAAG ACAGATTCTT GCCAGGAGGA 1200
 CTCAGGGGGA CCCCTCGTCT GTTCCCTCCA AGGCCGATG ACTTTGACTG GAATTGTGAG 1260
 CTGGGGCCGT GGATGTGCCC TGAAGGACAA GCCAGGCGTC TACACGAGAG TCTCACACTT 1320
 CTTACCTCTG ATCCGAGTGC ACACCAAGGA AGAGAATGTC CTGGCCCTCT GAGGGTCCCC 1380
 AGGGAGGAAA CGGGCACCAAC CCGCTTTCTT GCTGGTTGTC ATTTTTCAG TAGAGTCATC 1440
 TCCATCAGCT GTAAGAGAG ACTGGGAAGA TAGGCTCTGC ACAGATGGAT TTGCTGTGG 1500
 CACCACGAG GTGAACGACA ATAGCTTTAC CTTACGGAT AGGCCTGGGT GCTGGCTGCC 1560
 CAGACCTCTT GGCAGGATG GAGGGGTGGT CTTGACTCAA CATGTTACTG ACCAGCAACT 1620
 TGCTTTTTC TGACCTGAAG CCTGCAGGAG TTAAGAAAGG CAGGGCATCT CCGTGTGATG 1680
 GGCTCGAAGG GAGAGCCAGC TCCCGGACCC GGTGGGCATT TGTGAGGCC ATGGTTGAGA 1740
 AATGAATAAT TTCCCAATTA GGAAGGTGTA GCAGCTGAGG TCTCTGAGG GAGCTTAGCC 1800
 AATGTGGGAG CAGCGGTTTG GGGAGCAGAG ACCTAACGA CTTCAGGGCA GGGCTCTGAT 1860
 ATTCCATGAA TGTATCAGGA AATATATATG TGTGTGTATG TTTGCACACT TGTGTGTGG 1920
 GCTGTGAGTG TAAGTGTGAG TAAGAGCTGG TGTCTGATTG TTAAGTCTAA ATATTCTCTT 1980
 AAATCTGTG GACTGTGATG CCACACAGAG TGGTCTTTCT GGAGAGGTTA TAGGCTACTC 2040
 CTGGGGCCTC TTGGGTCCCC CACGTGACAG TGCCCTGGGA TGACTTATT CTGCAGCATG 2100
 ACCTGTGACC AGCACTGTCT CAGTTTCACT TTCACATAGA TGTCCCTTTC TTGGCCAGTT 2160
 ATCCCTTCTT TTAGCCCTAG TTCATCCAAT CCTCACTGGG TGGGGTGAGG ACCACTCCTT 2220
 AACTGAATA TTTATATTTC ACTATTTTTA TTTATATTTT TGTAATTTTA AATAAAGTG 2280

ATCAATAAAA TGTGATTTTT CTGA

Seq ID NO: 292 Protein sequence:

Protein Accession #: NP_002649.1

1	11	21	31	41	51	
MRALLARLLL	CVLVVSDESKG	SNELHQVPSN	CDCLNGGTCV	SNKYFSNIHW	CNCPKKFGGQ	60
HCEIDKSKTC	YEGNGHFYRG	KASTDTMGRP	CLPWN SATVL	QQTYHAHRSD	ALQLGLGKHN	120
YCRNPDNRRL	PWCYVQVGLK	PLVQECMVHD	CADGKKPSSP	PEELKFQCGQ	KTLRPRPKII	180
GGFEFTIENQ	PWFAAIYRRH	RGGSVTVVCG	GSLISPCWVI	SATHCFIDYP	KKEDYIVVLG	240
RSRLNSNTQG	EMKFEVENLI	LHKDYSADTL	AHNDIALLLK	IRSKEGRCQA	PSRTIQTICL	300
PSMYNDPQFG	TSCEITGFGK	ENSTDYLYPE	QLKMTVVVKLI	SHRECQPHY	YGSEVTTKML	360
CAADPQWKTD	SCQDSDGGPL	VCSLQGRMTL	TGIVSWGRGC	ALKDKPGVYT	RVSHFLPWIR	420
SHTKEENGLA	L					

Seq ID NO: 293 DNA sequence

Nucleic Acid Accession #: NM_001498

Coding sequence: 93...2006

1	11	21	31	41	51	
GGCAGGAGGC	TGAGTGTCGG	TCTCGCGCCC	GGAAGCGGGC	GACCGCCGTC	AGCCCGGAGG	60
AGGAGGAGGA	GGAGGAGGAG	GAGGGGGCGG	CCATGGGGCT	GCTGTCCAG	GGCTCGCGCG	120
TGAGCTGGGA	GGAAACCAAG	CGCCATGCCG	ACCACGTGCG	GCGGCACGGG	ATCCTCCAGT	180
TCCTGCACAT	CTACCACGCC	GTCAAGSACC	GGCACAAGGA	CGTTCTCAAG	TGGGGCGATG	240
AGGTGGAATA	CATGTTGTA	TCTTTTGATC	ATGAAAATAA	AAAAGTCCCG	TTGGTCTGT	300
CTGGGGAGAA	AGTTCTTGAA	ACTCTGCAAG	AGAAGGGGGA	AAGGACAAAC	CCAAACCATC	360
CTACCCCTTG	GAGACCGAG	TATGGGAGTT	ACATGATTGA	AGGGACACCA	GGACAGCCCT	420
ACGAGGAAAC	AATGTCCGAG	TTCAATACAG	TTGAGGCCAA	CATGCGAAAA	CGCCGGAAGG	480
AGGCTACTTC	TATATTAGAA	GAAAATCAGG	CTCTTTGCAC	AATAACTTCA	TTTCCAGAT	540
TAGGCTGTCC	TGGGTTCCAA	CTGCCCCAGG	TCAAACCCAA	CCCAGTGGAA	GGAGGAGCTT	600
CCAAGTCCCT	CTTCTTTCCA	GATGAAGCAA	TAAACAAGCA	CCCTCGCTTC	AGTACCTTAA	660
CAAGAAATAT	CCGACATAGG	AGAGGAGAAA	AGGTTGTGAT	CAATGTACCA	ATATTTAAGG	720
ACAAGAAATC	ACCATCTCCA	TTTATAGAAA	CATTACTGA	GGATGATGAA	GCTTCAAGGG	780
CTTCTAAGCC	GGATCATATT	TACATGGATG	CCATGGGATT	TGGAATGGGC	AATTGCTGTC	840
TCCAGGTGAC	ATTCACAGCC	TGCAGTATAT	CTGAGGCCAG	ATACCTTTAT	GATCAGTTGG	900
CTACTATCTG	TCCAAATGTT	ATGGCTTTGA	GTGCTGCATC	TCCCTTTTAC	CGAGGCTATG	960
GTGCAGACAT	TGATTGTGCG	TGGGGAGTGA	TTTCTGCATC	TGTAGATGAT	AGAACTCGGG	1020
AGGAGCGAGG	ACTGGAGCCA	TTGAAGAAC	ATAACTATAG	GATCAGTAAA	TCCCGATATG	1080
ACTCAATAGA	CAGCTATTTA	TCTAAGTGTG	GTGAGAAATA	TAATGACATC	GACTTGACGA	1140
TAGATAAAGA	GATCTACGAA	CAGCTGTTGC	AGGAAGGCAT	TGATCATCTC	CTGGCCCAGC	1200
ATGTTGCTCA	TCTCTTTATT	AGAGACCCAC	TGACACTGTT	TGAAGAGAAA	ATACACCTGG	1260
ATGATGCTAA	TGAGTCTGAC	CATTTTGAGA	ATATTCACTC	CACAAATTGG	CAGACCAATG	1320
GATTTAAGAC	CCCTCTCCCA	AAGTTCAGCA	TTGGATGGAG	AGTAGAATTT	CGACCCATGG	1380
AGGTGCAATT	AACAGACTTT	GAGAACTCTG	CCTATGTGGT	GTTTGTGGTA	CTGCTCACC	1440
GAGTGATCCT	TTCCTACAAA	TTGGATTTC	TCATTCCACT	GTCAAAGGTT	GATGAGAAAC	1500
TGAAGGTAGC	ACAGAAAAGA	GATGCTGTCT	TGCAGGGAAT	GTTTTATTTC	AGGAAAGATA	1560
TTTGCAAGG	TGGCAATGCA	GTGGTGGATG	GTGTGCGCAA	GGCCCAAGAC	AGCACGGAGC	1620
TCGCTGAGAG	GGGATGACCA	CTCATGAGCA	TAGACACCAT	CATCAATGGG	AAGGAAGGTG	1680
TGTTTCTCGG	ACTGATCCCA	ATTCTGAACT	CTTACCTTGA	AAACATGGAA	GTGGATGTGG	1740
ACACCCAGATG	TAGTATTCTG	AACTACCTAA	AGCTAATTAA	GAAGAGAGCA	TCTGGAGAAC	1800
TAATGACAGT	TGCCAGATGG	ATGAGGGAGT	TTATCGCAAA	CCATCCTGAC	TACAAGCAAG	1860
ACAGTGTGAT	AAGTATGAAA	ATGAATTATA	GCCTTATTTT	GAAGTGTAAC	CAAAATGCAA	1920
ATGAATTATG	TGAATGCCCA	GAGTTACTTG	GATCAGCATT	TAGGAAAGTA	AAATATAGTG	1980
GAAAGTAAAC	TGACTCATCC	AAGTAGACAT	TCTACAGAAA	GAAAAATGCA	TTATTGACGA	2040
ACTGGCTACA	TGACCATGCC	TCTCAGCCCG	TGTGTATAAT	ATGAAGACCA	AATGATAGAA	2100
CTGTACTGTT	TTCTGGGCCA	GTGAGCCAGA	AATTGATTAA	GGCTTTCTTT	GGTAGGTAAA	2160
CTTAGAGTTT	ATACAGTGTA	CATGTACATA	GTAAGATATT	TTTGATTAA	AATGTATTTT	2220
AATAACATAT	CTAAAGTCAT	CATGAACCTG	CTTGATACAT	TTTAAATTCT	TACTCTGGAG	2280
CAACCTACTG	TCTAAGCAGT	TTGTAAATG	TACTGGTAAT	TGTACAATAC	TTGCATTCCA	2340
GAGTTAAAT	GTTTACTGTA	AATTTTGTG	CTTTAAAGA	CTACCTGGGA	CCTGATTAT	2400
TGAAATTTT	CTCTTAAAA	ACATTTCTC	TGTTAATTT	TCCTTTGTCA	TTTCCTTTGT	2460
TGCTACATT	AAATCATTG	AATCCATTGA	AAGTGCTTCA	AGGGTAATCT	TGGGTTTCTA	2520
GCACCTTATC	TATGATGTTT	CTTTGCAAT	TGGAATAATC	ACTTGGTCAC	CTTGCCCCAA	2580
GCTTTCCCT	CTGAATAAAT	ACCCATTGAA	CTCTGAAAAA	AAAAAATAAA	AAAA	

Seq ID NO: 294 Protein sequence:

Protein Accession #: NP_001489

1	11	21	31	41	51	
MGLLSQGSPL	SWEETKRHAD	HVRRHGILQF	LHIYHAVKDR	HKDVLKWGDE	VEYMLVSFDH	60
ENKKVRLVL	GEKVLTLQE	KGERTNPNHP	TLWRPEYGSY	MIEGTPGQPY	GGTMSEFNTV	120
ENAMRKRRKE	ATSLILEENQA	LCTITSFPRL	GCPGPTLPEV	KPNPVEGGAS	KSLFFPDDEAI	180
NKHPREFTLT	RNIHRRRGEK	VVINVPFKD	KNTPSFFIET	FTEDDEASRA	SKPDHIYMDA	240
MGFGMGNCCL	QVTFQACIS	EARYLYDQLA	TICPIVMALS	AASPFYRGYV	SDIDCRWGI	300
SASVDDRTRE	ERGLEPLKNN	NYRISKSRID	SIDSYLSKCG	EKYNDIDLTI	DKEIYEQLLQ	360
EGIDHLLAQH	VAHLEFIRPL	TLFEEKIHLD	DANESDHFPN	IQSTNWTQMR	FKPPPNDSI	420
GWRVEFRPME	VQLTDFENSA	VYVFPVLLTR	VILSYKLDLF	IPLSKVDENM	KVAQKRDAVL	480
QGMFYFRKDI	CKGNAVDVG	CGKAQNSTEL	AAEYTLMSI	DTIINGKEGV	FPGLIPILNS	540
YLENMEVDVD	TRCSILNLYK	LIKKRASGEL	MTVARWMMREF	IANHPDYKQD	SVITDEMNY	600
LILKCNQIAN	ELCEPELLG	SAFKRVKYS	SKTDSSN			

WO 02/086443

PCT/US02/12476

Seq ID NO: 295 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 247-816

```

5      1      11      21      31      41      51
      |      |      |      |      |      |
      AGTGTTCGGC TGGGGCAGGC ACGCTGTGGC TGGCTACTTC CCTTCCTCCC ATCCCCCTTG 60
      GGCCAAACGG GATCGGTGCT TCTGGTGAGA CGCCTCCCCA TGCACATCAC TCCCAGGTGC 120
10     CCTAGGGGGC ACATTTCCCA CAACTCCCAG AGGGCAGGTT TCTAGAAAGT GCCACCAGTG 180
      GGGAGGGCGC ACAACTTCAC TGCCATTTTG TGAGGTGCCG CCGTCTCTCC TCCAGCAAGG 240
      GAAACAATGA CCGATAAAAC AGAGAAGGTG GCTGTAGATC CTGAAACTGT GTTTAAACGT 300
      CCCAGGGAAT GTGACAGTCC TTCGTATCAG AAAAGGCAGA GGATGGCCCT GTTGGCAAGG 360
      AAACAAGGAG CAGGAGACAG CCTTATTGCA GGCTCTGCCA TGTCCAAAGA AAAGAAGCTT 420
      ATGACAGGAC ATGCTATTCC ACCCAGCCAA TTGGATTCTC AGATTGATGA CTTCACTGGT 480
15     TTCAGCAAGG ATAGGATGAT GCAGAAACCT GGTAGCAATG CACCTGTGGG AGGAAACGTT 540
      ACCAGCAGTT TCTCTGGAGA TGACCTAGAA TGCAGAGAAA CAGCCTCCTC TCCCAAAGC 600
      CAACGAGAAA TTAATGCTGA TATAAAACGT AAATTAGTGA AGGAACTCCG ATGCGTTGGA 660
      CAAAAATATG AAAAAATCTT CGAAATGCTT GAAGGAGTGC AAGGACCTAC TGCAGTCAGG 720
      AAGCGATTTT TTGAATCCAT CATCAAGGAA GCAGCAAGAT GTATGAGACG AGACTTTGTT 780
20     AAGCACCTTA AGAAGAAACT GAAACGTATG ATTTGAGAAT ACTTGTCCCT GGAGGATTAT 840
      CACACCCCAA ATGATAAATC TCCTTAATGA TTGAGGAGAG AAAAGGATCA GATTGCTGTT 900
      TTCTACAATG GAGCAGGATA TTGCTGAAGT CTCCTGGCAT ATGTTACCGA ATCAATAGC 960
      CTTCCAGAGG CTAAGAAATT TCTGTTAGTA AAAGATGTTT TTTTCCCAA AGCATTTTAT 1020
      TTGAAAGGAT AACTTGTGTT TTGGTTATT TGTATTCCTA CCTGTGCTGG TAGATATTAT 1080
25     TAACCCATTA GGTAAATACT ATTACAGTCG TGGTTTCTGC A
  
```

Seq ID NO: 296 Protein sequence:
Protein Accession #: Eos sequence

```

30     1      11      21      31      41      51
      |      |      |      |      |      |
      MTDKTEKVAV DPETVFKRPR ECDSPSYQKR QRMALLARKQ GAGDSLIIAGS AMSKEKKLMT 60
      GHAIPPSQLD SQIDDFTFPS KDRMMQKPGS NAPVGGNVTS SFGDDLECR ETASSPKSQR 120
35     EINADIKRKL VKELRCVGQK YEKIFEMLEG VQGPTAVRKR PFESIIEKAA RCMRRDFVKH 180
      LKKKLKRLMI
  
```

Seq ID NO: 297 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 247-815

```

40     1      11      21      31      41      51
      |      |      |      |      |      |
      AGTGTTCGGC TGGGGCAGGC ACGCTGTGGC TGGCTACTTC CCTTCCTCCC ATCCCCCTTG 60
      GGCCAAACGG GATCGGTGCT TCTGGTGAGA CGCCTCCCCA TGCACATCAC TCCCAGGTGC 120
45     CCTAGGGGGC ACATTTCCCA CAACTCCCAG AGGGCAGGTT TCTAGAAAGT GCCACCAGTG 180
      GGGAGGGCGC ACAACTTCAC TGCCATTTTG TGAGGTGCCG CCGTCTCTCC TCCAGCAAGG 240
      GAAACAATGA CCGATAAAAC AGAGAAGGTG GCTGTAGATC CTGAAACTGT GTTTAAACGT 300
      CCCAGGGAAT GTGACAGTCC TTCGTATCAG AAAAGGCAGA GGATGGCCCT GTTGGCAAGG 360
      AAACAAGGAG CAGGAGACAG CCTTATTGCA GGCTCTGCCA TGTCCAAAGA AAAGAAGCTT 420
      ATGACAGGAC ATGCTATTCC ACCCAGCCAA TTGGATTCTC AGATTGATGA CTTCACTGGT 480
50     TTCAGCAAGG ATAGGATGAT GCAGAAACCT GGTAGCAATG CACCTGTGGG AGGAAACGTT 540
      ACCAGCAGTT TCTCTGGAGA TGACCTAGAA TGCAGAGAAA CAGCCTCCTC TCCCAAAGC 600
      CAACAAGAAA TTAATGCTGA TATAAAACGT AAATTAGTGA AGGAACTCCG ATGCGTTGGA 660
      CAAAAATATG AAAAAATCTT CGAAATGCTT GAAGGAGTGC AAGGACCTAC TGCAGTCAGG 720
      AAGCGATTTT TTGAATCCAT CATCAAGGAA GCAGCAAGAT GTATGAGACG AGACTTTGTT 780
55     AAGCACCTTA AGAAGAAACT GAAACGTATG ATTTGAGAAT ACTTGTCCCT GGAGGATTAT 840
      CACACCCCAA ATGATAAATC TCCTTAATGA TTGAGGAGAG AAAAGGATCA GATTGCTGTT 900
      TTCTACAATG GAGCAGGATA TTGCTGAAGT CTCCTGGCAT ATGTTACCGA ATCAACTGGC 960
      CTTCCAGAGG CTAAGAAATT TCTGTTAGTA AAAGATGTTT TTTTCCCAA AGCGTTTAT 1020
      TTGAAAGGAT AACTTGTGTT TTGGTTATT TGTATTCCTA CCTGTGCTGG TAGATATTAT 1080
60     TAACCCATTA GGTAAATACT ATTACAGTCG TGGTTTCTGC A
  
```

Seq ID NO: 298 Protein sequence:
Protein Accession #: Eos sequence

```

65     1      11      21      31      41      51
      |      |      |      |      |      |
      MTDKTEKVAV DPETVFKRPR ECDSPSYQKR QRMALLARKQ GAGDSLIIAGS AMSKEKKLMT 60
      GHAIPPSQLD SQIDDFTFPS KDRMMQKPGS NAPVGGNVTS SFGDDLECR ETASSPKSQ 120
70     EINADIKRKL VKELRCVGQK YEKIFEMLEG VQGPTAVRKR PFESIIEKAA RCMRRDFVKH 180
      LKKKLKRLMI
  
```

Seq ID NO: 299 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 247-815

```

75     1      11      21      31      41      51
      |      |      |      |      |      |
      AGTGTTCGGC TGGGGCAGGC ACGCTGTGGC TGGCTACTTC CCTTCCTCCC ATCCCCCTTG 60
      GGCCAAACGG GATCGGTGCT TCTGGTGAGA CGCCTCCCCA TGCACATCAC TCCCAGGTGC 120
80     CCTAGGGGGC ACATTTCCCA CAACTCCCAG AGGGCAGGTT TCTAGAAAGT GCCACCAGTG 180
      GGGAGGGCGC ACAACTTCAC TGCCATTTTG TGAGGTGCCG CCGTCTCTCC TCCAGCAAGG 240
      GAAACAATGA CCGATAAAAC AGAGAAGGTG GCTGTAGATC CTGAAACTGT GTTTAAACGT 300
      CCCAGGGAAT GTGACAGTCC TTCGTATCAG AAAAGGCAGA GGATGGCCCT GTTGGCAAGG 360
      AAACAAGGAG CAGGAGACAG CCTTATTGCA GGCTCTGCCA TGTCCAAAGC AAAGAGCTTA 420
85     TGACAGGACA TGCTATTCCA CCCAGCCAAT TGGATTCTCA GATTGATGAC TTCCTGGTT 480
  
```


WO 02/086443

PCT/US02/12476

5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85

TCAGCAAGA TAGATGATG CAGAAACCTG GTAGCAATGC ACCTGTGGGA GGAAACGTTA 540
CCAGCAGTTT CTCTGGAGAT GACCTAGAAT GCAGAGAAAC AGCCTCCTCT CCCAAAGCC 600
AACAGAAAT TAATGCTGAT ATAAACGTA AATTAGTGAA GGAACCTCGA TCGTGTGGAC 660
AAAAATATGA AAAATCTTC GAAATGCTTG AAGGAGTGCA AGGACCTACT GCAGTCAGGA 720
AACGATTTTT TGAATCCATC ATCAAGGAAG CAGCAAGATG TATGAGACGA GACTTTGTTA 780
AGCACCTTAA GAAGAAACTG AAACGTATGA TTTGAGAATA CTTGTCCCTG GAGGATTATC 840
ACACCCCAAA TGCATAAATCT CATTAATGAT TGAGGAGAGA AAAGGATCAG ATTGCTGTTT 900
TCTACAATGG AGCAGGATAT TGCTGAAAGTC TCCTGGCATA TGTTACCGAA TCAACTGGCC 960
TTCCAGAGGC TAAGAAATTT CTGTTAGTAA AAGATGTTCT TTTTCCCAA GCGTTTTATT 1020
TGAAAGGATA ACTTGTGTTT TGGTTATTTT GTATTCCAC CTGTGCTGGT AGATATTATT 1080
AACCCATTAG GTAAATACTA TTACAGTCGT GGTTCCTGCA

Seq ID NO: 300 Protein sequence:
Protein Accession #: Eos sequence

15
20
25
30
35
40
45
50
55
60
65
70
75
80
85

1 11 21 31 41 51
MTDKTEKVV DPETVFKRPR ECDSPSYQKR QRMALLARKQ GAGDSLIAGS AMSKAKKLMT 60
GHAIPPSQLD SQIDDFTFPS KDRMMQKPGS NAPVGGNVTS SFGDDLECR ETASSPKSQ 120
EINADIKRL VKELRCVQKQ YEKIFEMLEG VQGPTAVRKR PFESIIEKAA RCMRRDPVKH 180
LKKLKRMI

Seq ID NO: 301 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 247-812

1 11 21 31 41 51
AGTGTTCGGC TGGGGCAGGC ACGCTGTGGC TGGCTACTTC CCTTCCTCCC ATCCCCCTTG 60
GGCCAAACGG GATCGGTGCT TCTGGTGAGA CGCCTCCCCA TGCACATCAC TCCACAGGTG 120
CCTAGGGGGC ACATTTCCCA CACTCCCAG AGGGCAGGTT TCTAGAAAGT GCCACCAAGT 180
GGGAGGCGCC ACACTTCAC TGCCATTTTG TGAGGTGCCG CCGTCTCTCC TCCAGCAAGG 240
GAAACAATGA CCGATAAAAC AGAGAAGGTG GCTGTAGATC CTGAAACTGT GTTTAAACGT 300
CCCAGGGAAT GTGACAGTCC TTCGTATCAG AAAAGGCAGA GGATGGCCCT GTTGGCAAGG 360
AAACAAGGAG CAGGAGACAG CCTTATTGCA GGCTCTGCCA TGTCCAAAGA AAAGAGCTTA 420
TGACAGGACA TGCTATTCCA CCCAGCCAAT TGGATTCTCA GATTGATGAC TTCCTGGTT 480
TCAGCAAAAG TGGGATGATG CAGAAACCTG GTAGCAATGC ACCTGTGGGA GGAAATGTTA 540
CCAGCAATTT CTCTGGAGAT GACCTAGAAT GCAGAGGAAT AGCCTCCTCT CCCAAAGCC 600
AACAGAAAT TAATGCTGAT ATAAATGTC AAGTAGTGAA GGAATCCGA TGCCTTGGAC 660
AATATGAAAA AATCTTCGAA ATGCTTGAAG GAGTGCAAGG ACCTACTGCA GTCAGGAAAC 720
GATTTTTTGA ATCCATCATC AAGGAAGCAG CAAGATGTAT GAGACGAGAC TTTGTTAAGC 780
ACCTTAAGAA GAAATCTGAA CGTATGATTT GAGAATACTT GTCCCTGGAG GATTATCACA 840
CCCAAAATGC TAATCTCAT TAATGATTGA GGAGAGAAAA GGATCAGATT GCTGTTTCT 900
ACAATGGAGC AGGATATTGC TGAAGTCTCC TGGCATATGT TACCGAATCA ACTGGCCTTC 960
CAGAGGCTAA GAAATTTCTG TTAGTAAAAG ATGTTCTTTT TCCCAAAGCG TTTTATTGTA 1020
AAGGATAACT TGTGTTTGGG TTATTTTGTG TTCCACCTG TGCTGGTAGA TATTATTAA 1080
CCATTAGGTA AATACTATTA CAGTCGTGGT TTCTGCA

Seq ID NO: 302 Protein sequence:
Protein Accession #: Eos sequence

1 11 21 31 41 51
MTDKTEKVV DPETVFKRPR ECDSPSYQKR QRMALLARKQ GAGDSLIAGS AMSKEKKLMT 60
GHAIPPSQLD SQIDDFTFPS KDGMMQKPGS NAPVGGNVTS NFSGDDLECR GIASSPKSQ 120
EINADIKQV VKELRCVQKQ YEKIFEMLEG VQGPTAVRKR PFESIIEAAR CMRRDPVKHL 180
KXKLKRMI

Seq ID NO: 303 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 247-815

1 11 21 31 41 51
AGTGTTCGGC TGGGACAGGC ACGCTGTGGC TGGCTACTTC CCTTCCTTCC ATCCCCCTTG 60
GGCCAAACAG GATCGGTGCT TCTGGTGAGA CGTCTCCCCA TGCACATCAC TCCAGATGTC 120
CCTAGGGGGC ACATTTCCCA CACTCCCAG AGGGCAGGTT TCTAGAAAGT GCCACCAAGT 180
GGGAGGCGCC ACACTTCAC TGCCATTTTG TGAGGTGCCG CCGTCTCTCC TCCAGCAAGG 240
GAAACAATGA CCGATAAAAC AGAGAAGGTG GCTGTAGATC CTGAAACTGT GTTTAAACGT 300
CCCAGGGAAT GTGACAGTCC TTCGTATCAG AAAAGGCAGA GGATGGCCCT GTTGGCAAGG 360
AAACAAGGAG CAGGAGACAG CCTTATTGCA GGCTCTGCCA TGTCCAAAGC AAAGAGCTTA 420
TGACAGGACA TGCTATTCCA CCCAGCCAAT TGGATTCTCA GATTGATGAC TTCCTGGTT 480
TCAGCAAAAG TAGGATGATG CAGAAACCTG GTAGCAATGC ACCTGTGGGA GGAAACGTTA 540
CCAGCAGTTT CTCTGGAGAT GACCTAGAAT GCAGAGAAAC AGCCTCCTCT CCCAAAGCC 600
AACAGAAAT TAATGCTGAT ATAAACGTA AATTAGTGAA GGAACCTCGA TCGTGTGGAC 660
AAAAATATGA AAAATCTTC GAAATGCTTG AAGGAGTGCA AGGACCTACT GCAGTCAGGA 720
AACGATTTTT TGAATCCATC ATCAAGGAAG CAGCAAGATG TATGAGACGA GACTTTGTTA 780
AGCACCTTAA GAAGAAACTG AAACGTATGA TTTGAGAATA CTTGTCCCTG GAGGATTATC 840
ACACCCCAAA TGCATAAATCT CGTTAATGAT TGAGGAGAGA AAAGGATCAG ATTGCTGTTT 900
TCTACAATGG AGCAGGATAT TGCTGAAAGTC TCCTGGCATA TGTTACCGAA TCAACTGGCC 960
TTCCAGAGGC TAAGAAATTT CTGTTAGTAA AAGATGTTCT TTTTCCCAA GCGTTTTATT 1020
TGAAAGGATA ACTTGTGTTT TGGTTATTTT GTATTCCAC CTGTGCTGGT AGATATTATT 1080
AACCCATTAG GTAAATACTA TTACAGTCGT GGTTCCTGCA

Seq ID NO: 304 Protein sequence:
Protein Accession #: Eos sequence

1	11	21	31	41	51	
MTDKTEKVAV	DPETVFKRPR	ECDSPSYQKR	QRMALLARKQ	GAGDSLIAGS	AMSKAKKLMT	60
GHAIPPSQLD	SQIDDPFGFS	KDRMMQKPGS	NAPVGNVTS	SFSGDDLECR	ETASSPKSQQ	120
ENADIKRKL	VKELRCVQK	YEKIFEMLEG	VQGPTAVRKR	FFESIKEAA	RCMRRDFVKH	180
LKKKLKRLMI						

Seq ID NO: 305 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 87-689

1	11	21	31	41	51	
CGTGGAGGCA	GCTAGCGCGA	GGCTGGGGAG	CGCTGAGCCG	CGCGTCGTGC	CCTGCGCTGC	60
CCAGACTAGC	GAACAATACA	GTCAGGATGG	CTAAAGGTGA	CCCCAAGAAA	CCAAAGGGCA	120
AGATGTCCGC	TATGCGCTTC	TTTGTGCAGA	CATGCAGAGA	AGAACATAAG	AAGAAAAACC	180
CAGAGGTCCC	TGTCATTTT	GCGGAATTTT	CCAAGAAGTG	CTCTGAGAGG	TGGAAGACGA	240
TGTCGCGGAA	AGAGAAATCT	AAATTTGATG	AAATGGCAAA	GGCAGATAAA	GTGCGCTATG	300
ATCGGGAAT	GAAGGATTAAT	GGACCAAGCTA	AGGGAGGCAA	GAAGAAGAAG	GATCCTAATG	360
CTCCCAAAAG	GCCACCGTCT	GGATCTCTCC	TGTTCTGTTC	AGAATTCGCG	CCCAAGATCA	420
AATCCACAAA	CCCCGGCATC	TCTATTGGAG	ACGTGGCAAA	AAAGCTGGGT	GAGATGTGGA	480
ATAATTAAAA	TGACAGTGAA	AAGCAGCCTT	ACATCACTAA	GGCGGCAAG	CTGAAGGAGA	540
AGTATGAGAA	GGATGTGTCT	GACTATAAGT	CGAAAGGAAA	GTTTGATGGT	GCAAAGGGTC	600
CTGCTAAAGT	TGCCCGGAAA	AAGGTGGAAG	AGGAAGATGA	AGAAGAGGAG	GAGGAAGAAG	660
AGGAGGAGGA	GGAGGAGGAG	GATGAATAAA	GAAACTGTTT	ATCTGTCTCC	TTGTGAATAC	720
TTAGAGTAGG	GGAGGCGCAT	AATTGACACA	TCTCTTATT	GAGAAGTGTC	TGTTGCCCTC	780
ATTAGGTTTA	ATTACAAAAT	TTGATCACGA	TCATATTGTA	GTCTCTCAAA	GTGCTCTAGA	840
AATTGTCACT	GGTTTACATG	AAGTGGCCAT	GGGTGTCTGG	AGCACCTCGA	AACTGTATCA	900
AAGTTGTACA	GTATTTCCAA	CATTTTAAAA	ATGAAAAGGC	ACTCTCGTGT	TCTCTCACT	960
CTGTGCACAT	TGCTGTTGGT	GTGACAAGGC	ATTTAAAGAT	GTTTCTGGCA	TTTTCTTTTT	1020
ATTGTAAAG	TGTTGGTAAC	TATGTTTATT	GGCTAGAAAT	CCTGAGTTTT	CAACTGTATA	1080
TATCTATAGT	TTGTA AAAAG	AACAAAACAA	CCGAGACAAA	CCCTTGATGC	TCCTTGCTCG	1140
GCGTTGAGGC	TGTGGGGAAG	ATGCCTTTGG	GGAGAGGCTG	TAGCTCAGGG	CGTGCACTGT	1200
GAGGCTGGAC	CTGTTGACTC	TGCAGGGGGC	ATCCATTTAG	CTTCAGGTGT	TCTTGTCTCT	1260
GTATATAGTG	ACATAGCATT	CTGCTGCCAT	CTTAGCTGTG	GACAAAGGGG	GGTCAGCTGG	1320
CATGAGAATA	TTTTTTTTTT	TAGTGGCGGT	AGTTTTTAAA	CTGTTTGTGT	TTAAACAAAC	1380
TATAGAACTC	TTCAATTGTC	GCAAAACAAA	GAGTCACTGC	ATCAATGAAA	GTTCAAGAAC	1440
CTCCTGTACT	TAAACACGAT	TCGCAACGTT	CTGTTATTTT	TTTTGTATGT	TTAGAATGCT	1500
GAAATGTTTT	TGAAGTTAAA	TAAACAGTAT	TACATTTTTA	AAACTCTTCT	CTATTATAAC	1560
AGTCAATTTT	TGACTCACAG	CAGTGAACAA	ACCCCCACTC	CATTGTATTT	GGAGACTGGC	1620
CTCCCTATAA	ATGTGGTAGC	TTCTTTTATT	ACTCAGTGGC	CAGCTCACTT	AGGGCTGAGA	1680
TGAAGGAGAG	GGCTACTTGA	AGCTACTGTG	TGATTTTGT	TGTGTCTGAG	TGGCATTTCAG	1740
ATGAAGTCTG	GAGGAGTTAG	GAGAACGACA	TAGGCAAGGT	TCAGCAGCCT	TCCAAGGTAT	1800
AGGAAGGTGG	GTGATTAGGA	CTGAGGCTAT	CTAGGTTTAA	CTTTTGTCCC	ACCTCCACCC	1860
CCATTATTTG	GGGGCCCAAT	GCATTGCTAA	ACAGCAATTT	CAGAGTGTAT	GGTGTGTCAA	1920
AAATTAAGGC	TTTATTGTTT	TTCTCTTTCA	CCCCTACCCC	CCGTGCTCCT	GGCACATATC	1980
ACATTATTTG	TGCTGCCCAA	CATTGCGGCT	CTTGAGCCTG	CTGCTGGTCT	CCTGGATGCC	2040
AGTGAGGGTA	TGTGGGATGG	GGTGGTGGGG	TAGGGGACGG	TATCCTTTTT	TTGCTCTTAC	2100
TTGGAAACAC	CAAAACACCC	AAGGAAGATG	ATAGGCTCCA	TCITGGGCCA	CCTGAGCTAT	2160
AGGGCAGGCT	AATGGAATCA	ACCATTCTG	AGCACTAAAT	GTATCATGAA	AAGTTGAATG	2220
GCCTGCTCAT	GAATTTAGCT	CATTCAGTGG	AAATGTAGAT	TGATGTTCAA	TGTTAAACTG	2280
GAAGGAGCTT	GGTTTGTGTG	TCAGTGGTTA	TATTAGTGGG	TAGTGTAAAC	TTTATCCAG	2340
GTGCGGTGA	GGGGAGATGG	CCACAGTAGC	AAGTGGTGAC	ACTAAATACC	ATTTTGAAGG	2400
CTGATGTGTA	TATACATCAT	TACTGTCCGT	AGCAATGAAG	GATACAGTAC	TGTGTGTGG	2460
GTGAGTGTG	CTATTGCCCA	GCATTAATAT	TTGGGTGTGT	ATGTTTGAGG	CTATGAAACA	2520
CGCAGGAGTG	TTTTTGCTCT	ATTAATTTTA	AGAGAAAGCA	GCTTTTCTCT	AAAATTCACT	2580
GTGAGAAAC	TTGCATGTCT	GGAGGCGGTG	TCCTCTCCGC	CCGTGCGGGT	CCTGGATGAG	2640
TACGAGTTAT	GGTCACGCTG	CTCTTATGTG	TTCATAGCCA	TTGCTCTCC		2700
CATCAGAACT	GTTTGTCTG	AATGTGTCTC	TCTAGTTCTA	GAAAATGACC	ACTAATTTAA	2760
AAAACTCGGT	TGTGAGGTTT	GCCGAGAGGC	ACTTGTCTCA	GAATTTCCCC	TCCTGCTTCA	2820
GCCATGTCT	TGTCAGTTGG	CATTCTAAGC	TAAAGCTTTA	GCTTCCCAAT	TCGTGATGTG	2880
CTAGGCCAAG	ATTCGGGAGC	TGTTGCCAGC	CTCGTCAAAT	ATGGAAGAGA	AACAACCTGC	2940
GGTCAAAAGG	GAGTGAATTT	TAAAGTGGTG	CGCGTCTATC	TCATAACTAG	ATGTACCAAC	3000
CAGGGAAGGG	CCAAGGATGG	AAAGGGGTAA	CTTTTGTGCT	TCCAAGTAG	CTAAGCAGAA	3060
TGTGGGGAGC	AGTTTAGCCA	GATGATCTTT	GATTAGGCAA	ACATTGAGTT	TTAAAGAGGC	3120
TGTCAAGTTG	AGGCCACTTG	GTCCATTAGC	TGGGGCAGCA	AGATCACTAC	TCAACGTTTT	3180
CACACTGTGG	CAAGATTGCT	CTTCTAGTGG	ATAATGCCCC	TAGTTTCTCT	GAGATGATGT	3240
AAGTGGCATG	ATGTTACCTA	AGGCTTAGGC	TTAGCTTGAT	TTCTGGGCCC	ACTGTCTGTG	3300
TTCTTAAGAT	GCCAACCTGT	TGCTTTTTTT	TTTTTTTTCC	CCCATTTAAA	AGGATAGTAC	3360
CTACTCCCTC	TAACCACTCT	ACCCATTCT	TGAATGACAT	TTTATCCTTC	GGAAAGAACA	3420
AGGCTGTGAT	GTAGTGACTA	TTGTCTGTGT	CTCCGTGTGT	TGTCTGTCT	TGTCACAAAT	3480
GTATTTGGGG	ACGTTGGATG	CATTCATTTT	CTGTAATAAA	G		

Seq ID NO: 306 Protein sequence:
Protein Accession #: NP_005333.1

1	11	21	31	41	51	
MAKGDPPKKP	GKMSAYAFV	QTCREBHKKK	NPEVPVNFAB	FSKKCSERNK	TMSGKEKSKP	60
DEMAKADKVR	YDREMKDYGP	AKGGKKKKDP	NAPKRPSPGF	FLFCSEFRPK	IKSTNPGISL	120
GDVAKKLGE	WNLNDSBKQ	PYITKAAKLG	EKYEKDVADY	KSKGKFGAK	GPAKVARKKV	180
EEEEEEEEEE	EEEEEEEEEE					

Seq ID NO: 307 DNA sequence
Nucleic Acid Accession #: NM_022342
Coding sequence: 1..2178

	1	11	21	31	41	51	
5	ATGGGTACTA	GGAAAAAAGT	TCATGCATTT	GTCCGTGTCA	AACCCACCGA	TGACTTTGCT	60
	CATGAAATGA	TCAGATACGG	AGATGACAAA	AGAAGCATTG	ATATTCACCT	AAAAAAGAC	120
	ATTCGGAGAG	GAGTTGTCAA	TAACCAACAG	ACAGACTGGT	CGTTTAAGTT	GGATGGAGTT	180
	TTCACGATG	CCTCCACGGA	CTTGGTTTAT	GAGACAGTTG	CAAAGGATGT	GGTTTCTCAG	240
	CCCTCGATG	GCTATAATGG	CACCATCATG	TGTTATGGGC	AGACGGGAGC	TGGCAAGACA	300
10	ACACCATGA	TGGGGGCAAC	TGAGAATTAC	AAGCACCGGG	GGATCCTCCC	TCGTGCCCTG	360
	AGCAGGTTT	TTAGGATGAT	CGAAGAACGC	CCCACACATG	CCATCACTGT	GCGTGTTTCC	420
	ACCTGGAAA	TCTATAATGA	GAGCCTGTTT	GATCTCCTGT	CCACTCTGCC	CTATGTTGGA	480
	CCTCAGTCA	CACCAATGAC	CATCGTGAAA	AACCTCAAG	GAGTCTTCAT	TAAGGGCTTG	540
	CAGTTTACC	TCACAAGTCA	GGAGGAGGAT	GCATTCAGCC	TCCTTTTGA	GGGTGAGACC	600
15	ACAGGATTA	TAGCTCCCA	CACATGAAC	AAAAACTCTT	CCAGATCACA	CTGCATTTTC	660
	CCATCTACT	TAGAGGCCCA	TTCCCGGACC	TTATCAGAGG	AAAAGTACAT	CACCTCCAAA	720
	TTAAGTTGG	TGGATCTGGC	AGGCTCAGAG	AGGCTGGGGA	AGTCTGGGTC	TGAGGGCCAA	780
	TCCTGAAGG	AAGCCACCTA	CATCAACAAA	TCGCTCTCAT	TCCTGGAGCA	GGCCATCATT	840
	CCCTTGGGG	ACCAGAAAGC	GGACCACATC	CCCTTTCGGC	AGTGCAAGCT	CACCCACGCT	900
20	TGAAGGACT	CGTTAGGGGG	AAACTGCAAT	ATGGTCTCG	TGACAAACAT	CTATGGAGAA	960
	CTGCCAGT	TAGAAGAAAC	GCTATCTTCA	CTGAGATTTC	CCAGCAGGAT	GAAGCTAGTC	1020
	CCACTGAGC	TGCCCATCGA	TGAAAAGTAT	GATGCTGAGA	GAATGGTCAA	GAACCTGGAG	1080
	AGGAAGTAG	CACACTCTCA	GCAGGAGCTG	GCTATCCATG	ACAGCCTGAC	CAACCGCACC	1140
	TTGTGACCT	ATGACCCCAT	GGATGAAATC	CAGATTGCTG	AGATCAACTC	CCAGGTGCGG	1200
25	GGTACCTGG	AGGGGACACT	GGACGAGATC	GACATAATCA	GCCTTAGACA	GATCAAGGAG	1260
	GTGTTCAACC	AGTTCCGGGT	GGTCTGAGC	CAACAGGAAC	AGGAAGTGGG	GTCCACTTTG	1320
	GCAGGAAGT	ACACCTTCAT	TGACAGGAAT	GACTTTGCAG	CCATTTCTGC	TATCCAGAA	1380
	CGGGGCTTG	TGGATGTTGA	TGGCCACCTA	GTGGGTGAGC	CTGAAGGACA	AAACTTTGGA	1440
	TCGGAGTCG	CCCCTTTCTC	TACCAAACTT	GGGAAGAAAG	CCAAGTCCAA	GAAGACATTC	1500
30	AAGAGCCAC	TCAGAGCCGA	CACCCACCCC	TCCAAACCCG	TGGCCCTTGA	GGAGTTTAAG	1560
	ATGAGCAAG	GTAGTGAGAT	CAACCGAATT	TTCAAAGAAA	ACAATCCAT	CTTGAATGAA	1620
	GGAGGAAAA	GGCCGAGCGA	GACCAACACG	CACATCAATG	CCATCAAGCG	GGAGATTGAT	1680
	TGACCAAGG	AGGCCCTGAA	TTTCCAGAAG	TCACTACGGG	AGAAGCAAGG	CAAGTACGAA	1740
	ACAAGGGGC	TGATGATCAT	CGATGAGGAA	GAATTCCTGC	TGATCCTCAA	GCTCAAAGAC	1800
35	TCAAGAAGC	AGTACCGCAG	CGAGTACCAG	GACCTGCGTG	ACCTCAGGGC	TGAGATCCAG	1860
	ATTGCCAGC	ACCTAGTGGG	TCAGTGTGCG	CACCGCCTGC	TCATGGAATT	TGACATCTGG	1920
	ACAATGAGT	CCTTTGTGAT	CCCTGAGGAC	ATGCAGATGG	CACTGAAGCC	AGGCGGCAGC	1980
	TCCGGCCAG	GCATGCTCCC	TGTGAACAGG	ATTGTGTCTC	TGGGAGAAGA	TGACCAGGAC	2040
	AATTGAGCC	AGCTGCAGCA	GAGGGTGCTT	CCTGAGGGCC	CTGATTCAT	CTCCTTCTAC	2100
40	ATGCCAAAG	TCAAGATAGA	GCAGAAGCAT	AATTACTTGA	AAACCATGAT	GGGCTCCAG	2160
	AGGCACATA	GAATAATG					

Seq ID NO: 308 Protein sequence:
Protein Accession #: NP_071737

45	1	11	21	31	41	51	
	MGTRKKVHAF	VRVKPTDDFA	HEMIRYDDDK	RSIDIHLKID	IRRGVVNNQ	TDWSFKLDGV	60
	LHDASQDLVY	ETVAKDVVSQ	ALDGYNGTIM	CYGGTGAAGT	YTMGATENY	KHRGILPRAL	120
50	QQVFRMIER	PTHAITVRVS	YLEIYNESLF	DLLSTLPYVG	PSVTPMIVE	NPQGVPIKGL	180
	SVHLTSQED	AFSLPPEGET	NRIIASHTMN	KNSSRSHCIF	TIYLEAHSRT	LSEKYITSK	240
	INLVDLAGE	RLGKSGGEG	VLKEATYINK	SLSFLEQAI	ALGDQKRDI	PFRQCKLTHA	300
	LKDSLGNCN	MVLVTNLYGE	AAQLEETLSS	LRFASRMKLV	TTEPAINEKY	DAERMVKNLE	360
	KELALLKQEL	AIHDSLTNRT	FVTYDPMDEI	QIAEINSQVR	RYLEGLDEI	DIISLRQIKE	420
55	VFNQFRVVL	QQEQEVSTL	RRKYTLIDRN	DFAAISAIQK	AGLVDDVDGHL	VGEPEQGNFG	480
	LGVAPESTK	GKKAKSKKTP	KEPLRPDTPP	SKPVAEEFCK	NEQGSSEINRI	FKENKSIKLE	540
	RRKRASETQ	HINAIKREID	VTKEALNFQK	SLREKQGYE	NKGLMIIDEE	EPFLILKLD	600
	LKKQYRSEYQ	DLRLDLRAEQ	YCQHLVDQCR	HRLLMEFDIW	YNESFVIPED	MQMALKPGGS	660
60	IRPGMVPVNR	IVSLGEDDQD	KFSQLQQRVL	PEGPDSISFY	NAKVKIEQKH	NYLKTMMGLQ	720
	QAHRK						

Seq ID NO: 309 DNA sequence
Nucleic Acid Accession #: CAT cluster

65	1	11	21	31	41	51	
	TTTTTTTTTT	TTTTTTTTAA	TGCTGCTGT	CATGCTCTGT	CTACCAGGGT	GAATTTCCAA	60
	AAATTTCTGC	ATAGCAATTT	TAGCCAAAAC	TATATATGTT	CTGGGGAGGA	TAGGCATAGG	120
	CACATTGAAG	ACCAAGAGAA	AGAGTGAAGA	AGTGTAGTTG	GGTCATTGTG	AATGGATGTT	180
70	TAGATTGTCA	AGAAAAGTGG	GCCAGAGGCC	CCACCTCACA	CTAGGACGGC	AATGCTCTCT	240
	CATTAGTATC	TCAGGCACCA	TGGGTCTTAT	TTGGTGTGTC	AAGAAACACC	CTCAACAAAG	300
	TAATGAACCC	TCAGCCTCCA	GCTTCTCTTC	TTCCGGGATTC	TTCTTAGGGC	CTCCTTTTTC	360
	CTTTTATGTT	TCCAGTACCC	TGAATTTCTT	ATTCCCATCC	CCCATTAATA	TCGTCTTCAA	420
	AGAAAAAACA	AGAAGGACAC	ATTCATTTTA	AGATCCAAAT	GAATGATAAG	AGCTTAAAC	480
75	ATTATACTTA	TCAGTATTAT	TTGCATTTTT	ATAGAAACCA	AAACCATATT	TCAACAAAC	

Seq ID NO: 310 DNA sequence
Nucleic Acid Accession #: NM_018622.2
Coding sequence: 1-1140

80	1	11	21	31	41	51	
	ATGGCGTGGC	GAGGCTGGGC	GCAGAGAGGC	TGGGGCTGGC	GCCAGGCGTG	GGGTGCGTCG	60
	GTGGGCGGGC	GCAGCTGCGA	GGAGCTCACT	GCGGTCCTAA	CCCCGCGCGA	GCTCCTCGGA	120
85	CGCAGGTTTA	ACTTCTTTAT	TCAACAAAAA	TGCGGATTCA	GAAGAAGCACC	CAGGAAGGTT	180
	GAACCTCGAA	GATCAGACCC	AGGGACAAGT	GGTGAAGCAT	ACAAGAGAAG	TGCTTTGATT	240
	CCTCCTGTGG	AAGAAACAGT	CTTTTATCCT	TCTCCCTATC	CTATAAGGAG	TCTCATAAAA	300
	CCTTTATTTT	TTACTGTTGG	GTTTACAGGC	TGTGCATTGG	GATCAGCTGC	TATTTGGCAA	360

TATGAATCAC TGAATCCAG GGTCCAGAGT TATTTTGATG GTATAAAAGC TGATTGGTTG 420
 GATAGCATAA GACCACAAAA AGAAGGAGAC TTCAGAAAGG AGATTAACAA GTGGTGGAAAT 480
 AACCTTAAGTG ATGCCCAGCG GACTGTGACA GGTATTATAG CTGCAAAATGT CCTTGTATTTC 540
 TGGTTATGGA GAGTACCTTC TCTGCAGCGG ACAATGATCA GATATTTTAC ATCGAATCCA 600
 GCCTCAAAGG TCCTTTGTTC TCCAATGTTG CTGTCAACAT TCAGTCACTT CTCTTATTTC 660
 CACATGGCAG CAAATATGTA TGTTTGTGG AGCTTCTCTT CCAGCATAGT GAACATTCTG 720
 GGTCAAGAGC AGTTCATGGC AGTGTACCTA TCTGCAGGTG TTAATTTCCAA TTTTGTCACT 780
 TACCTGGGTA AAGTTGCCAC AGGAAGATAT GGACCATCAC TTGGTGCATC TGGTGGCATC 840
 ATGACAGTCC TCGCAGCTGT CTGCACTAAG ATCCCAAGAG GGAGGCTTGC CATATTTTTC 900
 CTTCGGATGT TCACGTTTCA AGCAGGGAAT GCCCTGAAAG CCATATCTGC CATGGATACA 960
 GCAGGAATGA TCCTGGGATG GAAATTTTTT GATCATGCGG CACATCTTGG GGGAGCTCTT 1020
 TTTGGAATAT GGTATGTTAC TTACGGTCAT GAACTGATTT GGAAGAACAG GGAGCCGCTA 1080
 GTGAAATCT GGCATGAAAT AAGGACTAAT GGCCCCAAAA AAGGAGGTGG CTCTAAGTAA

Seq ID NO: 311 Protein sequence:
 Protein Accession #: NP_061092.2

1 11 21 31 41 51
 MANRWQAQRG WGCQQAQWAS VGGRSCEELT AVLTPPQLLG RRFNFFIQOK CGFRKAPRKV 60
 EPRRSDPGTS GEAYKRSALI PPVEETVFYP SPYPFIRSLIK PLFPTVGFPTG CAFGSAAIWQ 120
 YSLKSRVQS YFDGIKADWL DSRPQKEGD FRKEINKWNN NLSDGQRTVT GIIAANVLVF 180
 CWMRVPSLQR TMIRYFTSNP ASKVLCSPLM LSTFHSFSLF HMAANMYVLW SFSSSIVNII 240
 GGEQFMAYVL SAGVISNFVS YLGKVAATRY GPSLGAAGAI MVLVAAVCTK IPEGLRAIIF 300
 LPMFTFTAGN ALKAIANDT AGMILGWKFP DHAHLGGAL FGIWYVTYGH ELIWKNNREPL 360
 VKIWHEIRTN GPKKGGGSK

Seq ID NO: 312 DNA sequence
 Nucleic Acid Accession #: NM_000625
 Coding sequence: 195..3656

1 11 21 31 41 51
 CTCTCGGCCA CCTTTGATGA GGGGACTGGG CAGTTCTAGA CAGTCCCGAA GTTCTCAAGG 60
 CACAGGTCTC TTCCTGGTTT GACTGTCTCT ACCCCGGGGA GGCAGTGCAG CCAGCTGCAA 120
 GCCCCACAGT GAAGAACATC TGAGCTCAAA TCCAGATAAG TGACATAAGT GACCTGCTTT 180
 GTAAAGCCAT AGAGATGGCC TGTCTTGGGA AATTTCTGTT CAAGACCAAA TTCCACCAGT 240
 ATGCAATGAA TGGGGAAAAA GGCATCAACA ACAATGTGGA GAAAGCCCCC TGTGCCACCT 300
 CAGTCCAGT GACACAGGAT GACCTTCAGT ATCACAACCT CAGCAAGCAG CAGAATGAGT 360
 CCCCCGAGCC CCTCGTGGAG ACGGGAAGA AGTCTCCAGA ATCTCTGGTC AAGCTGGATG 420
 CAACCCCATT GTCCTCCCCA CGGCATGTGA GGATCAAAAA CTGGGGCAGC GGGATGACTT 480
 TCCAAGACAC ACTTCACCAT AAGGCCAAAG GGATTTTAAC TTGCAGGTCC AAATCTTGCC 540
 TGGGGTCCAT TATGACTCCC AAAAGTTTGA CCAGAGGACC CAGGGACAAG CCTACCCCTC 600
 CAGATGAGCT TGTACCTCAA GTATCGAAT TTGTCAACCA ATATTACGGC TCCCTCAAAG 660
 AGGCAAAAT AGAGGAACAT CTGGCCAGGG TGGAAAGCGT AACAAAGGAG ATAGAAACAA 720
 CAGTAACCTA CCAACTGACG GGAGATGAGC TCATCTTCGC CACCAAGCAG GCCTGGCGCA 780
 ATGCCCCACG CTGCATTGGG AGGATCCAGT GGTCCAACCT GCAGGTCTTC GATGCCCGCA 840
 GCTGTTCCAC TGCCCGGGAA ATGTTTGAAC ACATCTGCAG ACACGTGCGT TACTCCACCA 900
 ACAATGGCAA TCGGAAGTTC GGCATCACCG TGTCCCCCA GCGGAGTGAT GGCAAGCAG 960
 ACTTCGGGTT GTGGAATGCT CAGCTCATCC GCTATGCTGG CTACCAAGATG CCAGATGGCA 1020
 GCATCAGAGG GGACCTGACC AACGTGGAAT TCACTCAGCT GTGCATCGAC CTGGGCTGGA 1080
 AGCCCAAGTA CGGCCGCTTC CATGTGGTCC CCCTGGTCTC GCAGGCCAAT GGCCGTGACC 1140
 CTGAGCTCTT CGAATCCCA CCTGACCTTG TGCTTGAGGT GGCCATGGAA CATCCCAAT 1200
 ACGAGTGGTT TCGGAAGTTC GAGCTAAAGT GGTACGCCCT GCCTGCAGTG GCCAACATGC 1260
 TGCTTGAGGT GGGCGGCTCG GAGTTCCTCAG GGTGCCCTCT CAATGGCTGG TACATGGGCA 1320
 CAGAGATCGG AGTCGGGAGC TCTGTGATG TCCAGCGCTA CAACATCTCG GAGGAAGTGG 1380
 GCAGGAGAAT GGGCCTGGAA ACGCACAAGC TGGCCTCGCT CTGGAAGAGC CAGGCTGTCT 1440
 TTGAGATCAA CATTTGCTGT CTCCATAGTT TCCAGAAGCA GAATGTGACC ATCATGGACC 1500
 ACCACTCGGC TGCAGAAATC TTCTGAAAGT ACATGCAGAA TGAATACCGG TCCCGTGGGG 1560
 GCTGCCCGGC AGACTGGATT TGGCTGGTCC CTCCCATGTC TGGGAGCATC ACCCCCGTGT 1620
 TTCACCAGGA GATGCTGAAC TACGTCCTGT CCCCCTTCTA CTACTATCAG GTAGAGGCCT 1680
 GGAAAACCCA TGTCTGGCAG GACGAGAAGC GGAGACCCAA GAGAAGAGAG ATTCCATTGA 1740
 AAGTCTTGTT CAAAGCTGTG CTCTTTGCCT GTATGCTGAT GCGCAAGACA ATGGCGTCCC 1800
 GAGTCAGAGT CACCATCTCT TTTGCGACAG AGACAGGAAA ATCAGAGGCG CTGGCCTGGG 1860
 ACCTGGGGGC CTTATTGAGC TGTGCTTCA ACCCCAAAGT TGTCTGCATG GATAAGTACA 1920
 GGCTGAGCTG AGCTGGAGAG GAACGGCTGC TGTGGTGGT GACCAAGTAC TTTGGCAATG 1980
 GAGACTGCCC TGGCAATGGA GAGAACTGA AGAAATCGCT CTTATGCTG AAAGAGCTCA 2040
 ACAACAAATT CAGGTACGCT GTGTTTGGCC TGGGCTCCAG CATGTACCTT CGGTTCTGCG 2100
 CCTTTGCTCA TGACATTGAT CAGAAGCTGT CCCACTGGG GGCCTCTCAG CTCACCCGGA 2160
 TGGGAGAAGG GGATGAGCTC AGTGGGCAAG AGGACGCCCT CCGCAGCTGG GCCGTGCAAA 2220
 CCTTCAAGGC AGCTGTGAGT ACGTTTGATG TCCGAGGCAA ACAGCACATT CAGATCCCCA 2280
 AGCTCTACAC CTCCAAATGT ACCTGGGACC CGCACCACTA CAGGCTCGTG CAGGACTCAC 2340
 AGCCTTTGGA CCTCAGCAAA GCCTCAGCA GCATGCATGC CAAGAACGTG TTCACCATGA 2400
 GGCTCAAAAT TCGGCAGAAAT CTACAAAGTC CGATGCCAGC CCGTGCCACC ATCTGGTGG 2460
 AACTCTCTCT TGAGGATGGC CAAGGCTTGA ACTACCTGCC GGGGGAGCAC CTGGGGTTT 2520
 GCCCAGGCAA CACGCCGGCC CTGGTCCAA GATCTCTGGA GCGAGTGGTG GATGGCCCCA 2580
 CACCCACCA GGCAGTGGC CTGGAGGCC TGGATGAGAG TGGCAGTAC TGGGTGAGT 2640
 ACAAGAGGCT GCCCCCTGCT TCACTCAGCC AGGCCCTCAC CTACTTCTTG GACATCACA 2700
 CACCCCAAC CACGCTGTCTG TCCAAAAGC TGGCCAGGTG GGCCACAGAA GAGCCTGAGA 2760
 GACACAGGCT GAGAGCCCTG TGCCAGCCCT CAGAGTACAG CAAGTGGAGG TTCACCAACA 2820
 GCCCACAATT CTGGAGGTG CTAGAGGAGT TCCCGTCCCT GCGGTGTCTG GCTGGCTTCC 2880
 TGCTTTCCCA GCTCCCAATT CTGAAGCCCA GGTCTACTCT CATCAGTCTC CCCCAGGATC 2940
 ACACGCCCCC GGAGATCCAC GTGACTGTGG CCGTGGTCTC CTACCAACAC CGAGATGGCC 3000
 AGGTTCCCT GACCCAGGCT GTCTGCAGCA CATGGCTCAA CAGCCTGAAG CCCCAAGACC 3060
 CAGTGCCTCT CTTTGTGCGG AATGCCAGCG GCTTCCACTT CCCCAGGAGT CCTTCCCTATC 3120

CTTGATCCT CATCGGGCT GGCACAGGCA TCGCGCCCTT CCGCAGTTTC TGGCAGCAAC 3180
GGCTCCATGA CTCCAGCAC AAGGGAGTGC GGGGAGGCCG CATGACCTTG GTGTTTGGGT 3240
GCCGCGCCCC AGATGAGGAC CACATCTACC AGGAGGAGAT GCTGGAGATG GCCCAGAAGG 3300
GGGTGCTGCA TCGGCTGCAC ACAGCCTATT CCGCCTGCCC TGGCAAGCCC AAGGTCTATG 3360
5 TTGAGGACAT CCTGCGGCGAG CAGCTGGCCA GCGAGGTGCT CCGTGTGCTC CACAAGGAGC 3420
CAGGCCACCT CTATGTTTGC GGGGATGTGC GCATGGCCCG GGACGTGGCC CACACCCTGA 3480
AGCAGCTGGT GGCTGCCAAG CTGAAATTGA ATGAGGAGCA GGTGAGGAC TATTTCTTTC 3540
AGCTCAAGAG CCAGAAGCGC TATCAGCAAG ATATCTTTGG TGCTGTATT CTTCAGAGG 3600
10 CGAAGAAGGA CAGGGTGGCG GTGCAGCCCA GCAGCCTGGA GATGTGAGG CTCTGAGGCG 3660
CTACAGGAGG GGTAAAGCT GCCGCGACAG AACTTAAGGA TGGAGCCAGC TCTGCATTAT 3720
CTGAGGTAC AGGCCTGGG GAGATGGAGG AAAGTGATAT CCCCAGCCT CAAGTCTTAT 3780
TTCCTCAAG TTGCTCCCA TCAAGCCCTT TACTTGACCT CCTAACAAAG AGCACCTGG 3840
ATTGATCGGA GCCTC

Seq ID NO: 313 Protein sequence:
Protein Accession #: NP_000616

1 11 21 31 41 51
MACPWKFLPK TKFHQYAMNG EKGINNVEK APCATSSPVT QDDLQYHNLS KQONESPQPL 60
VETGKKSPES LVKLDATPLS SPRHVRKNW GSGMTFQDTL HRKAKGILTC RSKSCLGSIM 120
TPKSLTRGRP DKPTPPDELL PQAIEFVNQY YGSLKEAKIE EHLARVEAVT KEIETTIVTYQ 180
25 LTGDELIPAT KQAWRNAEPRC IGRIQWSNLQ VFDARSCSTA REMPEHICRH VRYSTNNNGNI 240
RSAITVFPQR SDGKHDPRVW NAQLIRYAGY QMPDGSIRGD PANVEFTQLC IDLGWPKPYG 300
RFDVVLVLQ ANGRDPELFE IPPDLVLEVA MEHPKYEWFR EELKWKYALP AVANMLLEVE 360
GLEPPGCPFN GWYMGTEIGV RDPFDVQRYN ILEEVGRRMG LETHKLASLW KDQAVVEINI 420
AVLHSFQKQN VTIMDHSSAA ESPMKYMQNE YRSRGCCPAD WILVPPMSG SITPVFHEQM 480
30 LNYVLSPPFY YQVFAWKTHV WQDEKRRPKR REIPLKVLVK AVLPAFMLMR KTMASRVVVT 540
ILFATETGKS EALAWDLGAL FSCAPNPKVV CMDKYRLSCL EEEERLLVVT STFGNGDCPG 600
NGEKLKLSLF MLKELNNKFR YAVFGLGSSM YPRFCFAFHD IDQKLSHLGA SOLTPMGECD 660
ELSGQEDAFR SWAVQTFKAA CETFDVRGKQ HIQIPKLYTS NVTWDPHYR LVQDSQPLDL 720
SKALSSMHAK NVFTMRKLSR QNLQSPSSR ATILVELSCE DGQGLNLYPG EHLGVCPGNQ 780
35 PALVQGILER VVDGTPHQVA VRLEALDESG SYWVSDKRLP PCSLSQALTY FLDITTPPTQ 840
LLLQKLAQVA TEEPERQRL EALCQPSSEYK WKFTNSPTFL EVLEEFPSLR VSAGFLLSQL 900
PILKPRFYSI SSPRDHTFTE IHLTVAVVTV HTRDGGGPLH HGVCSTWLSN LKQDFVPCF 960
VRNAGFHLF EDPSPHCILI GPGTGIAPFR SFWQQRHDS QHKGVRGGRM TLVFGCRRPD 1020
EDHIYQEML EAMQKGLVLA VHTAYSRLPG KPKVYVDIL RQQLASEVLR VLEKEPGHLY 1080
40 VCGDVRMARD VAHLKQLVA AKLKLNEEQV EDYFFQLKSQ KRYHEDIFGA VFPYEAKKDR 1140
VAVQPSSELM SAL

Seq ID NO: 314 DNA sequence
Nucleic Acid Accession #: XM_087254
Coding sequence: 47..2332

1 11 21 31 41 51
AGAGTACGTG TTACAGATA AAACCTGGTAC ACTGACAGAA AATGAGATGC AGTTTCGGGA 60
50 ATGTTCAATT AATGGCATAA AATACCAAGA AATTAATGGT AGACTTGTAC CCGAAGGACC 120
AACACAGAC TCTTCAGAGA GAAACTTATC TTATCTTAGT AGTTTATCCC ATCTTAACAA 180
CTTATCCCAT CTACACCAAG GTTCTCTTT CAGAACCACT CCTGAAATG AACTGAACT 240
AATTAAGAA CATGATCTCT TCTTTAAAGC AGTCAGTCTC TGTCACACTG TACAGATTAG 300
CAATGTTCAA ACTGACTGCA CTGGTGATGG TCCCTGGCAA TCCAACCTGG CACCATCGCA 360
55 GTTGGAGTAC TATGATCTT CACCATGATGA AAAGGCTCTA GTAGAAGCTG CTGCAAGGAT 420
TGGTATTGTC TTTATTGGCA ATTCTGAAGA AACTATGGAG GTTAAAACTC TTGAAAACT 480
GGAACGGTAC AAACCTGCTC ATATTCTGGA ATTTGATTCA GATCGTAGGA GAATGAGTGT 540
AATTGTTTCA GCACCTGTCAG GTGAGAAGTT ATTATTGCTT AAAGGAGCTG AGTCATCAAT 600
60 TCTCCCTAAA TGTATAGGTG GAGAAATAGA AAAAACCAGA ATTCATGTAG ATGAATTGTC 660
TTTGAAGAGG CTAAGAATCT TGTGTATAGC ATATAGAAAA TTTACATCAA AAGAGTATGA 720
GGAAATAGAT AAACGCTATG TTGAAGCCAG GACTGCCTTG CAGCAGCGGG AAGAGAAAT 780
GGCAGCTGTT TCCAGTTCAT TAGAGAAAGA CCTGATATTA CTGGAGCCCA CAGCAGTAGA 840
AGACAGCTA CAAGATAAAG TTCGAGAAAC TATTGAAGCA TTGAGAATGG CTGGTATCAA 900
65 AGTATGGGTA CTACTGGGG ATAAACATGA AACAGCTGTT AGTGTGAGTT TATCATGTGG 960
CCATTTCAT AGAACCATGA ACATCCTTGA ACTTATAAAC CAGAAATCAG ACAGCGAGTG 1020
TGCTGAACAA TTGAGGCAGC TTGCCAGAAG AATTACAGAG GATCATGTGA TTCAGCATGG 1080
GCTGGTAGTG GATGGGACCA GCCTATCTCT TGCACTCAGG GAGCATGAAA AACTATTTAT 1140
70 GGAAGTTTGC AGAATTTGTT CAGCTGTATT ATGCTGTGCT ATGGCTCCAC TGCAGAAAGC 1200
AAAAGTAATA AGACTAATAA AAATATCACC TGAGAAACCT ATACATTTGG CTGTTGGTGA 1260
TGGTGCTAAT GACGTAAGCA TGATACAAGA AGCCCATGTT GGCATAGGAA TCATGGGTAA 1320
AGAAGGAAGA CAGGCTGCAA GAAACAGTGA CTATGCAATA GCCAGATTTA AGTTCTCTC 1380
CAAAATGCTT TTTGTTGATG GTCAATTTTA TTATATTAGA ATAGCTACCC TTGTACAGTA 1440
TTTTTTTAT AAGAATGTGT GCTTTATCAC ACCCCAGTTT TTATATCATG TCTACTGTTT 1500
75 GTTTTCTCAG CAAACATTGT ATGACAGCGT GTACCTGACT TTATACAATA TTTGTTTAC 1560
TTCCCTACCT ATCTGATAT ATAGTCTTTT GGAACAGCAT GTAGACCCTC ATGTGTTACA 1620
AAATAAGCCC ACCCTTTATC GAGACATTAG TAAAAACCGC CTCTTAAGTA TTAACATT 1680
TCTTTATTGG ACCATCTGGG GCTTCAGTCA TGCTTTTATT TTCTTTTITG GATCCTATT 1740
ACTAATAGGG AAAGATACAT CTCTGCTTGG AAATGGCCAG ATGTTTGGAA ACTGGACATT 1800
TGGCACTTTG GTCATCAGAG TCATGTTTAT TACAGTCACA GTAAAGATGG CTCTGGAAC 1860
80 TCATTTTGG ACTTGGATCA ACCATCTGCT TACCCTGGGA TCTATTATAT TTTATTTTGT 1920
ATTTTCTTGG TTTTATGGAG GGATTCCTCTG GCCATTTTGG GGCTCCCGA ATATGTATT 1980
TGTGTTTATT CAGCTCCTGT CAAGTGGTTC TGCTTGGTTT GCCATAATCC TCATGTTTGT 2040
TACATGTCTA TTTCTTGATA TCATAAGAA GGTCTTTGAC CGACACCTCC ACCCTACAAG 2100
TACTGAAAAG GCACAGCTTA CTGAAACAAA TGCAAGTATC AAGTGCTTGG ACTCCATGTG 2160
85 CTGTTTCCCG GAAGGAGAAG CAGCTGTGCT ATCTGTGGA AGAATGCTGG AACGAGTTAT 2220
AGGAAGATGT AGTCCAACCC ACATCAGCAG ATCATGGAGT GCATCGGATC CTTTCTATAC 2280
CAACGACAGG AGCATCTTGA CTCTCTCCAC AATGGACTCA TCTACTTGT AAAGGGGAG 2340

Seq ID NO: 315 Protein sequence:
Protein Accession #: XP_087254

Seq ID NO: 316 DNA sequence
Nucleic Acid Accession #: NM_004473
Coding sequence: 661..1791

85 1 11 21 31 41 51
 | | | | |
CTCGCCAGCG GTCCGCGGGG CTGGAGACCC ACGCCGTGGA GAGGACCAGC CTCAGGTCCG 60

	CCCGCCTGGG	CCCGCGCCCC	GACCTCGCTG	CCCCCGCCTC	GCCTCTCTGC	CGTGGCGCT	120
	TACCGCCACC	TTGGCCTCGG	GGGCAGGBCA	TGGCGGGCCC	CCGCCAGATC	GCCCAGCGCC	180
	AGTACTAACT	GCCCTCGCTC	TGGCCTTCGA	GCCCGAAGCC	TCTTCTGCGC	GCACAACCTA	240
5	GGCAGTAATC	CTAAACTAGC	GGGCACCACA	GACCACTGTC	AGCCACCCCA	ACCCAGGGAT	300
	CACCTCCGGA	CCCCTCGACC	GCCCGGCACC	AGCGCGCAAG	GGACCCCTCA	GCCGAGAGCC	360
	AGAGTCCAGT	CCCCTCGCGG	AGGCCACCGC	CGCTGCCCGC	CTCGAGAAGC	ACAACGCGGG	420
	CTGAGCCGTC	GGCTAGCGGG	TCACTCCCGA	GCCTCTGTCT	GCACCGCGCC	AGCCCCAGAC	480
	CACGACGCT	GAGCCTCCAG	CGCGCGCCAG	CCTGGGCGCG	TGGGCTCTCC	GGGCCAGCCC	540
10	GCGACGATCC	CCTGAGCTCT	CGCAGAAAGG	GCCGAGCGTC	CGTTCGCGGG	ACGCCAGGCC	600
	CGCCCCCGCC	CCCCGACAGC	CGCGGGGATC	CAGAGCCCGG	GGGTGCGGGA	CGCCCCGCGC	660
	ATGACTGCCG	AGAGCGGGCC	GCCCGCGCCG	CAGCCGAGAG	TGCTGGCTAC	CGTGAAGGAA	720
	GAGCGCGGGG	AGAGCGGCAG	AGGGGCGGGG	GTCCCGAGGG	AGGCCACGGG	CGCGGGGCGG	780
	GGCGGGCGGC	GCCCAAGCGG	CCCCCTGCAG	CGCGGGAAGC	CGCCCTACAG	CTACATCGCG	840
	CTCATCGCCA	TGGCGCTGCG	GACGCGCGCC	GAGCGCGCGC	TCACGCTGGG	CGGCATCTAC	900
15	AAGTTTATCA	CCGAGCGCTT	CCCCTTCTAC	CGCGACAACC	CCAAAAAGTG	GCAGAACAGC	960
	ATCCGCCACA	ACCTCACACT	CAACGACTGC	TTCCTCAAGA	TCCGCGCGCA	GGCGGCGCGC	1020
	CCGGGTAAGG	GCAACTACTG	GGCGCTCGAC	CCCAACGCGG	AGGACATGTT	CGAGAGCGGC	1080
	AGCTTCTCTC	GCCCGCGCAA	GCGCTTCAAG	CGCTCGGACC	TCTCCACCTA	CCCGGCTTAC	1140
	ATGACGAGC	CGGCGCTGCG	CGCAGCCGCG	GCTGCCGCGC	CCGCGCGCGC	CGCGCGCGCC	1200
20	GCGGCCATCT	TCCAGGCGCG	GGTGCCCGCC	GCGCGCGCCC	CCTACCCGGG	CGCGGCTCTAT	1260
	GCAGGCTACG	CGCGCGCGCG	CGCGCTCCAG	TCTACTACCC	CGCGGCGTCG		1320
	CCGCGCCCTT	GCCGCGCTCT	CGGCGTGGTT	CCTGAGCGGC	CGCTCAGCCC	AGAGCTGGGG	1380
	CCCGCACCGT	CGGGGCGCGG	CGGCTCTTGC	GCCTTTGCGT	CCGCGCGCGC	CCCCGCTACC	1440
	ACCCACGGCT	ACCGCCCGCG	AGGCTGCACC	GGGGGCGCGC	CGGCCAACCC	CTCTGCCTAT	1500
25	GCGGCTGCCT	ACGCGGGCGC	CGACGGCGCG	TACCGCGAGG	GGCGCGCGAG	TGCGATCTTT	1560
	GCCGCTGCTG	GCCGCTGCGC	GGGACCGCGT	TCCGCGCGAG	CGGGCGCGAG	CAGTGGCGGC	1620
	GTGGAGACCA	CGGTGGACTT	CTACGGGCGC	ACGTGCGCGG	GCCAGTTCGG	AGCGCTGGGA	1680
	GCCTGCTACA	ACCTTGGCGG	GCAGCTCGGA	GGGGCCAGTG	CAGGCGCCTA	CCATGCTCGC	1740
30	CATGCTGCGC	CTTATCCCGG	TGGGATAGAT	CGGTTCTGTG	CCGCCATGTG	AGCCAGCGTA	1800
	GGGACGAAAA	CTCATAGACA	CATCGGCTGT	TCACAGCTTC	CCCGCAACCT	GAGAACGAAAC	1860
	AGGAATGGAG	ACGAGACTCA	ACTGGGACCC	ACGTGGAAAA	GACCGAGCAG	GCCACAGAGG	1920
	CTCGGTCTCC	CCGCGCACAG	CGTAGGCACC	CTGTGTACTC	TGTAAACGGG	AGGAGGTGGG	1980
	GCGAGGCAGC	CAGAGCCCTT	GGACTGGCAC	AGGGACCCCT	GATGGAGCGA	AGCCCTCAA	2040
35	CGGGATGCTT	TCTGGCATTC	TATCGGGGAG	GGTCTTGGC	GGTAACGAGA	GGGCGAGCGTA	2100
	GTGTCAACAC	CAGAGACGAG	GATCCAAATT	GTGGGGAATC	AGTTTACGCC	TTCCATGTGC	2160
	TGCCGGAACT	CGGGCCTTTT	TACGCGGTTT	GTCTCTAGT	GCCTTTAACT	CGGTTACTAC	2220
	AATAAAAGGC	TGCGGCAGCG	CCTTCTTCTT	TAAAGTGAGG	AGGACAAATT	TGCAAAAGAA	2280
	ATAGGCTTTT	CTTCTTTT	AAATTGGAGA	AATCTCTGCT	CTGGTTGACC	TGGGCTGGTT	2340
40	TTCCCTGTCT	CTGAGAACTT	GAGACCTAGC	TCCGAGTTGA	ACTGTGCGTC	AGCACTCCAG	2400
	TCCCATCACC	TGAACCTTCA	GTCTCCCCCA	TCTGTTACAC	TAGAGGGCTG	CAGGACTCTA	2460
	TCACCGCGCC	CGGGGTTATC	ATTCAAGGCC	CCATCATCTT	GGATGCTGCC	CTGCGTATTT	2520
	GGCAGCAATG	GTGGGCCACC	CAGGGCCTCT	GAGTAGCCAC	CAAAGCCCTA	GCCGCTGTTC	2580
	TAGGGAACGG	AAAAGAGTTC	ATGGCCAGGC	GTCTAACCTA	AAGTCCCAGG	ATTGGCTCCA	2640
45	GGCAGCAATT	ATATCATAAC	TTATGAACT	TTTGAGCAGG	ACGTGCTGGT	AATTTTCATG	2700
	CTGTACTGCG	CCAGTCATAA	ATCTGCTTTT	CCATTATAAG	GCAGAGAGAA	GTACATTCGT	2760
	TCATTTGTCC	ACTGTTTCTT	GTCAACAGC	AGCCCTGGAC	CCAAAGGGTG	AACTAAAGTT	2820
	TAAGGAGATG	AGAGGATTCA	AGGAGCCCGT	TGGTGACGCC	TTTCAGTAGC	TGGGGAGGGC	2880
	TCTTCCATCC	CCAGCACCCC	CTGCTACACC	TCAGCAGCCT	CCCCCATGCA	AAAAGGAAAG	2940
50	AGAAAAATTA	AGTTAGGGCA	GTCACTAAAG	TGAGCTTTAG	AAAGAAACTG	GAATTTTAAAC	3000
	TTCAATTTGT	ATCTTGCTTA	AGTAGCAGGC	TCACTAAAAA	TAGAGAAAGT	CCAATAACTC	3060
	TCCCGCTTTC	CCTTGAGAAA	TCTTTAAGTT	TGGAATCTGG	AGCAAAAACT	TTCAAGATTA	3120
	AATATTTTCAG	AGGCTCCATT	CACAGCTTTC	AGATAAACTG	GAGTGTTTCA	ATGGACTGTT	3180
	TTAATAAAAA	TCTTTGAGCA	AGTGAGTTAT	GGCAAGAGAA	ACTCAGCCTC	TTTCTGTATA	3240
55	AACTTAACAG	GGAGGGGCTG	GGGTGTGAAA	AAGAAGATTG	TATGAAAACC	ATTGGTAATT	3300
	TTTATTTTTT	ATTTTGGGGA	CTGCACATATC	CTGTTACCGA	AGACATGTGA	ACTTGGTTCA	3360
	GTCAAATGG	GGATTGTTAT	AAACCAAGTG	TCTCCATTAG	AAATATGGTG	CAAGCCACAT	3420
	ATGTAATTTT	AAATATTCTA	GTAGCCACAT	TAATAAAGTN	AAAAGAAACA	AAAAAAAAAA	3480
	AA						

Seq ID NO: 317 Protein sequence:
Protein Accession #: NP_004464

	1	11	21	31	41	51	
65	FKHLTHYROI	DTRANSCRIP	TIONFACTOR	TFMTAESGP	PPPQPEVLAT	VKEERGETAA	60
	GAGVFPGEATG	RGAGGRRRKR	PLQRGKPPYS	YIALIAMAIA	HAPERRLTLG	GIYKFITERF	120
	PFYRDNPKKW	QNSIRHNLTL	ND CFLKIPRE	AGRPGKGNVW	ALDPNADMDF	ESGSFLRRRK	180
	RFKRSDLSTY	PAYMHDAAAA	AAAAAAAAAA	AAAAAIFPGA	VPAARPPYPG	AVYAGYAPPS	240
70	LAAPPVYYYP	AASPGPCRVP	GLVPERPLSP	ELGPAPSGPG	GSCAFASAGA	PATTTGYQPA	300
	GCTGARPNP	SAYAAAYAGP	DGAYPQGAGS	AIFAAAGRLL	GPASPPAGGS	SGGVETTVDF	360
	YGRTPGQFG	ALGACYNPFG	QLGGASAGAY	HARHAAAYPG	GIDRFVSAM		

Seq ID NO: 318 DNA sequence
Nucleic Acid Accession #: NM_005688
Coding sequence: 126..4439

	1	11	21	31	41	51	
80	CCGGGCAGGT	GGCTCATGCT	CGGGAGCGTG	GTGAGCGGC	TGGCGCGGTT	GTCTGGAGC	60
	AGGGGCGCAG	GAATTCTGAT	GTGAAACTAA	CAGTCTGTGA	GCCCTGGAAC	CTCCGCTCAG	120
	AGAAGATGAA	GGATATCGAC	ATAGGAAAAG	AGTATATCAT	CCCCAGTCTC	GGGTATAGAA	180
	GTGTGAGGGA	GAGAACCCAG	ACTTCTGGGA	CGCACAGAGA	CCGTGAAAGAT	TCCAAGTTCA	240
	GGAGAACTCG	ACCGTTGGAA	TGCCAAGATG	CCTTGGAAAC	AGCAGCCCGA	GCCGAGGGCC	300
85	TCTCTCTTGA	TGCCCTCATG	CATTCTCAGC	TCAGAACTCT	GGATGAGGAG	CATCCCAAGG	360
	GAAAGTACCA	TGATGGCTTG	AGCCCATCCG	GACTACTTCC	AAACACCAGC		420
	ACCCAGTGGA	CAATGCTGGG	CTTTTTCTCT	GTATGACTTT	TTCGTGGGCT	TCTTCTCTGG	480

	CCCGTGTGGC	CCACAAGAG	GGGGAGCTCT	CAATGGAAGA	CGTGTGGTCT	CTGTCCAAGC	540
	ACGAGTCTTC	TGACGTGAAC	TGCAGAAGAC	TAGAGAGACT	GTGGCAAGAA	GAGCTGAATG	600
	AAGTTGGGCC	AGACGCTGCT	TCCCTGCGAA	GGGTTGTGTG	GATCTTCTGC	CGCACCAGGC	660
5	TCATCTGTGC	CTACGTGTGC	CTGATGATCA	CGCAGCTGGC	TGGCTTCAGT	GGACCAGCCT	720
	TCATGGTGAA	ACACCTCTTG	GAGTATACCC	AGGCAACAGA	GTCTAACCTG	CAGTACAGCT	780
	TGTTTGTAGT	GCTGGGCTC	CTCCTGACGG	AAATCGTGCG	GTCTTGGTCT	CTTGCACTGA	840
	CTTGGGCATT	GAATTACCGA	ACCGGTGTCC	GCTTGGCGGG	GGCCATCTCTA	ACCATGGCAT	900
	TTAAGAAGAT	CCTTAAGTTA	AAGAACATTA	AAGAGAAATC	CCTGGGTGAG	CTCATCAACA	960
10	TTTGCTCCAA	CGATGGGCAG	AGAATGTTTG	AGGCAGCAGC	CGTTGGCAGC	CTGCTGGCTG	1020
	GAGGACCCGT	TGTTGCCATC	TTAGGCATGA	TTTATAATGT	AATTATTCTG	GGACCAACAG	1080
	GCTTCTCTGG	ATCAGCTGTT	TTTATCTCTT	TTTACCCAGC	AATGATGTTT	GCATCACGGC	1140
	TCACAGCATA	TTTCAGGAGA	AAATGCGTGG	CCGCCACCGA	TGAACGTGTC	CAGAAGATGA	1200
	ATGAAGTTCT	TACTTACATT	AAATTTATCA	AAATGTATGC	CTGGGTCAAA	GCATTTTCTC	1260
15	AGAGTGTCCA	AAAAATCCGC	GAGGAGGAGC	GTCCGATATT	GGAAAAAGCC	GGGTACTTCC	1320
	AGGGTATCAC	TGTGGGTGTG	GCTCCCATTT	TGGTGGTGAT	TGCCAGCGTG	GTGACCTTCT	1380
	CTGTTTATAT	GACCTTGGGC	TTGATCTGA	CAGCAGCACA	GGCTTTCACA	GTGGTGACAG	1440
	TCTTCAATTC	CATGACTTTT	GCTTTGAAAG	TAACACCGTT	TTCAGTAAAG	TCCCTCTCAG	1500
	AAGCCTCAGT	GGCTGTTGAC	AGATTTAAGA	GTTTGTCTCT	AATGGAAGAG	GTTTACATGA	1560
20	TAAAGAACAA	AGGAGGAGT	CCTCACATCA	AGATAGAGAT	GAAAAATGCC	ACCTTGGCAT	1620
	GGGACTCCTC	CCACTCCAGT	ATCCAGAACT	CGCCCAAGCT	GACCCCAAAA	ATGAAAAAAG	1680
	ACAAGAGGGC	TCCAGGGGCG	AGAAAGAGAG	AGGTGAGGCA	GCTGCAGCGC	ACTGAGCATC	1740
	AGGCGGTGCT	GGCAGAGCAG	AAAGGCCACC	TCTCTCTGGA	CAGTGACGAG	CGGCCAGTTC	1800
	CCGAAGAGGA	AGAAGGCAGG	CACATCCACC	TGGGCCACCT	GCGCTTACAG	AGGACACTGC	1860
25	ACAGCATCGA	TCTGGAGATC	CAAGAGGGTA	AACCTGGTGG	AATCTGCGCG	AGTGTGGGAA	1920
	TGTGAAAAAC	CTCTCTCAT	TCAGCCATTT	TAGGCCAGAT	GACGCTTCTA	GAGGGCAGCA	1980
	TTGCAATCAG	TGCAACCTTC	GCTTATGTGG	CCGAGCAGGC	CTGGATCTCT	AATGTACTTC	2040
	TGAGAGACAA	CATCTGTTT	GGGAAGGAAT	ATGATGAAGA	AAGATACAAC	TCTGTGCTGA	2100
	ACAGCTGCTG	CCTGAGGCCT	GACCTGGCCA	TTCTTCCAG	CAGCGACCTG	ACGGAGATTG	2160
30	GAGAGCGAGG	AGCCAACTGT	AGCGGTGGGC	AGCGCCAGAG	GATCAGCTTT	GCCCGGCCCT	2220
	TGTATAGTGA	CAGGAGCATC	TACATCTCTG	ACGACCCCTT	CAGTGCCTTA	GATGCCCATG	2280
	TGGGCAACCA	CATCTTCAAT	AGTGTATCTC	GGAAACATCT	CAAGTCCAAG	ACAGTTCTGT	2340
	TTGTTACCCA	CCAGTTACAG	TACCTGGTTG	ACTGTGATGA	AGTGTCTTTC	ATGAAAGAGG	2400
	GCTGTATTAC	GGAAAGAGGC	ACCCATGAGG	AACTGATGAA	TTTAAATGGT	GACTATGCTA	2460
35	CCATTTTAA	TAGCCTGTGG	CTGGAGAGAG	CACCCGCACT	TGAGATCAAT	TCAAAAAAAG	2520
	AAACCAAGTG	TTCACAGAA	AAGTCAACA	ACAAGGGTCC	TAAACACAGG	TCAAGTAAAG	2580
	AGGAAAAAGC	AGTAAAGGCA	GAGGAAGGGC	AGCTTGTGCA	GCTGGAAGAG	AAAGGGCAGG	2640
	GTTCAAGTGC	CTGGTCAGTA	TATGGTGTCT	ACATCCAGGC	TGCTGGGGGC	CCCTTGGCAT	2700
	TCTCTGGTTA	TATGGCCCTT	TTTATGCTGA	ATGTAGGCAG	CACCGCCTTC	AGCACCTGGT	2760
40	GGTTGAGTTA	CTGATATCA	CAAGGAAGCG	GGAAACACAC	TGTGACTCGA	GGGAACGAGA	2820
	CCTCGGTGAG	TGACAGCATG	AAGGACAATC	CTCATATGCA	GATCATATGC	AGCATCTACG	2880
	CCCTCTCCAT	GGCAGTCTG	CTGATCTCTG	AAGCCATTCT	AGGAGTTGTC	TTTGTCAAGG	2940
	GCACGCTGCG	AGCTTCTCTC	CGGCTGCATG	ACGAGCTTTT	CCGAAGGATC	CTTCGAAGCC	3000
	CTATGAAGTT	TTTTGACAGC	ACCCCCACAG	GGAGGATTCT	CAACAGGTTT	TCCAAAGACA	3060
45	TGGATGAAGT	TGACGTGCGG	CTGCCCTTCC	AGGCCGAGAT	GTTTATCCAG	AACGTTATCC	3120
	TGGTGTCTCT	CTGTGTGGGA	ATGATGCGAG	GAGTCTTCCC	GTGGTTCCTT	GTGGCAGTGG	3180
	GGCCCTCTGT	TAGCTCTTTT	TGAGTCTCTG	ACATTTCTCT	CAGGGTCTCT	ATTCGGGAGC	3240
	TGAAGCGTCT	GGACAATATC	ACCGAGTCAC	CTTCTCTCTC	CCACATCACG	TCCAGCATAC	3300
	AGGGCCTTGC	CACCATCCAC	GCCTACAATA	AAGGGCAGGA	GTTTCTGCAC	AGATACCAGG	3360
50	AGCTGTGGGA	TGACAAACCA	GCTCTTTTTT	TTTTGTTTAC	GTGTGCGATG	CGGTGGCTGG	3420
	CTGTGCGGCT	GGACCTCATC	AGCATCGCCC	TCATCACCAC	CACGGGGCTG	ATGATCGTTC	3480
	TTATGCAAGG	GATTTGGCTT	CCGAGCTATG	CGGGTCTGCG	CATCTCTTAT	GCTGTCCAGT	3540
	TAAAGGGGCT	GTTCCAGTTT	ACGGTCAGAC	TGGCATCTGA	GACAGAAGCT	CGATTCCACT	3600
	CGGTGGAGAG	GCTCAATCAC	TACATTAAGA	CTCTGTCTCT	GGAAGCACCT	GCCAGAATTA	3660
55	AGAACAAGGC	TCCCTCCCTT	GACTGGCCCC	AGGAGGGAGA	GGTGACCTTT	GAGAACGCGC	3720
	AGATGAGGTA	CCGAGAAAAA	CTCCCTCTTG	TCCTAAAGAA	AGTATCTCTC	ACGATCAAA	3780
	CTAAAGAGAA	GATTTGGCATT	GTGGGGCGGA	CAGGATCAGG	GAAGTCTCTG	CTGGGGATGG	3840
	CCCTCTTCCG	TCTGGTGGAG	TTATCTGGAG	GCTGCATCAA	GATTGATGGA	GTGAGAATCA	3900
	GTGATATTGG	CCTTGCAGAC	CTCCGAAGCA	AACTCTCTAT	CATTCCTCAA	GAGCCGGTGC	3960
60	TGTTCACTGG	CACCTGTGAG	TCAAATTGAG	ACCCCTTCAA	CCAGTACACT	GAAGACCAGA	4020
	TTTGGGATGC	CCTGGAGAGG	ACACACATGA	AAGAATGTAT	TGCTCAGCTA	CCTCTGAAC	4080
	TGAAATCTGA	TAGCTGTGG	AATGGGGATA	ACTTCTCAGT	GGGGGAACGG	CAGCTCTTGT	4140
	GCATAGCTAG	AGCCCTGCTC	CGCCACTGTA	AGATTCTGAT	TTTAGATGAA	GCCACAGCTG	4200
	CCATGGACAC	AGAGACAGAG	TTATTGATTC	AAGAGACCAT	CCGAGAAGCA	TTTGACAGCT	4260
65	GTACCATGCT	GACCATTGCC	CATCGCCTGC	ACACGCTTCT	AGGCTCCGAT	AGGATTATGG	4320
	TGCTGGCCCA	GGGACAGGTG	GTGGAGTTTG	ACACCCCATC	GTCCTTCTG	TCCAACGACA	4380
	GTTCGCCATT	CTATGCCATT	TTTGTGCTG	CAGAGAACAA	GGTCGCTGTC	AAGGGCTGAC	4440
	TCTCTCCCTG	TGACGAAGTC	TCTTTTCTTT	AGAGCAATTG	CATTCCTCTG	CTGGGGCGGG	4500
	CCCTCATGCG	GCTCTCTCTA	CCGAAACCTT	GCCTTTCTCG	ATTTTATCTT	TGCGACAGCA	4560
70	GTTCGGGATT	GGCTTGTGTG	TTTCACTTTT	AGGGAGAGTC	ATATTTTGAT	TATTGTATTT	4620
	ATTCCATATT	CATGTAAACA	AAATTTAGTT	TTTGTCTCTA	ATTGCACTCT	AAAAGGTTCA	4680
	GGGAACCGTT	ATTATAATTG	TATCAGAGGC	CTATAATGAA	GCTTTATACG	TGTAGCTATA	4740
	TCTATATATA	ATTCTGTACA	TAGCCTATAT	TTACAGTGAA	AATGTAAAGT	GTTTATTTTA	4800
	TATTAATAAT	AGCACTGTGC	TAATAACAGT	GCATATTCTT	TTCTATCATT	TTTGTACAGT	4860
75	TGCTGTACT	AGAGATCTGG	TTTTGCTATT	AGACTGTAGG	AAGAGTAGCA	TTTCACTTCT	4920
	CTCTAGCTGG	TGGTTTCCAG	GTGCCAGGTT	TTCTGGGTGT	CCAAAGGAAG	ACGTGTGGCA	4980
	ATAGTGGGCC	CTCCGACAGC	CCCTCTGCCC	GCCTCCCATC	AGCGCTCCCA	GGGGTGGCTG	5040
	GAGACGGGTG	GGCGGCTGGA	GACCATGCGA	AGCGCCGTGA	GTTCTCAGGG	CTCCTGCCTT	5100
	CTGTCTCTGT	GCTCTTACT	GTTCCTGTCA	GGAGAGCAGC	GGGGCGAAGC	CCAGGCCCTT	5160
80	TTTCACTCCC	TCCATCAAGA	ATGGGGATCA	CAGAGACATT	CCTCCGAGCC	GGGGAGTTTC	5220
	TTTCTGCTCT	TCTTCTTTT	GCTGTGTGTT	CTAAACAAGA	ATCAGTCTAT	CCACAGAGAG	5280
	TCCCATGCCC	TCAGGTTTCT	ATGGCTGGCC	ACTGCACAGA	GCTCTCCAGC	TCCAAGACCT	5340
	GTTGGTTCCA	AGCCCTGGAG	CCAACCTGCT	CTTTTGTAGG	TGGCACTTTT	TCAATTTGCT	5400
	ATTCACACAC	TATCCACAGT	CAGTGGCAGG	GCTCAGGATT	TGCTGGGTCT	GTTTTCCTTT	5460
	CTCACCGCAG	TGTCGACACA	GTCTCTCTCT	CTCTCTCCCC	TCAAAGTCTG	CAACTTTAAG	5520
85	CAGCTCTTGC	TAATCAGTGT	CTCACACTGG	CGTAGAAGTT	TTTGTACTGT	AAAGAGACCT	5580
	ACCTCAGGTT	GCTGGTGTCT	GTGTGGTTTG	GTGTGTTCCC	GCAAACCCCC	TTTGTGCTGT	5640
	GGGGCTGGTA	GCTCAGGTGG	GCGTGGTCAC	TGCTGTCTATC	AGTTGAATGG	TCAGCGTTGC	5700

ATGTCGTGAC CAACTAGACA TTCTGTCGCC TTAGCATGTT TGCTGAACAC CTTGTGGAAG 5760
 CAAAAATCTG AAAAAATGTA TAAATATTATT TTGGATTTTG TAAAAAATAA AAAAAAATAA 5820
 AAAAAAATAA AAAAAAATAA

5

Seq ID NO: 319 Protein sequence:
 Protein Accession #: NP_005679

1	11	21	31	41	51	
MKDIDIGKEY	IIPSPGYRSV	RERTSTSGTH	RDREDSKFRR	TRPLECQDAL	ETAARAEGLS	60
LDASMHSQLR	ILDEEHKPKG	YHHGLSALKP	IRTTSKHQHP	VDNAGLFSCM	TFSWLSSLAR	120
VAHKKGELSM	EDVNSLSKHE	SSDVNCRRLR	RLWQEELENEV	GPDAASLRV	VWIFCRTRLI	180
LSIVCLMITQ	LAFSGPAFM	VKHLEYTQA	TESNLQYSL	LVLGLLLTEI	VRWSLALTW	240
ALNYRTGVRL	RGAILTMAPK	KILKLKNIKE	KSLGELINIC	SNQGORMFEA	AAVGSLLAGG	300
PVVAILGMIY	NVILGPTGPF	LGSAPFILFY	PAMMFASRLT	AYFRKRCVAA	TDERVQKME	360
VLTYIKFKIM	YAWKAFPSQS	VQKIREEBERR	ILEKAGYFQG	ITVGVAPIV	VIASVVTFSV	420
HMTLGFDLTA	AQAFVTVTVF	NSMTFALKVT	PFSVKSLSSEA	SVAVDRFKSL	FLMEEVHMIK	480
NKPASPHIKI	EMKNATLAWD	SSHSSIQNSP	KLTPMKKKDK	RASRGKKEKV	RQLQRTEHQA	540
VLAEQKGLHL	LDSDERSPE	EEGKHIHLG	HLRLQRTLHS	IDLEIQEGKL	VGICGSVGS	600
KTSLISAILG	QMTLLEGSIA	ISGTFAYVAQ	QAWILNATLR	DNILFGKEYD	EERYNSVLNS	660
CCLRPDLAIL	PSSDLTEIGE	RGANLSGGQR	QRISLARALY	SDRSIYLDD	PLSALDAHVG	720
NHIFNSAIRK	HLKSKTVLHV	THQLQVLDVC	DEVIFMKEGC	ITERGTHEEL	MNLNGDYATI	780
FNNLLGPTP	EGEINSKKET	SGSQKKSQDK	GPKTGSVKKE	KAVKPEEGQL	VQLEEKGGQS	840
VPWSVYGVYI	QAAGGPIAFL	VIMALEMLNV	GSTAFSTWWL	SYWIKQSGSN	TTVTRGNETS	900
VSDSMKDNPH	MQYASIALY	SMAMVLLILK	IRGVVVFVKG	LRASSRLHDE	LFRRLRSFPM	960
KFPDTPPTGR	ILNRFSDKMD	EVDVRLPFQA	EMFIQNVILV	FFCVGMIAGV	FPWFLVAVGP	1020
LVILPSVLHI	VSRVLIRELK	RLDNITQSPF	LSHTSSSIQG	LATIHAYNKG	QEFLEHRYQL	1080
LDDNQAPFFL	FTCAMRLAV	RDLISIALI	TTTGLMIVLM	HGQIPPAYAG	LAISSAVQLT	1140
GLFQFTVRLA	SETARTSTSV	ERINHVIKTL	SLEAPARIKN	KAPSPDPWQE	GEVTFENAEM	1200
RYRENLPVLV	KKVSFTIKPK	EKIGIVGRTO	SKKSLGMLAL	FRLVELSGGC	IKIDGVRIISD	1260
IGLADLRSLK	SIIPQEPVLF	SGTVRSNLDP	FNQYTEDQIW	DALERTHMEK	CIAQLPLKLE	1320
SEVMENGDNF	SVGERQLLCI	ARALLRHCKI	LILDEATAAM	DTETDLIIQE	TIREAFADCT	1380
MLTIAHRLHT	VLGSDRIMVL	AQQQVVEFDT	PSVLLSNDSS	RFYAMFAAAE	NKVAVKVG	

Seq ID NO: 320 DNA sequence
 Nucleic Acid Accession #: AK022089.1
 Coding sequence: 181-1488

1	11	21	31	41	51	
AGCAGTTGCA	CAACTTCCAG	CAACTTCTC	AGCCCGCTAC	TAATGAGCTG	AAAGCCAGGA	60
ACATCCGAGG	AGAAGAGAAA	GCTTCCAGCC	CTCCTCCCTT	CACCTCGGAA	ATCCAGACAC	120
CCCCACCCCC	ACCCTCAGAT	CACCTTAAGA	TAATTTCTTT	ATTCTGTTGC	CCGACAGACC	180
ATGGCTCCCT	TTGGAAGAAA	CTTGCTAAAG	ACTCGGCATA	AAAACAGATC	TCCAACTAAA	240
GACATGGATT	CAGAAGAGAA	GGAAATTTGT	GTTTGGGTTT	GCCAAGAAGA	GAAGCTTGTC	300
TGTGGGCTGA	CTAAACGCAC	CACCTCTGCT	GATGTCATCC	AGGCTTTGCT	TGAGGAACAT	360
GAGGCTACGT	TTGAGAGAAA	ACGATTTCTT	CTGGGGAAGC	CCAGTGATTA	CTGCATCATA	420
GAGAAGTGGG	GAGGCTCCGA	AAGGGTTCTT	CCTCCACTAA	CTAGAATCCT	GAAGCTTTGG	480
AAAGCGTGGG	FTCATGAPKA	GCCCAATATG	CAATTTGTGT	TGGTTAAAGC	AGATGCTTTT	540
CTTCCAGTTC	CTTTGTGGCG	GACAGCTGAA	GCCAAATTAG	TGCAAAACAC	AGAAAAATTG	600
TGGGAGCTCA	GCCCGAGAAA	CTACATGAAG	ACTTTACCAC	CAGATAAACA	AAAAAGAAAT	660
GTCAGGAAAA	CTTTCCGGAA	ACTGGCTAAA	ATTAAGCAGG	ACACAGTTTC	TCATGATCGA	720
GATAATATGG	AGACATTAGT	TCATCTGATC	ATTTCCCAAG	ACCATACTAT	TCATCAGCAA	780
GTCAGAGAAA	TGAAGAGAGT	GGATCTGGAA	ATTGAAAGAT	GTGAAGCTAA	GTTCCATCTT	840
GATCGAGTAG	AAAATGATGG	AGAAAACAT	GTTCCAGGAT	CATATTTAAT	GCCCAGTTTC	900
AGTGAAGTTG	AGCAAAATCT	AGACTTGCAG	TATGAGGAAA	ACCAGACTCT	GGAGGACCTG	960
AGCGAAAGTG	ATGGAATTGA	ACAGCTGGAA	GAACGACTGA	AATATTACCG	AATACTCATT	1020
GATAAGCTCT	CTGCTGAAAT	AGAAAAAGAG	GTAAGAAAGT	TTTGATTTGA	TATAAATGAA	1080
GATGCGAAG	GGGAAGCTGC	AAGTGAACCT	GAAAGCTCTA	ATTTAGAGAG	TGTTAAGTGT	1140
GATTTGGAGA	AAAGCATGAA	AGCTGGTTTG	AAAATTCCT	CTCATTTGAG	TGGCATCCAG	1200
AAAGAGATTA	AATACAGTGA	CTCATTTGCT	CAGATGAAAG	CAAAAGAATA	TGAACTCCTG	1260
GCCAAGGAAT	TCAATTCCT	TCATATTAGC	AACAAAGATG	GGTGCCAGTT	AAAGGAAAC	1320
AGAGCGAAGG	AATCTGAGGT	TCCAGTAGC	AATGGGGAGA	TTCTCCCTT	TACTCAAAGA	1380
GTATTTAGCA	ATTACACAAA	TGACACAGAC	TCGGACACTG	GTATCAGTTC	TAACACAGT	1440
CAGGACTCCG	AAACAACAGT	AGGAGATGTG	GTGCTGTTGT	CAACATAGTT	CCAATGGCTC	1500
CTTTCTGACC	TGCTTTTCATG	TTTAAATGTT	TGTTTAATTT	AATAGGAAAC	CTCATTTTAA	1560
ATATAACACT	CAAAAAAATG	TAAATCATAT	TGTAGTATTC	AATAGTTAAT	AAAAACTCGA	1620
GAAATGTGTT	GTTTCTG					

Seq ID NO: 321 Protein sequence:
 Protein Accession #: NP_005438.1

1	11	21	31	41	51	
MAPFGRNLLK	TRHKNRSPTK	DMDSEEKEIV	VWVCQEEKLV	CGLTKRRTSA	DVIQALLEEH	60
EATFGKRLPL	LGPSPDYCII	EKWRGSEKRV	PPLTRILKLW	KAWGDEQPNM	QFVLVKADAF	120
LPVPLWRTAE	AKLVQNTTEK	WELSPANMYK	TLPPDKQKRI	VRKTFRKLAK	IKQDVTSHDR	180
DNMTLVHLII	ISQDHTIHQQ	VKRMKELDLE	IEKCBKAPHL	DRVENDGENY	VQDAYLMPSP	240
SEVEQNLDLQ	YEENQTLLED	SESDGIEQLE	ERLKYRILII	DKLSAEIEKE	VKSVCIDINE	300
DAEGEASSEL	ESSNLESVKC	DLEKSMKAGL	KIHSLSGIQ	KEIKYSDSL	QMKAKYELL	360
AKFENSLHIS	NKDGQCLKEN	RAKESEVPSS	NGEIPFFTOR	VFSNYTNDTD	SDTGISSNHS	420
QDSETTVGDV	VLLST					

Seq ID NO: 322 DNA sequence
 Nucleic Acid Accession #: NM_030920.1

Coding sequence: 317-1123

	1	11	21	31	41	51	
5	AGCATTTGAAG	GGGAAGGAAC	TGCGGGTGTG	GTGTGTGTAT	GTGTGTGTGT	ATGTGTGTGC	60
	GGCGCGTGGC	TGCGTGTGTG	TGCGCGCGCT	AGTGTGTGGA	CAAGGAGGTG	GGGGCAGCTG	120
	AGTTAGAGTC	CCAACTCTTG	GACTCCATTT	GCTATTCTCT	TCTTTCTCCC	CCACACCTAT	180
	CTGGTGGTGG	TAGTGGGCGT	TTATATTTCG	GTTCCTTTTC	ATTCAATTCT	AAATCTCTTA	240
	AAAATTTTGG	GTTGGGGGTA	TTGGGGAAGG	CAGGAAAGGG	AAAAGGAGAG	TAGTAGCTGA	300
10	AGAGCAAGAG	GAGGACATGG	AGATGAAGAA	GAAGATTAC	CTGGAGTTAA	GGAACAGATC	360
	CCCGGAGGAG	GTGACAGAGT	TAGTCCTTGA	TAATTGCCCTG	TGTGTCAATG	GGGAAATTGA	420
	AGGCCTGAAT	GATACTTTCA	AAGAAGTAGA	ATTTCTGAGT	ATGGCTAATG	TGGAAGTAAG	480
	TTGCTGGGCC	CGGCTTCCCA	GCTTAAATAA	ACTTCGAAAA	TTGGAGCTTA	GTGATAATAT	540
	AATTTCTGGA	GGCTTGGGAG	TCCTGGCAGA	GAAATGTCCA	AATCTTACCT	ACCTCAATCT	600
15	GAGTGGAAAC	AAAATAAAG	ATCTCAGTAC	AGTAGAAGCT	CTGCAAAATC	TTAAAAATTT	660
	GAAAACTCTT	GACCTGTTTA	ACTGTGAGAT	CACAAACCTG	GAAGATTATA	GAGAAAGTAT	720
	TTTTGAACCTA	TCGACGCAAA	TCACATACTT	AGATGGATTT	GATCAGGAGG	ATAATGAAGC	780
	GGCGGACTCT	GAAGAGGAGG	ATGATGAGGA	TGGAGATGAA	GATGATGAAG	AGGAAGAGGA	840
	AAATGAAGCT	GGTCCACCGG	AAGGATATGA	GGAAGAGGAG	GAGGAAGAGG	AAGAGGAGGA	900
20	TGAGGATGAG	GATGAAGATG	AAGATGAAGC	AGGTTGAGAG	TGGGAGAGG	GAGAAGAGGA	960
	AGTGGGCCCTC	TCATACTTAA	TGAAGAAGA	AATTGAGGAT	GAAGAAGATG	ATGATGACTA	1020
	TGTTGAAGAA	GGGGAAGAGG	AGGAAGAAGA	GGAAGAAGGA	GGTCTTCGAG	GGGAGAAGAG	1080
	GAAACGAGAT	GCTGAAGACG	ATGGAGAGGA	AGAAGATGAC	TAGATCATTC	TAAAGACCAGA	1140
	TTCTCTAATG	GGCTTGGGAT	TGCAATAGAG	TGATCACATC	TTTGTTCCTT	CATGTACGAT	1200
25	AGCTATCCCT	ACAGAAAGTA	ATGTGTAAC	TTTATAGGAA	AAAGTGTGGT	TTTACTATTT	1260
	TTGCCCTTATC	ATTCCAAATA	AGAACTAGTC	TGTTAATGAT	CATATTGTAT	GTAGAGAAAA	1320
	ATTTTCATTG	ACTCCCATTTG	TGGAATTCCC	TAGCAATTTA	TTTAGACTTA	ATTTTATAAA	1380
	TTCAAGCTTA	CTGTATTATG	CATTTTATAG	CCATAATTAA	AACATGATCA	CTTTTAAACA	1440
	GGTGTAGTAT	GGTGCATTTT	ATTCCTTATT	TATAGATTAA	CTGAAATTAC	AGTTTGTCTAT	1500
30	AATATAAAT	GACATAGTCT	TCTTGAGTGG	TAAGTTGGTT	ATTTTATTAG	AGGTGATCCA	1560
	GGAACTCTTA	GTTTGAAGGC	AGTTACCTTT	TTTTTTTTTT	TTTTTTTTTG	ACTAAGAGTG	1620
	TTTGGTTGCT	TTTTTGTGAC	AAGTAAGTGG	GAAATAGAAA	GCAGAAATAG	AAAGGTCTTA	1680
	TTGAGCAACA	TAGTTCAATG	ATTTTGTGGA	GGTCTTATTC	AGTAATATGG	TTGATGGATT	1740
	TAGTGTGAG	TGATTAAGAT	TTATTTTGA	AGGAAAAATT	GCTTATACTA	AGTCCAGAGA	1800
35	CATGAGGTG	AGCCCTTTTG	TCAGGCTGCA	AATCATGACA	TGCCGATGGT	TGTTTATTTT	1860
	GTTTTTAGGT	GTGCATTCCT	TTTCTTCTTA	GCAATTCCTT	TATGATCACC	TTCCCTTCTT	1920
	GTTTCACTCC	CTCCGCTCT	CTCAAAAGGA	ACTTGGGAAA	CTTGTGAAGC	CCAGGAAAAAC	1980
	CTTTAGTCTT	ATACCTCAAC	TACGTTTCAG	TCCTGTCTGG	GTTTTAAATA	AGTGAAGTAG	2040
	AAGAAATGTA	TAAATTTCTG	ACATAAGAAAT	ATATTATCAA	TACAGTTTAA	TGCAGTAAAG	2100
40	TCCTCTTACC	ATAAATGTTT	CTTGTTGAC	AACATCTAAG	ACAATATTAG	TGGGATGAAG	2160
	AAAGAAAGC	AGGGGTGCTT	TGGAAGCAG	TGTTAGTGT	CCTCAAAAGT	CGGAACAATT	2220
	GCCTGTTGAT	ATATTAAATA	GACATTAAAG	TCAAAATTTA	ATGTTGGCCT	CTCAATGAT	2280
	TTGGATACCA	CTCTGCAAG	TATTTCTAAC	CTTTAATCCC	CAGTTTAAAT	ACAGATATAA	2340
	TAAATAGCTA	TAAATGGAAT	ATACTAGGCA	GCTGGAAAAA	TATTTGAAAC	TAAATTGACA	2400
45	TAAATATTA	GATTTGTTTT	CAAGTGGATG	TCCATTAAAA	GTAGAAAAAT	ATTTGGGATA	2460
	AGTGAGTGTG	TGTTTCTCTTA	CATGGCTACT	AAATAAAATA	TAATGAGTAT	ACAAGTATAT	2520
	CTCCTCTTTT	GCTATGGAGG	CTCCATGTTT	AAGGCAATGG	CTTTTAAAT	CTTGGCTATC	2580
	TAAATTTTTT	TCCCTTTGTT	TTGAATATTT	GTAAGTTTTT	AAGAAGTTAG	TGTCAGCAAA	2640
	TAAATGAAG	TATATCTCTT	ATACTGGGAC	ATATTTAAAT	ACTGAGTATA	GTACTGCTGC	2700
50	TACTGCTTCT	ACAATGTAAA	ATGTATGACT	TGGTGTTTTA	AAGTAAAAAT	TATGATGTTA	2760
	CTTGTGGAGA	AACTAAAAAT	GTGTACAAC	TGACCGAAAG	AAAACCCCTG	GGGATAAGTT	2820
	TAGTGAGGGG	ATTGGAATCC	CCAAAAAGAT	AACATTTTTC	TTCTGCTTTT	AAAAACTGAA	2880
	ATTCCTGTTT	CTAGTTCTCA	ACAATTTCTA	TTACATACTA	TGCCAGATTA	CAAAATACCT	2940
	ATTTTAAAAA	TGAATCTAT	ATATTGACTT	TCTATCAAT	CATCTTACTG	TGCAATCAAA	3000
55	ATTAGAGTAA	TTTGGTTTGA	AAACAACACT	TAGAGCCTCC	AGATAACTTT	TAAAGACTTAT	3060
	TTAGCTTTGT	GCGGTGCTAT	TTTATGCAAA	TAAAGTAAAGG	TGGGTTTAT	ATTTTGTATA	3120
	AGTTTTCGGT	CCTATTTTAA	TGCTCTTGT	ATGGCAGTAT	GTATATATTG	TGTTAAGTTC	3180
	CTCAAGAATC	TCCTTAAAAA	CTTTGAAGTT	AATACTTTTG	TGCAACTGTG	TTTTGAATAA	3240
60	AGCCATGACA	TGTTTAAAAA	CAAAAC				

Seq ID NO: 323 Protein sequence:
Protein Accession #: NP_112182.1

	1	11	21	31	41	51	
65	MEMKKKINLE	LRNRSPEVET	ELVLDNCLCV	NGEIEGLNDT	FKELEFLSMA	NVELSSLARL	60
	PSLNKLRKLE	LSDNIISGGL	EVLAEKCPNL	TYLNLSGNKI	KDLSTVEALQ	NLKNLKSLLD	120
	FNCEITNLED	YRESIFELLQ	QITYLDGFDQ	EDNEAPDSEE	EDDEDGDEDD	EEEEENEAGE	180
70	PEGYEEEEEE	EEEEDEDEDE	DEDEAGSELG	EGEEEVGLSY	LMKEEIQDEE	DDDDYVEEGE	240
	EEEEEBEGGL	ROEKRRDAE	DDGEEEDD				

Seq ID NO: 324 DNA sequence
Nucleic Acid Accession #: NM_003812
Coding sequence: 224..2722

	1	11	21	31	41	51	
75	TCCTCTGCGT	CCCGCCCCGG	GAGTGGCTGC	GAGGCTAGGC	GAGCCGGGAA	AGGGGGCGCC	60
	GCCCAGCCCC	GAGCCCCCGG	CCCGGTGCCC	CGAGCCCGGA	GCCCCCTGCC	CGCGCGCGCA	120
80	CCATGCGCGC	CGAGCCGCGC	TGACCGGCTC	CGCCCGCGGC	CGCCCCGCGC	CTAGCCCGGC	180
	GCTCTCGCGC	GCCACACGGA	GCGGCGCCCG	GGAGCTATGA	GCCATGAAGC	CGCCCGGCGC	240
	CAGCTCGCGC	CAGCCGCCCC	TGGCGGGCTG	CAGCCTTGCC	GCGCTTCTCT	GCGGCCCCCA	300
	ACGCGGCCCC	GCGGCTGCTG	TGCTGCGCAG	CGCCCGCGCC	CGCAGCGCGC	CCTGCGCGCT	360
	GCTTCTCGTC	CTTCTCTCTG	TGCCTCGGCT	CGCCGCTCG	TCCCGGCCCC	GCGCTGGGG	420
85	GGCTGCTGCG	CCCAGCGCTC	CGCATTGGAA	TGAAACTGCA	GAAAAAATT	TGGGAGTCTT	480
	GGCAGATGAA	GACAATACAT	TGCAACAGAA	TAGCAGCAGT	AATATCAGTT	ACAGCAATGC	540
	AATGCAGAAA	GAAATCACAC	TGCCTTCAAG	ACTCATATAT	TACATCAACC	AAGACTCGGA	600

	AAGCCCTTAT	CACGTTCTTG	ACACAAAGGC	AAGACACCAG	CAAAAACATA	ATAAGGCTGT	660
	CCATCTGGCC	CAGGCAAGCT	TCCAGATTGA	AGCCTTCGGC	TCCAAATTCA	TTCTTGACCT	720
	CATACTGAAC	AATGGTTTGT	TGCTTCTGA	TTATGTGGAG	ATTCACTACG	AAAATGGGAA	780
5	ACCACAGTAC	TCTAAGGGTG	GAGAGCACTG	TTACTACCAT	GGAGCATCA	GAGGCGTCAA	840
	AGACTCCAAG	GTGGCTCTGT	CAACCTGCAA	TGGACTTCAT	GGCATGTTTG	AAGATGATAC	900
	CTTCGTGTAT	ATGATAGAGC	CAC TAGAGCT	GGTTTCATGAT	GAGAAAAGCA	CAGGTCGACC	960
	ACATATAATC	CAGAAAACCT	TGGCAGGACA	GTATTCTAAG	CAATGAAGA	ATCTCACTAT	1020
	GGAAAGAGGT	GACCAGTGGC	CCTTCTCTC	TGAATTACAG	TGGTTGAAAA	GAAGGAAGAG	1080
	AGCAGTGAAT	CCATCACGTG	GTATATTTGA	AGAAATGAAA	TATTTGGAAC	TTATGATTGT	1140
10	TAATGATCAC	AAAACGTATA	AGAAGCATCG	CTCTTCTCAT	GCACATACCA	ACAACCTTTC	1200
	AAAGTCCGTG	GTCAACCTTG	TGGATTCTAT	TTACAAGGAG	CAGCTCAACA	CCAGGTTTGT	1260
	CCTGGTGGCT	GTAGAGACCT	GGACTGAGAA	GGATCAGATT	GACATACCA	CCAACCCCTG	1320
	GCAGATGCTC	ACTGAATTCT	CAAAATACCG	GCAGCGCATT	AAGCAGCATG	CTGATGCTGT	1380
	GCACCTCATC	TGCGGGGTGA	CATTTCACTA	TAAAGAGAAGC	AGTCTGASTT	ACTTTGGAGG	1440
15	TGCTGTGTCT	CGCACAAAGG	GAGTTGGTGT	GAATGAGTAT	GGTCTTCCAA	TGGCAGTGGC	1500
	ACAAATATTA	TGCGAGAGCC	TGGCTCAAAA	CCTTGGAAATC	CAATGGGAAC	CTTCTAGCAG	1560
	AAAGCCAAAA	TGTAACCTGC	CAGAATCCCTG	GGGTGGCTGC	ATCATGGAGG	AAACAGGGGT	1620
	GTCCCATCTC	CGAAAATTTT	CAAAATGCGG	CATTTTGGAG	TATAGAGACT	TTTACAGAG	1680
	AGGAGGTGGA	GCCTGCCTTT	TCAACAGGCC	AACAAAGCTA	TTTGAGCCCA	CGGAATGTGG	1740
20	AAATGGATAC	GTGGAAGCTG	GGGAGGAGTG	TGATTGTGGT	TTTCATGTGG	AATGCTATGG	1800
	ATTATGCTGT	AAGAAATGTT	CCCTCTCCAA	CGGGGCTCAC	TGCAGCGAAG	GGCCCTGCTG	1860
	TAACAATACC	TCAATGCTTT	TTCAAGCCAG	AGGGTATGAA	TGCCGGGATG	CTGTGAACGA	1920
	GTGTGATATT	ACTGAATTCT	CTACTGGAGA	CTCTGGTCAG	TGCCCAACAA	ATCTTCATAA	1980
	GCAAGACGGA	TATGCATGCA	ATCAAAATCA	GGGCCGCTGC	TACAATGGCG	AGTGAAGAC	2040
25	CAGAGACAA	CAGTGTCACT	ACATCTGGGG	AACAAAGGCT	GCAGGGTCTG	ACAAGTTCTG	2100
	CTATGAAAAG	CTGAATACAG	AAGGCACTGA	GAAGGGAAGC	TGCGGGAAGG	ATGGAGACCG	2160
	GTGGATTACG	TGCAGCAAC	ATGATGTGTT	CTGTGGATTC	TTACTCTGTA	CCAATCTTAC	2220
	TCAGATCCCA	CGTATTGGTC	AACCTCAGGG	TGAGATCATT	CCAACCTCCT	TCTACCATCA	2280
	AGGCCGGGTG	ATTGACTGCA	GTGGTGCCCA	TGTAGTTTGA	GATGATGATA	CGGATGTGGG	2340
30	CTATGTAGAA	GATGGAACGC	CATGTGGCCC	GTCTATGATG	TGTTTAGATC	GGAAGTGCCT	2400
	ACAAATTCAA	GCCCTAAATA	TGAGCAGCTG	TCCACTCGAT	TCCAAGGGTA	AAGTCTGTTC	2460
	GGGCCATGGG	GTGTGTAGTA	ATGAAGCCAC	CTGCATTTGT	GATTTCACCT	GGGCAGGGAC	2520
	AGATTGCACT	ATCCGGGATC	CAGTTAGGAA	CCTTCAACCC	CCCAAGGATG	AAGGACCCAA	2580
	GGGTCTAGT	GCCACCAATC	TCATAATAGG	CTCCATCGCT	GGTGCCATCC	TGGTAGCAGC	2640
35	TATTGTCTCT	GGGGGCACAG	GCTGGGGATT	TAAAAATGTC	AAGAAGAGAA	GGTTCGATCC	2700
	TACTCAGCAA	GGCCCACTCT	GAATCAGCTG	CGCTGGATGG	ACACCGCCTT	GCATGTTGG	2760
	ATTCTGGGTA	TGACATCTC	GCAGCAGTGT	TACTGGAATC	ATTAAGTTTG	TAAACAAAAC	2820
	CTTTGGGTGG	TAATGACTAC	GGAGCTAAAG	TTGGGGTGAC	AAGGATGGGG	TAAAAGAAAA	2880
40	CTGTCTCTTT	TGGAATAAT	GTCAAAGAAC	ACCTTTCACC	ACCTGTGAGT	AAACGGGGGA	2940
	GGGGGCAGAA	GACCATGCTA	TAAAAAGAAC	TGTTCCAGAA	TCTTTTITTT	TCCCTAATGG	3000
	ACGAAGGAAC	AACACACACA	CAAAAATTAA	ATGCAATAAA	GGAATCATTA	AAAA	

Seq ID NO: 325 Protein sequence:
Protein Accession #: NP_003803

45	1	11	21	31	41	51	
	MKPPGSSSRQ	PPLAGCSLAG	ASCGPQRGPA	GSVPASAPAR	TPPCRLLLV	LLLPLLAASS	60
50	RPRAMGAAAP	SAPHWNTAE	KNLGVLADED	NTLQONSSSN	ISYSNAMQKE	ITLPSRLIYY	120
	INQDSESPYH	VLDTKARHQ	KHNKAVHLAQ	ASFQIEAFGS	KFILDILINN	GLLSSDYVEI	180
	HYENGKPYYS	KGGEHCYHNG	SIRGVKDSKV	ALSTCNGLHG	MFEDDTFVYM	IEPLELVHDE	240
	KSTGRPHIIQ	KTLAQVYSKQ	MKNLTMERGD	QWPFLESELQW	LKRRKRAVNP	SRGIFEEPMKY	300
	LELMIVNDHK	TYKHKRSSHA	HTNPFKSVV	NLVDLSIYKEQ	LNTRVVLVAV	ETWTEKDQID	360
55	ITTNVPQMLH	EFYSKYRQRIK	QHADAHLIS	RVTFHYKRSS	LSYFVGVCSSR	TRGVGVNEYG	420
	LPMVAQVLS	QSLAQNLGIQ	WEPSSRKPKK	DCTESWGGCI	MEETGVSHSR	KFSKCSILEY	480
	RDFLQRGGGA	CLFNRPRTKLF	EPTCEGNGYV	EAGEECDCGF	HVECYGLCKK	KCSLSNGAHC	540
	SDGPPCMMNTS	CLFPQRYGEC	RDVAVNCDIT	EYCTGDSGQC	PPNLHKQDGY	ACNQNGRCY	600
	NGECKTRNDG	CQYTWGTKAA	GSDKFCYEKL	NTEGTEKGNC	KGDGDRNIQC	SKHDVFCGLF	660
60	LCTNLTRAER	IGQLQGEIIP	TSFYHQGRVI	DCSGAHVVLDD	DDTDVGVYED	GTFCGFSMMC	720
	LDRKCLQIQ	LNMSSCPLDS	KGVKCSGHGV	CSNEATCICD	FTWAGTDCSI	RDPVRNLHPP	780
	KDEGPKGPSA	TNLIIGSIAG	AILVAAIVLG	GTGWGPKNVK	KRRFDPTQQG	PI	

Seq ID NO: 326 DNA sequence
Nucleic Acid Accession #: AK074418.1
Coding sequence: 244-1515

65	1	11	21	31	41	51	
	CTTTCTCCAA	GACGCGCCGC	CATGCTCTCC	TCCTCTGCCA	GTCTCTCCCA	CCACTCTCTA	60
70	ACCTGAGAGC	CTGTGGAACC	TGCCCGTCTC	CCCTCCTCCA	TCAGACACAC	CTGCCTAGGA	120
	AACAGATGGA	AAAAGTGAGG	GACCGGTGAG	TGACTTGCTG	CTAAAGTTTA	TACCAGATGC	180
	AAATGACAGA	GCTGGAGTTC	TGCTGTGCCT	GGAAAGGACC	TCGGAAGTCT	TCTAAGGAGA	240
	GTCTATGGCG	ATTACAGGGA	GCCTTCAGTG	GAGACCTCCA	TCATCAAGTT	CAAGACCCAG	300
	GACTTTACCA	CCTTGCAGGA	TCACTGCCTG	AGCATGGGCC	GGACGTTTAA	GGATGAGACA	360
75	TTCCCGCAG	CAGATTCTTC	CATAGGCCAG	AAGCTGCTCC	AGGAAAAACG	CCTCTCCAAT	420
	GTGATATGGA	AGCGGCCACA	GGATCTACCA	GGGGGTCTCT	CTCACTTCAT	CCTGGATGAT	480
	ATAAGCAGAT	TTGACATCCA	ACAAGGAGGC	GCAGCTGACT	GCTGGTTCTC	GGCAGCACTG	540
	GGATCCTTGA	CTCAGAACCC	ACAGTACAGG	CAGAAGATCC	TGATGGTCCA	AAGCTTTTCA	600
	CACCAATATG	CTGAGCACTT	CCGTTTCCGG	TTCTGGCAAT	GTGGCCAGTG	GGTGGAAAGT	660
80	GTGATTGATG	ACCGCCTTAC	TGTCCAGGGA	GATAAATGCC	TCTTTGTGCG	TCCTCGCCAC	720
	CAAAACCAAG	AGTTCTGACC	CTGCCTGCTG	GAGAAGGCCT	ATGCCAAGCT	GCTCGGATCC	780
	TATTCGATC	TGCACTATGG	CTTCTCGAG	GATGCCCTGG	TGGACCTCAC	AGGAGGCGTG	840
	ATCACCAACA	TCCATCTGCA	CTCTTCCCCT	GTGGACCTGG	TGAAGGCAGT	GAAGACAGCG	900
	ACCAAGGCAG	GCTCCCTGAT	AACTGTGCCC	ACTCCAAGTG	GGCCCAACAGA	TACAGCACAG	960
85	GCGATGGAGA	ATCGGCTGGT	GAGTCTCCAT	GCCTCACTG	TGACTGGGGG	TGAGCAGATT	1020
	CAATACCGAA	GGGGCTGGGA	AGAAATTATC	TCCTGTGGGA	ACCCCTGGGG	CTGGGGCGAG	1080
	ACCAATGGA	GAGGGCGCTG	GAGTGATGGG	TCTCAGGAGT	GGGAGGAAAC	CTGTGATCCG	1140

	CGGAAAAGCC	AGCTACATAA	GAAACGGGAA	GATGGCGAGT	TTTGGATGTC	GTGTCAAGAT	1200
	TTCCACACAG	AATTCATCGC	CATGTTTATA	TGTAGCGAAA	TTCCAAATTAC	CCTGGACCAT	1260
	GGAAACACAC	TCCACGAAGG	ATGGTCCCAA	ATAATGTTTA	GGAAGCAAGT	GATTCTAGGA	1320
5	AACACTGCAG	GAGGACCTCG	GAATGATGCT	CAATTCAACT	TCTCTGTGCA	AGAGCCAATG	1380
	GAAGGCACCA	ATGTTGTGCT	GTGCGTCACA	GTGCTGTGCA	CACCATCAAA	TTTGAAGCA	1440
	GAAGATGCAA	AATTTCCACT	CGATTTCCAA	GTGATTCTGG	CTGGCTCACA	GAAACACTGT	1500
	CCAAAGCTCA	AATAATAAAT	TCCGCGCGAA	CTTCACCATG	ACTTACCATC	TGAGCCCTGG	1560
	GAACATATGT	GTGGTTGCAC	AGACACGGAG	AAAATCAGCG	GAGTTCCTGC	TCCGAATCTT	1620
10	CCTGAAAATG	CCGACAGATG	ACAGGCACCT	GAGCAGCCAT	TTCAACCTCA	GAATGAAGGG	1680
	AAGCCCTTCA	GAACATGGCT	CCCAACAAAG	CATTTTCAAC	AGATATGCTC	AGCAGGTATG	1740
	GTACCTAGCA	CCCAGGGGCC	TTACGTGGGA	TTGGAGAAAG	GGGACCTGAG	GGAGGGACAG	1800
	CCCTCACAGG	CCCTTACTGG	GATGCAGAGA	GGAGAAGTGA	CTTGATGGAC	TATTTTACCT	1860
	GCCTCTCTTC	CTGGATCGTC	TCCAGAACTG	CTGTGGCTGC	CAAGCTCGGT	AGAGACGTGG	1920
	CGCCCCACCC	AGTCTCATCC	GGGGGACTTC	AAGCTGGAAT	GCAGAGCTTA	GAAAGGGAGG	1980
15	GGATAATTAT	GGGGTGTGAG	GTGCATTGCC	CTCTAAATCT	TTAAACAAGC	AATTGGCAGT	2040
	ACCCCGTGAA	AACTTTCTCT	CTCTACTCTG	GCCACCTCCC	ACCAACCTGG	CATCGTTCTT	2100
	CCCGGGAGCT	AGCCAGCTTC	AGAAAGCACA	TACAGCATCC	TTGCTGCCAA	ACCACCTATG	2160
	TGCACACAGG	ATTTCCTTAA	TGGCTTAATA	AACTGTTATA	AAGAACTCCT	TGACTTGTCA	2220
20	GAATAAAATA	GCTGCCAGGG	GCTCTGCACA	ATGAGCCTCT	TACCGTTAAA	AAAAAAAAAA	2280
	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA				

Seq ID NO: 327 Protein sequence:
Protein Accession #: BAB85075.1

25	1	11	21	31	41	51	
	MAYYQEPSVE	TSIIKFKDQD	FTTLRDHCLS	MGRITFKDET	PAADSSIGQK	LLQEKRLSNV	60
	IWKRPQDLBG	GPPHFILDDI	SRFDIQQGG	ADCFWLAALG	SLTNPQYVRQ	KILMVQSPFH	120
30	QYAGIFRFRF	WQCQGWVEVV	IDRLRFVQGD	KCLFVRPRHQ	NQBFWPCLE	KAYAKLLGSY	180
	BDLHYGLFED	ALVDLTGTVI	TNIHLHSSPV	DLVKAVKTAT	KAGSLITCAT	PSGPTDTAQA	240
	MENGLVSLHA	YTVVTGAELQ	IYRGWEEIIS	LWNPWGNET	ENRGRWSDGS	QWEETCDPR	300
	KSQHLHKRED	GEFWMSCQDF	QQKFIAMFIC	SEIPITLDHG	NTLHEGWSQI	MFRKQVILGN	360
	TAGGPRNDAQ	FNFSVQEPME	GTNVVVCVTV	AVTPSNLKA	DAKFLDFQV	ILAGSQKHCP	420
35	KLK						

Seq ID NO: 328 DNA sequence
Nucleic Acid Accession #: BC017490.1
Coding sequence: 74-2788

40	1	11	21	31	41	51	
	GTGGGTCACG	TGAACCACTT	TTGCGCGGAA	ACCTGGTTGT	TGCTGTAGTG	GCGGAGAGGA	60
	TGCTGGTACT	GCTATGGCGG	AATCATCGGA	ATCCTTCACC	ATGGCATCCA	GCCCGGCCCA	120
45	GCGTGGCGCA	GGCAATGATC	CTCTCACCTC	CAGCCCTGGC	CGAAGCTCCC	GGCGTACTGA	180
	TGCOCTACCC	TCCAGCCCTG	GCCGTGACCT	TCCACCATTT	GAGGATGAGT	CCGAGGGGCT	240
	CCTAGGCACA	GAGGGGCCCC	TGGAGGAAGA	AGAGGATGGA	GAGGAGCTCA	TTGGAGATGG	300
	CATGGAAGGG	GACTACCGCG	CCATCCGAGA	GCTGGACGCC	TATGAGGCGG	AGGGACTGGC	360
	TCTGGATGAT	GAGGACGTAG	AGGAGCTGAC	GGCCAGTCAG	AGGGAGGCAG	CAGAGCGGGC	420
50	CATGCGGCAG	CGTGACCCTG	AGGCTGGCCG	GGCCCTGGGC	CGCATGCGCC	GTGGGCTCCT	480
	GTATGACAGC	GATGAGGAGG	ACGAGGAGCG	CCTTGCCCGC	AAGCGCCGCC	AGGTGGAGCG	540
	GGCCACGGAG	GACGCGGAGG	AGGACGAGGA	GATGATCGAG	AGCATCGAGA	ACCTGGAGGA	600
	TCTCAAAGGC	CACCTCTGTG	TCCAGTGGGT	GAGCATGGCG	GGCCCCCGCG	TGGAGATCCA	660
	CCACCGCTTC	AAGAACTTCC	TGCGCACTCA	CGTCCGACGC	CACGCCACCA	ACGTCTTCAA	720
55	GGAGCGCATC	AGCGACATGT	GCAAAGAGAA	CCGTGAGAGC	CTGGTGGTGA	ACTATGAGGA	780
	CTTGGCAGCC	AGGGAGCACG	TGCTGGCCTA	CTTCTGCCT	GAGGCACCGG	CGGAGCTGCT	840
	GCAGATCTTT	GATGAGGCTG	CCCTGGAGGT	GGTACTGGCC	ATGTACCCCA	AGTACGACCG	900
	CATCACCAAC	CACATCCATG	TCCGCACTCT	CCACCTGCCT	CTGGTGGAGG	AGCTGCGCTC	960
	GCTGAGGCAG	CTGCATCTGA	ACCACTGAT	CCGCACCACT	GGGGTGGTGA	CCAGCTGCAC	1020
60	TGGCGTCTTG	CCCCAGCTCA	GCATGGTCAA	GTACAACTGC	AACAAGTGCA	ATTTCGTCTT	1080
	GGGTCTCTTC	TGCCAGTCCC	AGAAACGAGG	GGTGAACCA	GGCTCCTGTC	CTGAGTGCCA	1140
	GTGCGCGCGC	CCCTTTGAGG	TCAACATGGA	GGAGACCATC	TATCAGAACT	ACCAGCGTAT	1200
	CCGAATCCAG	GAGATCCAG	GCAAAGTGGC	GGCTGGCCGG	CTGCCCCGCT	CCAAGGACGC	1260
	CATTCTCTCT	CAGACATCTG	TGGACAGCTG	CAAGCCAGGA	GACGAGATAG	AGCTGACTGG	1320
65	CATCTATCAC	AACAACTATG	ATGGCTCCCT	CAACACTGCC	AATGGCTTCC	CTGTCTTTGC	1380
	CACTGTCTATC	CTAGCCAACC	ACGTGGCCAA	GAAGGACAAC	AAGGTTGCTG	TAGGGGAAC	1440
	GACCGATGAA	GATGTGAAGA	TGATCACTAG	CCTCTCCAAG	GATCAGCAGA	TCGGAGAGAA	1500
	GATCTTTGCC	AGCATTTGCT	CTTCCATCTA	TGGTCATGAA	GACATCAAGA	GAGGCCTGGC	1560
	TCTGGCCCTG	TTCCGAGGGG	AGCCCAAAAA	CCCAAGTGGC	AAGCACAAGG	TACGTGGTGA	1620
70	TATCAACGTG	CTCTGTGTGG	GAGACCTTGG	CACAGCGAAG	TCCAGATTTC	TCAAGTATAT	1680
	TGAGAAAGTG	TCCAGCCGAG	CCATCTTCAC	CACCTGGCCAG	GGGGCGTCCG	CTGTGGGCTT	1740
	CACGCGGTAT	GTCCAGCGGC	ACCCTGTTCAG	CAGGGAGTGG	ACCTTGGAGG	CTGGGGCCCT	1800
	GGTTCTGGCT	GACCGAGGAG	TGTGTCTCAT	TGATGAATTT	GACAAGATGA	ATGACCAAGG	1860
	CAGAACCAAG	ATCCATGAGG	CCATGGAGCA	ACAGAGCATC	TCCATCTCGA	AGGCTGGCAT	1920
75	CGTCACTCCC	CTGCAGGCTC	GCTGCACGGT	CATTGCTGCC	GCCCAACCCA	TAGGAGGGCG	1980
	CTACGACCCC	TGCTGACTTT	TCTCTGAGAA	CGTGGACCTC	ACAGAGCCCA	TCTCTCACG	2040
	CTTTGACATC	CTGTGTGTGG	TGAGGGACAC	CGTGGACCCA	GTCCAGGACG	AGATGCTGGC	2100
	CCGCTTCTGT	GTGGGACGCC	ACGTCAGACA	CCACCCAGC	AACAAGGAGG	AGGAGGGGCT	2160
	GGCCAAATGC	AGCGCTGCTG	AGCCCGCCAT	GCCTAACACG	TATGGCGTGG	AGCCCTTGCC	2220
80	CCAGGAGGTC	CTGAAGAAGT	ACATCATCTA	CGCCAAAGGAG	AGGGTCCACC	CGAAGCTCAA	2280
	CCAGATGGAC	CAGGACAAGG	TGGCCAAGAT	GTACAGTGAC	CTGAGGAAAG	AATCTATGGC	2340
	GACAGGCAGC	ATCCCCATTA	CGGTGCGGCA	CATCGAGTCC	ATGATCCGCA	TGGCGGAGGC	2400
	CCAAGCGCGC	ATCCATCTGC	GGGACTATGT	GATCGAAGAC	GACGCTCAAC	TGGCCATCCG	2460
	CGTGATGCTG	GAGAGCTTCA	TAGACACACA	GAAGTTCAGC	GTCATGCGCA	GCAATGCGCA	2520
85	GACTTTTGCC	CGCTACCTTT	CATTCCGGCG	TGACAACAAT	GAGCTGTGTC	TCTTCATACT	2580
	GAAGCAGTTA	GTGGCAGAGC	AGGTGACATA	TCAGCGCAAC	CGCTTTGGGG	CCGACGAGGA	2640
	CACATATTGAG	GTCCCTGAGA	AGGACTTGGT	GGATAAGGCT	CGTCAGATCA	ACATCCACAA	2700

CCTCTCTGCA TTTTATGACA GTGAGCTCTT CAGGATGAAC AAGTTCAGCC ACGACCTGAA 2760
 AAGGAAAAATG ATCCTGCAGC AGTTCCTGAGG CCCTATGCCA TCCATAAGGA TTCCTTGGGA 2820
 TTCTGGTTTG GGGTGGTCAG TGCCCTCTGT GCTTTATGGA CACAAAACCA GAGCACTTGA 2880
 TGAACCTCGGG GTACTAGGGT CAGGGCTTAT AGCAGGATGT CTGGCTGCAC CTGGCATGAC 2940
 TGTTTGTTC TCCAGCCTG CTTTGTGCTT CTCACCTTTG GGTGGGATGC CTGGCCAGTG 3000
 TGCTTACTT GGTGTCTGAA CATCTTGCCA CCTCCGAGTG CTTTGTCTCC ACTCAGTACC 3060
 TTGGATCAGA GCTGCTGAGT TCAGGATGCC TGCCTGTGTT TTAGGTGTTA GCCTTCTTAC 3120
 ATGGATGTCA GGAGAGCTGC TGCCCTCTTG GCGTGAAGTG CGTATTCAGG CTGCTTTTGC 3180
 TGCCCTTTGGC CAGAGAGCTG TTGGAAGATG TTTGTAATCG TTTTCAGTCT CTGTCAGGTT 3240
 TCTGTGCCCC TGTGGTGGAA GAGGGCAGCA CAGTGGCAGC GCAGCGTTCT GGGCTCCTCA 3300
 GTCGCAGGGG TGGGATGTGA GTCATGCGGA TTATCCACTC GCCACAGTTA TCAGCTGCCA 3360
 TTGCTCCCTG TCTGTTTCCC CACTCTCTTA TTTGTGCATT CGGTTTGTTT TCTGTAGTTT 3420
 TAATTTTAA TAAAGTTGAA TAAATATATA AAAAAAAAAA AAAAAA

Seq ID NO: 329 Protein sequence:
Protein Accession #: AAH17490.1

1 11 21 31 41 51
 MAESSESFTM ASSPAQRRRG NDPLTSSPGR SSRRTDALTS SPGRDLPPFE DSEGLLGTE 60
 GPLEEEDGE ELIGDGMERD YRAIPELDAY EAELALDDE DVEELTASQR EAAERAMRQR 120
 DREAGRGLGR MRRGLLYDS D EDEERFARK RRQVERATED GEDEEMIES IENLEDLKGH 180
 SVREWSMAG PRLEIHRFK NFLRTHVDSH GHNVFKERIS DMCKENRESL VVNYEDLAAR 240
 EHVLAFLPE APAELLQIFD EAALEVVLAM YPKYDRITNH IHVRISHLPL VBEELSLRQL 300
 HLNQLIRTSQ VVTSCTGVLP QLSMVKYNCN KCFVLGPFC QSQNQEVKPG SCPECQSAGP 360
 FEVNMERTIY QNYQIRIQE SPGKVAAGR L PRSKDAILLA DLVDSCKPGD EIELTGIYHN 420
 NYDGSJLNTAN GFPVPATVIL ANHVAKDKNK VAVGELTDED VKMTISLSKD QQIGEKIFAS 480
 IAPSIYGHED IKRGLALALF GBEPKNPGOK HKVRGDINVL LCGDPGTAKS QFLKYIEKVS 540
 SRAIFTTGGQ ASAVGLTAYV QRHPVSREWT LEAGALVLAD RGVCLIDEFD KMNDQDRTSI 600
 HEAMEQSSIS ISKAGIVTSL QARCTVIAAA NPIGGRYDPS LTFSENVDLT EPIISRFDIL 660
 CVVRDTPDVP QDEMLARFV GSHVRHHPN KEEGLANGS AAEPAMPNTY GVEPLPQEV 720
 KKYIYAKER VHPKLNQMDQ DKVAKMYS DL RKESMATGSI PITVRHIESM IRMAEAHARI 780
 HLRDVIYEDD VNMALRVMLB SFIDTQKPSV MRSMRKTPAR YLSFRDRDNE LLLFILKQLV 840
 AEQVTYQRNR PGAQQDTIEV PEKDLVDKAR QINIHNLSAF YDSELFRMKN FSHDLKRKMI 900
 LQQF

Seq ID NO: 330 DNA sequence
Nucleic Acid Accession #: M17254
Coding sequence: 257-1645

1 11 21 31 41 51
 GTCCGCGCGT GTCCGCGCCC GCGTGTGCCA GCGCGGCTGC CTTGGCCGCTG CGCGCGAGC 60
 CGGGTCGCAC TAACTCCCTC GCGCGCGACG GCGCGGCTAA CCTCTCGGTT ATTCCAGGAT 120
 CTTTGGAGAC CCGAGGAAAG CCGTGTGAC CAAAAGCAAG ACAATGACT CACAGAGAAA 180
 AAAGATGGCA GAACCAAGGG CAACATAAGC CGTCAGGTTG TGAACAGCTG GTAGATGGGC 240
 TGCTTACTG AAGGACATGA TTCAGACTGT CCCGAGCCCA GCAGCTCATA TCAAGGAAAGC 300
 CTTATCAGTT AGCAGTGGAG ACCAGTCTGT GTTGTAGTGT GCCTACGGAA CGCCACACCT 360
 GGCTAAGACA GAGATGACCG CGTCTCTCTC CAGCGACTAT GGACAGACTT CCAAGATGAG 420
 CCCACGCGTC CTTGAGCAGG ATTGGCTGTC TCAACCCCCA GCCAGGGTCA CCATCAAAAT 480
 GGAATGTAAC CTTAGCCAGG TGAATGGCTC AAGGAACCTC CCTGATGAAT GCAGTGTGGC 540
 CAAAGGCGGG AAGATGTGGG GCAGCCGAGA CACCGTTGGG ATGAACATAC GCAGCTACAT 600
 GGAGGAGAA GACATGCCAC CCCCAAACAT GACCAAGAAC GAGCGCAGAG TTATCGTGCC 660
 AGCAGATCCT ACGCTATGGA GTACAGACCA TGTGCGGCAG TGGCTGGAGT GGGCGGTGAA 720
 AGAATATGGC CTTCCAGACG TCAACATCTT GTTATTCAG AACTCGATG GGAAGGAACT 780
 GTGCAAGATG ACCAAGGACG ACTTCCAGAG GCTCACCCCC AGCTACAACG CCGACATCCT 840
 TCTCTCACAT CTCCACTACC TCAGAGAGAC TCCTCTTCCA CATTGACTT CAGATGATGT 900
 TGATAAAGCT TTACAAACT CTCCACGGTT AATGCATGCT AGAAACACAG ATTTACCATA 960
 TGAGCCCCCG AGGAGATCAG CCTGGACCGG TCACGGCCAC CCCACGCCCC AGTCGAAAGC 1020
 TGCTCAACCA TCTCTCTTCA CAGTGCCCAA AACTGAAGAC CAGCGTCTCT AGTTAGATAT 1080
 TTATCAGATT CTTGAGACCA CAAGTAGCCG CTTTGCAAT CCAGGCAGTG GCCAGATCCA 1140
 GCTTTGGCAG TTCCTCTGCG AGCTCCTGTC GGACAGCTCC AACTCCAGCT GCATCACCTG 1200
 GGAAGGCACC AACCGGGAGT TCAAGATGAC GGATCCCGAC GAGGTGGCCC GCGCTGGGG 1260
 AGAGCGGAAG AGCAAAACCA ACATGAACCT CGATAAGCTC AGCCGCGCCC TCCGTTACTA 1320
 CTATGACAAG AACATCATGA CCAAGGTCCA TGGGAAGCGC TACGCTTACA AGTTTCGACTT 1380
 CCACGGGATC GCCCAGGCCC TCCAGCCCCA CCCCCCGGAG TCATCTCTGT ACAGTACCTC 1440
 CTCAGACCTC CGGTACATGG GCTCCTATCA CGCCACCCA CAGAAGATGA ACTTTGTGGC 1500
 GCCCCACCTC CCAGCCCTCC CCGTGACATC TTCCAGTTTT TTTGCTGCCC CAAACCCATA 1560
 CTGGAATCA CCACTGGGG GTATATACCC CAACACTAGG CTCCCCCA GCCATATGCC 1620
 TTCTCATCTG GGCACCTTACT ACTAAAGACC TGGCGGAGGC TTTTCCCATC AGCGTGCACT 1680
 CACCAGCCCA TCGCCACAAA CTCTATCGGA GAACATGAAT CAAAGTGCC TCAAGAGGAA 1740
 TGAAGAAAGC TTTACTGGGG CTGGGGAAGG AAGCCGGAAG AGAGATCCAA AGACTCTTG 1800
 GAGGGAGTTA CTGAAGTCTT ACTACAGAAA TGAGGAGGAT GCTAAAAATG TCACGAATAT 1860
 GGACATATCA TCTGTGGAAT GACCTTGTA AAGACAGTGT ATGTAGAAGC ATGAAGTCTT 1920
 AAGGACAAAG TGCCAAAGAA AGTGGTCTTA AGAAATGTAT AAACCTTAGA GTAGAGTTTG 1980
 AATCCCACTA ATGCAAACTG GGATGAAACT AAGCAATAG AAACAACACA GTTTTGACCT 2040
 AACATACCGT TTATAATGCC ATTTAAAGGA AAACCTACCTG TATTTAAAAA TAGTTTCATA 2100
 TCAAAACCAA GAGAAAAGAG ACAGAGAGAGA CTGTGGCCCA TCAACAGACG TTGATATGCA 2160
 ACTGCATGCG ATGTGCTGTT TTGGTTGAAA TCAAAATACAT TCGGTTTGAT GGACAGCTGT 2220
 CAGCTTTCTG AAACCTGTGA GATGACCCAA AGTTTCCAAC TCCTTTACAG TATTACCGGG 2280
 ACTATGAAC AAAAGGTGGG ACTGAGGATG TGTATAGAGT GAGCGTGTGA TTGTAGACAG 2340
 AGGGGTGAAG AAGGAGAGG AAGAGGCAGA GAAGGAGGAG ACCAGGCTGG GAAAGAACT 2400
 TCTCAAGCAA TGAAGACTGG ACTCAGGACA TTTGGGACT GTGTACAATG AGTTATGGAG 2460
 ACTCGAGGGT TCATCAGCTG AGTGTATAC CAAACCCAGT GTTAGGAGAA AGGACACAGC 2520
 GTAATGGAGA AAGGGAATCA GTAGAAATCA GAAACAAAAA TGCGCATCTC TTTCTTTGTT 2580
 TGTCAAATGA AAATTTTAA TGGAAATGTC TGATATTTAA GAGAAACATT CAGGACCTCA 2640
 TCATTATGTG GGGCTTTGT TCTCCACAGG GTCAGGTAAG AGATGGCCTT CTGGCTGCC 2700

ACAATCAGAA ATCACGCAGG CATTGTGGGT AGGCGGCCTC CAGTTTTCCT TTGAGTCGCG 2760
 AACGCTGTGC GTTTGTGAGA ATGAAGTATA CAAGTCAATG TTTTTCCTCC TTTTATATA 2820
 ATAATTATAT AACTTATGCA TTTATACACT ACGAGTTGAT CTGCGGCAGC CAAAGACACA 2880
 CGACAAAGA GACAAATCGAT ATAATGTGGC CTTGAATTTT AACTCTGTAT GCTTAATGTT 2940
 TACATATGA AGTTATTAGT TCTTAGAATG CAGAATGTAT GTAATAAAT AAGCTTGGCC 3000
 TAGCATGGCA ATACAGATTT ATACAGGAGT CTGCATTGTC ACTTTTTTTA GTGACTAAAG 3060
 TTGCTTAATG AAAACATGTG CTGAATGTTG TGGATTTTGT GTTATAATTT ACTTTGTCCA 3120
 GGAACCTGTG CAAGGGAGAG CCAAGGAAT AGGATGTTTG GCACCC

Seq ID NO: 331 Protein sequence
 Protein Accession #: AA52398

1 11 21 31 41 51
 MIQTVDPFAA HIKEALSVVS EDQSLFECAY GTPHLAKTEM TASSSSDYGQ TSKMSPRVPO 60
 QDWLSQPPAR VTIKMCNPS QNGSRNSPD ECSVAKGGKM VGSPTDVGMM YGSYMEEKHM 120
 PPPNMTTNER RVIVPADPTL WSTDHVRQWL EWAVKEYGLP DVNILLFQNI DGKELCKMTK 180
 DDFQLRTPSY NADILLSHLH YLRETPPLHL TSDDVDKALQ NSPRLMHARN TDLPEYPPRR 240
 SAWTGHGHTP PQSKAAQPSF STVPKTEDQR PQLDPYQILG PTSRLANPG SQQIQLWQFL 300
 LELLSDSSNS SCITWEGTNG EFKMTDPDEV ARRWGERKSK FNNYDKLSR ALRYYIDKNI 360
 MTKVHGKRYA YKDFDFGIAQ ALQPHPESS LYKYPDLFY MGSYHAHPQK MNFVAPHEPA 420
 LPVTSSSFFA APNPYNSPT GGIYPNTRLP TSHMPSHLGT YY 462

Seq ID NO: 332 DNA sequence
 Nucleic Acid Accession #: NM_000020
 Coding sequence: 283-1794

1 11 21 31 41 51
 AGGAAACGGT TTATTAGGAG GGAGTGGTGG AGCTGGGCCA GGAGGAAGA CGCTGGAATA 60
 AGAAACATT TTGCTCCAGC CCCATCCCA GTCCCGGAG GCTGCGCGC CAGCTGCGCC 120
 GAGCGAGCCC CTCCCAGGCT CAGCCCGGT CCGGGGCGC GCCGAGCCC AGCCCGCGT 180
 CCAGCGCTGG CGGTGCAACT GCGGCGCGC GGTGGAGGG AGGTGGCCC GGTCCGCGA 240
 AGGCTAGCGC CCCGACACCC CCAGAGCGG CCAATGACCT GGGCTCCGCC 300
 AGGAAAGGCC TTCTGATGCT GCTGATGGCC TTGTGACCC AGGGAGACC TGTGAAGCCG 360
 TCTCGGGGCC CGCTGTGTGAC CTGCACGTGT GAGAGCCAC ATTGCAAGGG GCCTACCTGC 420
 CCGGGGGGCT GGTGCACAGT AGTGTCTGTG CCGGAGGAG GGAGGCACC CCAGGAACAT 480
 CGGGGCTGCG GGAACCTGCA CAGGAGCTC TGCAGGGGC GCCCACCGA GTTCTCAAC 540
 CACTACTGCT GCGACAGCCA CCTCTGCAAC CACAACGTGT CCCTGGTGTG GGAGGCCACC 600
 CAACCTCCTT CGGAGCAGCC GGAACAGAT GGCCAGCTGG CCCTGATCCT GGGCCCGGTG 660
 CTGGCCTTGC TGGCCTGGT GTCCCTGGGT GTCTGGGCC TGTGGCATGT CCGACGGAGG 720
 CAGGAGAAGC AGCGTGGCCT GCACAGCGAG CTGGGAGAGT CCAGTCTCAT CCTGAAAGCA 780
 TCTGAGCAGG GCGACACGAT GTTGGGGGAC CTCCTGGACA GTGACTGCAC CACAGGGAGT 840
 GGCTCAGGGC TCCCTTCCT GGTGCAGAG ACAGTGGCAC GGCAGTTGC CTTGGTGGAG 900
 TGTGTGGGAA AAGGCGCTTA TGGCGAAGTG TGGCGGGCT TGTGGCAGCG TGAGAGTGTG 960
 GCGGTCAAGA TCTTCTCCTC GAGGATGAA CAGTCTGGT TCCGGGAGAC TGAGATCTAT 1020
 AACACAGTAT TGCTCAGACA GCACACATC CTAGGCTTCA TCGCCTCAGA CATGACCTCC 1080
 CGCAACTCGA GCACGAGCT GTGGCTCATC ACGCACTACC ACGAGCACGG CTCCTCTAC 1140
 GACTTCTGCG AGAGCAGAC GCTGGAGCCC CATCTGGCTC TGAGGCTAGC TGTGTCCGCG 1200
 GCATTCGGCG TGGCGCACCT GCACGTGGAG ATCTTCGGTA CACAGGGCAA ACCAGCCATT 1260
 GCCCACCGCG ACTTCAAGAG CGCAATGTG CTGGTCAAGA GCAACCTGCA GTGTTCATC 1320
 GCCGACCTGG GCCTGGCTGT GATGCACTCA CAGGGCAGCG ATTACCTGGA CATCGGCAAC 1380
 AACCGAGAG TGGGCAACAA GCGGTACATG GCACCCGAGG TGCTGGACGA GCAGATCCG 1440
 ACGGACTGCT TTGAGTCTTA CAGTGGACT GACATCTGGG CCTTGGCCT GGTGCTGTGG 1500
 GAGATTGCCC GCGGAGACCT CGTGAATGGC ATCGTGGAG ACTATAGACC ACCCTTCTAT 1560
 GATGTGGTGC CCAATGACCC CAGCTTGGAG GACATGAAGA AGGTGGTGTG TGTGGATCAG 1620
 CAGACCCCA CCATCCCTAA CCGGCTGGCT GCAGACCCGG TCCTCTCAGG CCTAGCTCAG 1680
 ATGATGCGGG AGTGTGGTA CCAAAACCCC TCTGCCGAC TCACCGCGCT GCGGATCAAG 1740
 AAGACACTAC AAAAATTAG CAACAGTCCA GAGAAGCCTA AAGTGATTCA ATAGCCAGG 1800
 AGCACCTGAT TCCTTTCTGC CTGCAGGGG CTGGGGGGGT GGGGGGCACT GGATGTTGCC 1860
 CTATCTGGGT AGAGGTAGTG TGAGTGTGGT GTGTGCTGGG GATGGGAGC TGCGCCTGCC 1920
 TGCTCGGCCC CCAGCCCAACC CAGCCAAAAA TACAGCTGGG CTGAAACCTG ATCCCTGTCT 1980
 GTCTGGCCTG CTCAAAGCG CAGGCTCCCT GACGCTGGC TCTCTCCCA CCCCTATGGC 2040
 CAGCATGGTG CACCCCTAC CACTCCCGGG ACAGGATGCA AAGAGGCTC CAGAGTCAGA 2100
 GTGCCAAGCC AGGGAATCCC AGTCCAGAG TCAGAGCCCG GGCCTGCACT TTGCCCTCTG 2160
 CCCTTGATCA ACCCCACTGC CCCACAGAG CTGCCAGGGT GGCACAGGGC CCTGTCCAGC 2220
 CCCTGGCACA CACTTCCCTG CCAGGCCTCA GCCTCTAGCA TAAGCTCCAG AGAGCCAGGG 2280
 CCCATCAGTT TCTCTCTGTG GATTTGTATC TCAGCTCCAT GATGCTTGG GCTTCTGTCT 2340
 TCCTCAACAA GAGTGCAGCT TGCTGAATGT CAGCTGCTGG AGAGAGCTGG GGCCTGACTT 2400
 ACTAGGGCAT TAAATCCTAA GAGTCTCTAC TGAGGTGTGG CAGGATCACA GGCCAGTGA 2460
 AAAAGGGCAG CTCAGATGGG CAAGGCCAG GACTTTCAGA TTAAGTGA GAATATCGAG 2520
 GCCAAGCATG GCAGGGGGA GGTCAGTGGG TGTCAAGAGA CCCAGGTCTG ACCCGGATG 2580
 TTTGCTCCAT GTGACAAAAG CAGGCCTGTC TCAGGACCTT TTTCTTTCTT TTTCTCTCT 2640
 TTTTTTTTTT GACACGGAGT TTCCTCTGTG TTGTCCAGGC TAGAGTGCAA TGGCATGATC 2700
 CCAGCTCACC GCAACGTCTA CTTCCAGGT TCAATCATT CTCTGCCTC AGACTCCCGA 2760
 GTAGCTGGGA TTACAGGCAC ATGCCACCAT GCCTGGCTAA TTTTGTATAT TTAGTAGAAA 2820
 CAGGTTTCA CCATGCTGGC CATGCTGGTT CTCGAATCTC TGACCTCAGG TGTTCACCT 2880
 ACCTCAGCTT GCAAAAGTGC TGGGTTACA GGTGTGAGCC ATCGCGCTG GCCAGGACCT 2940
 TTGTTTCTTA TCTACATATT GGAAGATTG GTCTGATGT CCTTTAGGC TTCTTTAGCT 3000
 CTAGTTCTCT GACACTTCAG CTTATATCAC AGCTAACTTC YTCAGTCTCA TCTATTCTCT 3060
 ATGCTCCAGC CCCTGGCAAT TTGCCCTCAG ATGGGGGTTT GAAAATAACT TTAACCTGACT 3120
 CAAGGAGTGT CTGGAGCACC TCCTAGTCTA AGTCTGCAAG CTCAGTCTCT TGCCTAAAAC 3180
 CATGCCAGTG GGCACCTTGG GCTCAGACA GCTCTGGGCC TTTTGACCA AGCCAGCCC 3240
 CTCGCCCTCT CTGTGGCATA GTCTTCTCTG CCCAGGACT GCAGGGGCGC TTCCTCAGG 3300
 GCTTCCAAAG CTCAAAAGAA ATTGGCTCC ATCCAAAGA GCTCCAGCTC CCTACTGGC 3360
 CCCTGGCTTC AGGCCACAC CCCTGGGCCA GGSCCAGAGA GTGTGTCTCA GGAGATTTCA 3420
 ATGGGCTCTA GAGAGACACA CAGAAAGTTT GGGCATTGGG GAAATTTTCA AGGRTGTATG 3480

TATGGYTCAC GTATGGWCCA GGTGTGCTCTG GTCCYKGGGT GCAGGGAAGT GGGCTGCAGG 3540
GAAGTGGATT GGAGGGGAGC TTGAGGAATA TAAGGAGCGG GGGTGGAGAC TCAGGCTATG 3600
GACAAAGACA GCCCAAGGT TGGGAAGACC TGGCCTTAGT CGTCCTCAGC CTAGGGCAGG 3660
GCAGTGAAGA AGCCTCTCCC CGCTCCTGCT GTAATGACCC AGAGTAGCCT CCCAAGGCCG 3720
GCATCTTATG TGTGTCTTCC ACCATCTCTCA TGGTGGCACT TTTCTAGGCC TGTCTCCAG 3780
CATTGTGCAA GGCTCGGAAG AGAACCAGGA AGTGAACTG GGTGAAAACA GAAAGCTCAA 3840
TGGATGGGCT AGGTTCCAG ATCATTAGGG CAGAGTTTGC ACGTCTCTG GTTCACTGGG 3900
AATCCACCCA GCCCAGCAAT CATCTCCCTC TTTGAAGGAT TTTWATTCT ACTGGGTTTT 3960
GGAACAACT CCTGCTGAGA CCCACAGCC AGAACTGAA AGCAGCAGCT CCCCAAAGCC 4020
TGGAAATCC CTAAGAGAAG GCCTGGGGGA MAGGAATGG AGTGACAGGG GACAGGTAGA 4080
GAGAAGGGGG CCCAATGGCC AGGAGTGAA GGAGGTGGCG TTGCTGAGAG CAGTCTGCAC 4140
ATGCTTCTGT CTGAGTGACG GAAGGTGTTT CAGGCTCGAA ATTACACTTC TCGTACCTGG 4200
AGACGCTGTT TGTGGGAGCA CTGGGCTCAT GCCTGGCACA CAATAGGTCT GCAATAAACC 4260
ATGGTTAAAT CCTGAAAAA AAAAAA

Seq ID NO: 333 Protein sequence
Protein Accession #: NP_000011

1 11 21 31 41 51
MTLSPRKGL LMLLMALVTQ GDPVKPSRGP LVTCTCESPH CKGPTCRGAW CTVVLVREEG 60
RHPQEHRCGG NLHRELRCGR PTEFVNHYCC DSHLCNHVNS LVLEATQPPS EQPGTDGQLA 120
LILGPVLALL ALVALGVLGL WHVRRRQEKQ RGLHSELGES SLILKASEQG DTMLGDLLDS 180
DCTTSGSGSL PFLVQRTVAR QVALVECVGK GRYGEVWRGL WHGESVAVKI FSSRDEQSWF 240
RETEIYNTVL LRHDNILGFI ASDMTSRNSS TQLWLITHYH EHGSLYDFLQ RQTLPEPLAL 300
RLAVSAACGL AHLHVEIFGT QGKPAIAHRD FKSRNVLVKS NLQCCIDILG LAVMHSQGS D 360
YLDIGNNPRV GTRKRYMAPEV LDEQIRTDCE ESYKWTDIWA FGLVLWEIAR RTIVNGIVED 420
YRPPFYDVVP NDPSPEDMKK VVCVDQQTPT IPNRLAADPV LSLGAQMMRE CWYPNPSPARL 480
TALRIKKTILQ KISNSPEKPK VIQ

Seq ID NO: 334 DNA sequence
Nucleic Acid Accession #: NM_004126.1
Coding sequence: 108-329

1 11 21 31 41 51
GGCAGGAGCT CGTGCCGGCC TTCAGTTGTT TCGGGACGCG CCGAGCTTCG CCGCTCTTCC 60
AGCGGCTCCG CTGCCAGAGC TAGCCCGAGC CCGGTTCTGG GCGGAAAATG CCTGCCCTTC 120
ACATCGAAGA TTTGCCAGAG AAGGAAAAAC TGAAAATGGA AGTTGAGCAG CTTCGCAAG 180
AAGTGAAGTT GCAGAGACAA CAAGTGTCTA AATGTTCTGA AGAAATAAAG AACTATATTG 240
AAGAACGTTT TGGAGAGGAT CCTCTAGTAA AGGGAATTCC AGAAGACAAG AACCCCTTTA 300
AAGAAAAAGG CAGCTGTGTT ATTTTCATAA TAACTTGGGA GAACTGCAT CCTAAGTGGG 360
AGAACTAGTT TGTTTATGTT TTCCAGATA AAACCAACAT GCTTTTAAAG GAAGGAAGAA 420
TGAAATTAAG AGGAGACTTT CTTAAGCACC ATATAGATAG GGTATGTAT AAAAGCATAT 480
GTGCTACTCA TCTTTGCTCA CTATGCAGTC TTTTAAAGA GAGCAGAGAG TATCAGATGT 540
ACAATTATGG AAATAAGAAC ATTACTTGAG CATGACACTT CTTTCAGTAT ATTGCTTGAT 600
GCTTCAAATA AAGTTTGTCT TT

Seq ID NO: 335 Protein sequence
Protein Accession #: NP_004117.1

1 11 21 31 41 51
MPALHIEDLP EKEKLMKEVE QLRKEVKLQR QQVSKCSEBI KNYIEERSGE DPLVKGIPED 60
KNPFFKEKGC VIS

Seq ID NO: 336 DNA sequence
Nucleic Acid Accession #: NM_005795
Coding sequence: 555-1940

1 11 21 31 41 51
GCACGAGGGA ACAACCTCTC TCTCTSCAGC AGAGAGTGTC ACCTCCTGCT TTAGGACCAT 60
CAAGCTCTGC TAACTGAATC TCATCCTAAT TGCAGGATCA CATTGCAAGG CTTTCACTCT 120
TTCCACCTTT GCTTGTGGGT AAATCTCTTC TGCGGAATCT CAGAAAGTAA AGTTCCATCC 180
TGAGAAATATT TCACAAGAA TTTCTTAAAG AGCTGGACTG GGTCTTGACC CCTGGAATTT 240
AAGAAATTCT TAAAGACAAT GTCAAATATG ATCCAAGAGA AAATGTGATT TGAGTCTGGA 300
GACAATTGTG CATATCGTCT AATAATAAAA ACCCATACTA GCCTATAGAA AACAATATTT 360
GAATAATAAA AACCCATACT AGCCTATAGA AAACAAATAT TGAAAGATTG CTACCACTAA 420
AAGAAAACT ACTACAACCT GACAAGACTG CTGCAAACTT CAATTGGTCA CCACAACCTG 480
ACAGGTTGCG TATAAAACAA GATTGCTACA ACTTCTAGTT TATGTTATAC AGCATATTTT 540
ATTTGGGCTT AATGATGGAG AAAAAGTGTA CCCTGTATTT TCTGGTTCTC TTGCCTTTTT 600
TTATGATTCT TGTACAGCA GAATTAGAAG AGAGTCTGTA GGACTCAATT CAGTTGGGAG 660
TTACTAGAAA TAAATCATG ACAGCTCAAT ATGAATGTTA CCAAAGATTG ATGCAAGACC 720
CCATTCAACA AGCAGAAAGG GTTTACTGCA ACAGAACCTG GGATGGATGG CTTCTGCTGGA 780
ACGATGTTGC AGCAGGAACT GAATCAATGC AGCTCTGCCC TGATTACTTT CAGGACTTTG 840
ATCCATCAGA AAAAGTTACA AAGATCTGTG ACCAAGATGG AAATGGTTT AGACATCCAG 900
CAAGCAACAG AACATGGACA AATTATACCC AGTGTAATGT TAACACCCAC GAGAAAGTGA 960
AGACTGCAC TAAATTGTTT TACCTGACCA TAATTGGACA CGGATTGTCT ATTGCATCAC 1020
TGCTTATCTC GCTTGGCATA TTCTTTTATT TCAAGAGCCT AAGTTGCCAA AGGATTACCT 1080
TACACAAAAA TCTGTTCTTC TCATTTGTTT GTAACCTCTG TGAACAAATC ATTCACCTCA 1140
CTGCAGTGGC CAACAACCG GCCTTAGTAG CCACAATCC TGTAGTTGCG AAAGTGTCCC 1200
AGTTCAATCA TCTTTACCTG ATGGGCTGTA ATTACTTTT GATGCTCTGT GAAGGCATT 1260
ACCTACACAC ACTCATTGTG GTGGCCGTGT TTGCAGAGAA GCAACATTTA ATGTGTATT 1320
ATTTCTTGG CTGGGAGATT CCACTGATTC CTGCTGTAT ACATGCCATT GCTAGAAGCT 1380

TATATTACAA TGACAAATGCG TGGATCAGTT CTGATACCCA TCTCCTCTAC ATTATCCATG 1440
 GCCCAATTGG TGCTGCTTTA CTGGTGAATC TTTTTCCTT GTTAAATATT GTACGCGTTC 1500
 TCATCACCAA GTTAAAGATT ACACACCAAG CGGAATCCAA TCTGTACATG AAAGCTGTGA 1560
 GAGCTACTCT TATCTTGGTG CCATTGCTTG GCATTGAATT TGTGCTGATT CCATGGCGAC 1620
 CTGAAGGAAA GATTGCAGAG GAGGTATATG ACTACATCAT GCACATCCTT ATGCACTTCC 1680
 AGGGTCTTTT GGTCTCTACC ATTTTCTGCT TCTTTAATGG AGAGGTTCAA GCAATTCTGA 1740
 GAAGAACTCG GAATCAATAC AAAATCCAAT TTGGAACAG CTTTTCACAC TCAGAAGCTC 1800
 TTCTAGTGC GTCTTACACA GTGTCAACAA TCAGTGATGG TCCAGGTTAT AGTCATGACT 1860
 TCCCTAGTGA ACACCTAAAT GGAAGAAAGCA TCCATGATAT TGAAAATGTT CTCTTAAAC 1920
 CAGAAAATTT ATATAATTGA AAATAGAAGG ATGGTGTGCT CACTGTTTGG TGCTTCTCCT 1980
 AACTCAAGGA CTTGGACCCA TGACTCTGTA GCCAGAAGAC TTCATATTA AATGACTTTG 2040
 GGGAAATGTA TAAAGAAGAG CCTTCACATG AAATTAGTAG TGTGTTGATA AGAGTGTAAC 2100
 ATCCAGCTCT ATGTGGGAAA AAAGAAATCC TGGTTTGTAA TGTTTGTGAG TAAATACTCC 2160
 CACTATGCGT GATCTGAGCG TACTAACCTG ACATCACCAA GTGTGGAATT GGAGAAAAGC 2220
 ACAATCAACT TTTCTGAGCT GGTGAAGCC AGTTCAGCA CACCATTGAT GAATTCAAAC 2280
 AAATGGCTGT AAAACTAATC ATCATGTTG GGCATGATC TACCCTTATT CSCCCCAAGA 2340
 GACCTAGCTA AGGTCTATAA ACATGAAGGG AAAATTAGCT TTTAGTTTAA AAACCTCTTA 2400
 TCCCATCTTG ATTGGGGCAG TTGACTTTTT TTTTTCCTCA GAGTGCCGTA GTCTCTTTTG 2460
 TAACTACCTC CTCAAATGGA CAATACCAGA AGTGAATTAT CCTGCTGGC TTTCTTTTCT 2520
 CTATGAAAAG CAACCTGAGTA CAATTGTTAT GATCTACTCA TTTGCTGACA CATCAGTTAT 2580
 ATCTTGTGGC ATATCCATTG TGGAACTGG ATGAACAGGA TGTATAATAT GCAATCTTAC 2640
 TTCTATATCA TTAGGAAAAC ATCTTAGTTG ATGCTACAAA ACACCTTGTC AACCTCTTCC 2700
 TGTCTTACCA AACAGTGGGA GGGAAATCCT AGCTGTAAAT ATAAATTTTG CCCTTCCATT 2760
 TCTACTGTAT AAACAAATTA GCAATCATT TATATAAAGA AAATCAATGA AGGATTTCCT 2820
 ATTTTCTTGG AATTTGTAA AAAGAAATG TGAATAATGA GCTTGTAAAT ACTCCATTAT 2880
 TTTATTTTAT AGTCTCAAT CAAATACATA CAACCTATGT AATTTTAA GCAATATAT 2940
 AATGCAACAA TGTGTGTATG TTAATATCTG ATACTGTATC TGGGCTGATT TTTTAAATAA 3000
 AATAGAGTCT GGAATGCT

Seq ID NO: 337 protein sequence
 Protein Accession #: NP_005786.1

1 11 21 31 41 51
 MEKKCTLYFL VLLPFFMILV TAELEESPED SIQLGVTRNK IMTAQYECYQ KIMQDPIQQA 60
 EGVYCNRTWD GNLWNVDVAA GTESMQLCPD YFQDFDPSEK VTKICDQDGN WFRHPASNRT 120
 WNYNTQCNVN THEKVKTALN LFYLTIIHGH LSIALSLISL GIFFYFKSLR QORITLHKNL 180
 FFSFVNCNVV TIIHLTAVAN NQALVATNPV SKVBSQFIHL YLMGCNYPWM LCEGIYHLTL 240
 IVVAVPAEKQ HLMWYFLLGW GFPLIPACIH AIARSLYND NCWISSDTHL LYIHHGPICA 300
 ALLVNLFELL NIVRVLITKL KVTHQAESNL YMKAVRATLI LVPLLGIEFV LIPWRPEGKI 360
 AEEVYDIYMH ILMHFQGLLV STIFCFPNEG VQAILRRNWN QYKIQFGNSF SNSEALRSAS 420
 YTVSTISDGP GYSHDCPSEH LNGKSIHDIE NVLLKPNLY N

Seq ID NO: 338 DNA sequence
 Nucleic Acid Accession #: NM_001795
 Coding sequence: 25-2379

1 11 21 31 41 51
 GCACGATCTG TTCCTCCTGG GAAGATGCAG AGGCTCATGA TGCTCCTCGC CACATCGGGC 60
 GCCTGCTCTG CCCTGCTGGC AGTGGCAGCA GTGGCAGCAG CAGGTGCTAA CCCTGCCCAA 120
 CGGGACACCC ACAGCTCTGT GCCCACCCAC CGGCGCCAAA AGAGAGATTG GATTTGGAAC 180
 CAGATGCACA TTGATGAAGA GAAAACACC TCACTTCCCC ATCATGTAGG CAAGATCAAG 240
 TCAAGCGTGA GTCGCAAGAA TGCCAAGTAC CTGCTCAAAG GAGAATATGT GGGCAAGGTC 300
 TTCGGGCTCG ATGCAGAGAC AGGAGACGTG TTCGCCATTG AGAGGCTGGA CCGGAGAAAT 360
 ATCTCAGAGT ACCACCTCAC TGCTGTCAAT GTGGACAAGG ACACTGTTGA AAACCTGGAG 420
 ACTCTCTCCA GCTTCAACAT CAAAGTTCAT GACGTGAACG ACAACTGGCC TGTGTTCAAG 480
 CATCGGTTGT TCAATGCGTC CGTGCTGAG TCGTGGCTG TGGGGACCTC AGTCATCTCT 540
 GTGACAGCAG TGGATGCAGA CGACCCCACT GTGGGAGACC ACGCTCTGT CATGTACCAA 600
 ATCTCTGAAG GGAAGAGATA TTTTGCCATC GATAATTCTG GACGTATTAT CACAATAACG 660
 AAAAGCTTGG ACCGAGAGAA GCAGGCCAGG TATGAGATCG TGGTGAAGC GCGAGATGCC 720
 CAGGGCCTCC GGGGGGAGTC GGGCACGGCC ACCGTGCTGG TCACTCTGCA AGACATCAAT 780
 GACAACCTTC CCTTCTTAC CCAGACCAAG TACACATTTG TCGTGCTGTA AGACACCCGT 840
 GTGGGCACCT CTGTGGGCTC TCTGTTTGTG GAGGACCCAG ATGAGCCCCA GAACCGGATG 900
 ACCAAGTACA GCATCTTGCG GGGCGACTAC CAGGACGCTT TCACCATTTA GACAAACCCC 960
 GCCCACAAAC AGGGCATCAT CAAGCCCATG AAGCCTCTGG ATTATGAATA CATCCAGCAA 1020
 TACAGCTTCA TCGTCAAGGC CACAGACCCC ACCATCGACC TCCGATACAT GAGCCCTCCC 1080
 GCGGGAAACA GAGCCCAAGT CATTATCAAC ATCACAGATG TGGACGAGCC CCCCATTTTC 1140
 CAGCAGCCTT TCTACCATT CCAGCTGAAG GAAAACCAAG AGAAGCCTCT GATTGGCACA 1200
 GTGCTGGCCA TGGACCTGTA TCGGCTAGG CATAGCATTG GATACTCCAT CCGCAGGACC 1260
 AGTGACAAGG GCCAGTCTTT CCGAGTCACA AAAAAGGGGG ACATTTACAA TGAGAAAGAA 1320
 CTGGACAGAG AAGTCTACCC CTGGTATAAC CTGACTGTGG AGGCCAAAGA ACTGGATTCC 1380
 ACTGGAACCC CCACAGGAAA AGAATCCATT GTGCAAGTCC ACATTGAAGT TTTGGATGAG 1440
 AATGACAATG CCCCAGGATT TGCCAAGCCC TACCAGCCCA AAGTGTGTGA GAACGCTGTC 1500
 CATGGCCAGC TGGTCTCGCA GATCTCGCA ATAGACAAGG ACATAACACC ACGAAACGTG 1560
 AAGTTCAAAT TCACCTTGAA TACTGAGAAC AACTTTACCC TCACGGATAA TCACGATAAC 1620
 ACGGCCAACA TCACAGTCAA GTATGGGCGG TTTGACCGGG AGCATACCAA GGTCCACTTC 1680
 CTACCCGTGG TACTCTCAGA CAATGGGATG CCAAGTCGCA CGGGCACCCG CACGCTGACC 1740
 GTGGCCGTGT GCAAGTGCAA CGAGCAGGGC GAGTTCACCT TCTGCGAGGA TATGGCCGCC 1800
 CAGGTGGGCG TGAGCATCCA GGCAGTGGTA GCCATCTTAC TCTGCATCCT CACCATCACA 1860
 GTGATCACCC TGCTCATCTT CCTGCGGCGG CGGCTCCGGA AGCAGGCCCG CGCGCACGGC 1920
 AAGAGCGTGC CGAGATCCA CGAGCAGCTG GTCACCTACG ACGAGGAGGG CGGCGGCGAG 1980
 ATGGACACCA CCAGCTACGA TGTGTCGGTG CTCACCTCGG TGCCTCCGCG CGGGGCCAAG 2040
 CCCCCTGGCG CGCGCTGGA CGCCCGGCCCT TCCCTCTATG CGCAGGTGCA GAAGCCACCG 2100
 AGGCACGCGC CTGGGGCACA CGGAGGGGCC GGGGAGATGG CAGCCATGAT CGAGGTGAAG 2160
 AAGGACGAGG CGGACACAGA CGGCGACGGC CCCCCTACG ACACGCTGCA CATCTACGGC 2220
 TACGAGGCT CCGAGTCCAT AGCCGAGTCC CTCAGCTCCC TGGGCACCGA CTCATCCGAC 2280

5	TCTGACGTGG	ATTACGACTT	CCTTAACGAC	TGGGGACCCA	GGTTTAAGAT	GCTGGCTGAG	2340
	CTGTACGGCT	CGGACCCCGG	GGAGGAGCTG	CTGTATTAGG	CGGCCGAGGT	CACTCTGGGC	2400
	CTGGGGACCC	AAACCCCCCTG	CAGCCCAGGC	CAGTCAGACT	CCAGGCACCA	CAGCCTCCAA	2460
	AAATGGCAGT	GACTCCCCAG	CCAGCACCC	CTTCCTCGTG	GGTCCCAGAG	ACCTCATCAG	2520
	CCTTGGGATA	GCAAACTCCA	GGTTCTTGAA	ATATCCAGGA	ATATATGTCA	GTGATGACTA	2580
	TTCTCAAAATG	CTGGCAAATC	CAGGCTGGTG	TTCTGTCTGG	GCTCAGACAT	CCACATAACC	2640
	CTGTACCCCA	CAGACCGCCG	TCTAACTCAA	AGACTTCCTC	TGGCTCCCCA	AGGCTGCAAA	2700
	GCAAAACAGA	CTGTGTTTAA	CTGCTGCAGG	GTCTTTTCTT	AGGGTCCCTG	AACGCCCTGG	2760
10	TAAGGCTGGT	GAGGTCTCTG	TGCCTATCTG	CCTGGAGGCA	AAGGCCTGGA	CAGCTTGACT	2820
	TGTGGGGCAG	GATTCTCTGC	AGCCCATTC	CAAGGGAGAC	TGACCATCAT	GCCCTCTCTC	2880
	GGGAGCCCTA	GCCCTGCTCC	AACCTCCATC	TCCACTCCAA	GTGCCCCACC	ACTCCCCAAC	2940
	CCCTCTCCAG	GCCTGTCAAG	AGGGAGGAAG	GGGCCCCATG	GCAGCTCCTG	ACCTTGGGTC	3000
	CTGAAGTGAC	CTCACTGGCC	TGCCATGCCA	GTAACCTGTG	TGTACTGAGC	ACTGAACCAC	3060
15	ATTCAGGGAA	GCTCTTATTA	AACCTTGAAG	CAACTGTGAA	TTCATTCTGG	AGGGGCAGTG	3120
	GAGATCAGGA	GTGACAGATC	ACAGGGTGAG	GGCCACCTCC	ACACCCACCC	CCTCTGGAGA	3180
	AGGCTTGGAA	GAGCTGAGAC	CTTGCTTTGA	GACTCCTCAG	CACCCCTCCA	GTTTTCCTTG	3240
	AGAAGGGGCA	GATGTTCCCG	GAGATCAGAA	GACGCTCTCC	CTTCTCTGCC	TCACCTGGTC	3300
	GCCAAATCCAT	GCTCTCTTTC	TTTTCTCTGT	CTACTCCTTA	TCCCTTGGTT	TAGAGGAACC	3360
20	CAAGATGTGG	GCTCTTATTA	AACCTTGAAG	CAACTGTGAA	TTCATTCTGG	AGGGGCAGTG	3420
	GCCGAGCATG	TGCTTTTACA	CCTCGCTGTT	GTCCATATCT	AGGGAATGTA	CCCTCAGGGA	3480
	CACCTTGGAA	AGGGAAGGCC	CTGCCCTGCC	CAACCTCTGT	GGTCACCCAT	GCATCATTTCC	3540
	ACTGGAACGT	TTCCTGCAA	ACACACCTTG	GAGAAGTGGC	ATCAGTCAAC	AGAGAGGGGC	3600
	AGGGAAGGAG	ACACCAAGCT	CACCCCTCGT	CATGACCCGA	GGTTCCTCACT	CTGGCAAAGC	3660
25	CCCTCACACT	GCAAGGGATT	GTAGATAACA	CTGACTTGTG	TGTTTTAAAC	AATAACTAGC	3720
	TTCTTATAAT	GATTTTTTTC	CTAATGATAC	TTACAAGTTT	CTAGCTCTCA	CAGACATATA	3780
	GAATAAGGGT	TTTTGCTATA	TAAGCAGGTT	GTATTATTAG	TTAACAATAT	TAATTCAGGT	3840
	TTTTTAGTTG	GAAAAACAAT	TCCTGTAACC	TTCTATTTTC	TATAATTGTA	GTAATTGCTC	3900
	TACAGATAAT	GTCTATATAT	TGGCCAAACT	GGTGCAATGAC	AAGTACTGTA	TTTTTTTATA	3960
30	CCTAAATAAA	GAAAAATCTT	TAGCCTGGGC	AACAAAAAAA			

Seq ID NO: 339 Protein sequence
Protein Accession #: NP_001786

35	1	11	21	31	41	51	
	MQRLMMLLAT	SGACLGGLLAV	AAVAAGANP	AQRDTHSLLP	THRRQRKDWI	WNQMHIIDEK	60
	NTSLPHHVKG	IKSSVSRKQA	KYLLKGEYVG	KVFRVDAETG	DVFAIERLDR	ENISEYHLTA	120
	VIVDKDTGM	LETPSSFTIK	VHDVNDNWPV	FTHRLFNASV	PSSAVGTSV	ISVTAVDADD	180
40	PTVGDHASVM	YQILKGKEYF	AIDNSGRIIT	ITKSLDREKQ	ARYEIVVEAR	DAQGLRGDSG	240
	TATVLVTLQD	INDNFPPFTQ	TKYTFVVPED	TRVGTSVGSL	FVEDPDEFQV	RTMKYSILRG	300
	DYQDAFTIET	NPAHNEGIIK	PMKPLDYEYI	QYQSFIYEAT	DPTIDLRYMS	PPAGNRAQVI	360
	INITVDDEPP	IFQQPFYHFQ	LKENQKKPLI	GTVLAMDPA	ARHSIGYSIR	RTSDKGQFFR	420
	VTKKGDYNE	KELDREVPW	YNLTVEAKBL	DSTGTPTGKE	SIVQVHIEVL	DENDNAPEFA	480
45	KPYQPKVCN	AVHGQLVLQI	SAIDKDIPT	NVKFKFTLNT	ENNFLTLDNH	DNTANITVKY	540
	GQFDRHRTV	HFLPVVISDN	GMPSRTGTST	LTVAVCCKNE	QGEPTFCEDM	AAQVGVSIQA	600
	VVAILLCLIT	ITVITLLIFL	RRRLRKQARA	HGKSVPEIHE	QLVTYDEEGG	GEMDTSYDV	660
	SVLNSVRRGG	AKPRPALDA	RPSLYAQVQK	PPRHAPGAHG	GPGEMAAMIE	VKKBADHDG	720
50	DGPPYDTLHI	YGYEGSESIA	ESLSGLGTD	SDSDVDYDFL	NDWGRPRFML	AELYGSDPRE	780
	ELLY						

Seq ID NO: 340 DNA sequence
Nucleic Acid Accession #: NM_003088
Coding sequence: 112-1593

55	1	11	21	31	41	51	
	CGCGAGGGTG	CGTGCGGGGC	GCGGCAGCCG	AACAAAGGAG	CAGGGGCGCC	GCCGAGGGA	60
60	CCCGCCACCC	ACCTCCCGGG	GCCGCGCAGC	GGCCTCTCGT	CTACTGCCAC	CATGACCGCC	120
	AACGCGACAG	CCGAGGCGGT	GCAGATCCAG	TTCCGCTCTA	TCAACTGCGG	CAACAAGTAC	180
	CTGACGCGCG	AGGGCTTCCG	GTTCAAGGTG	AACGCGTCCG	CCAGCAGCCT	GAAGAAGAAG	240
	CAGATCTGGA	CGCTGGAGCA	GCCCCCTGAC	GAGGCGGGCA	GCGCGGCGGT	GTGCTCGCGC	300
	AGCCACCTGG	GCCGCTACCT	GCGGCGGAC	AAGGACGGCA	ACGTGACCTG	CGAGCGCGAG	360
65	GTGCCCGGTC	CCGACTGCGG	TTTCTCTATC	GTGGCGCACG	ACGACGCTCG	CTGGTCTGCTG	420
	CAGTCCGAGG	CGCACCAGCG	CTACTTCCGC	GGCACGCGAG	ACCGCTCTGC	CTGCTTCGCG	480
	CAGACGGTGT	CCCCGCGCGA	GAAGTGGAGC	GTGCACATCG	CCATGACCCG	TCAGGTCAAC	540
	ATCTACAGTG	TCACCCGTAA	GCGCTACGCG	CACCTGAGCG	CGCGGCGGGC	CGACGAGATC	600
	GCGGTGGACC	GGACGCTGCC	CTGGGGCGTC	GACTCGCTCA	TCACCTCTCG	CTTCCAGGAC	660
70	CAGCGCTACA	GCGTGCAGAC	CGCCGACCC	CGCTTCTCTG	GCCACGACGG	GCGCTGCTGTG	720
	GCGCGCCCCG	AGCCGCGCC	TGGCTACACG	CTGGAGTTCC	GCTCCGCGAA	GGTGGCCTTC	780
	CGCGACTGCG	AGGGCCGTTA	CCTGGCGCGG	TGCGGGCCCA	GCGGCACGCT	CAAGGCGGGC	840
	AAGGCCACCA	AGGTGGGCAA	GGACGAGCTC	TTTGCTCTGG	AGCAGAGCTG	CGCCAGGTC	900
	GTGCTGCAGG	CGGCCAACGA	GAGGAACGTG	TCCACGCGCC	AGGGTATGGA	CCTGTCTGCC	960
75	AATCAGGACG	AGGAGACCGA	CCAGGAGACC	TTCCAGCTGG	AGATCGACCG	CGACACCAA	1020
	AAGTGTGCCT	TCCGTACCCA	CACGGGCAAG	TACTGGACGC	TGACGGCCAC	CGGGGCGGTG	1080
	CAGTCCACCG	CTCCAGCAAA	GAATGCCAGC	TGCTACTTTG	ACATCGAGTG	CGGTGACCCG	1140
	CGCATCACAC	TGAGGGCGTC	CAATGGCAAG	TTTGTAACCT	CCAAGAAGAA	TGGGCGAGCTG	1200
	GCGGCTCGGG	TGAGACAGC	AGGGGACTCA	GAGCTCTTCC	TCATGAAGCT	CATCAACCCG	1260
80	CCCATCATCG	TGTTCCGCGG	GGAGCATGGC	TTTCATCGGT	GCCGCAAGGT	CACGGGCACC	1320
	CTGGACGCCA	ACCGCTCCAG	CTATGACGTC	TTCCAGCTGG	AGTTCACCGA	TGGCGCTTAC	1380
	AACATCAAG	ACTCCACAGG	CAAACTACTG	ACGGTGGGCA	GTGACTCCGC	GGTCAACGAC	1440
	AGCGGCGACA	CTCTGTGCTA	CTTCTTCTTC	GAGTTCTGCG	ACTATAACAA	GGTGGCCATC	1500
	AAGGTGGGCG	CGGCTTACCT	GAGGGGCGAC	CACGACGGCG	TCCTGAAGGC	CTCGGCGGAA	1560
	ACCGTGGACC	CGGCTCTGCT	CTGGGAGTAC	TAGGGCCGGC	CGGTCTCTCC	CGGCCCTCTC	1620
85	CCACATGGGG	GCTCTGCTCA	ACCCTCCCTG	CTAACCCCTT	CTCCGCGAGG	TGGGCTCCAG	1680
	GGCGGGAGGC	AAGCCCCCTT	GCCTTCAAAA	CTGGAACCC	CAGAGAAAC	GGTGGCCCA	1740
	CCTGTGCGCC	CTATGGACTC	CCCACTCTCC	CCTCGCGCCG	GGTTCCTTAC	TCCCTCGGG	1800

TCAGCGGCTG CGGCCTGGCC CTGGGAGGGA TTTCAGATGC CCCTGCCCTC TTGCTCTGCCA 1860
 CGGGGCGAGT CTGGCACCTC TTTCTTCTGA CCTCAGACGG CTCTGAGCCT TATTTCTCTG 1920
 GAAGCGGCTA AGGAGCGGTT GGGGGCTGGG AGCCCTGGGC GTGTAGTGTA ACTGGAATCT 1980
 TTTGCTCTC CCAGCCACCT CCTCCAGCC CCCCAGGAGA GCTGGGCACA TGTCCCAAGC 2040
 CTGTCACTGG CCTCCCTGG TCACTGTCC CCGAAACCCC TGCTTGGGAA GGGAACTGT 2100
 CGGGAGGGCT AGGACTGACC CTTGTGGTGT TTTTGGGT GGTGGCTGGA AACAGCCCCT 2160
 CTCCACGCTG GGAGAGGCTC AGCCTGGCTC CCTCCCTGG AGCGGCAGGG CGTGACGGCC 2220
 ACAGGGTCTG CCCGCTGCAC GTTCTGCCAA GGTGGTGGTG GCGGGCGGGT AGGGGTGTGG 2280
 GGGCGCTCTT CTTCTGTCTT CTTTCTTTC ACCCTAGCCT GACTGGAAGC AGAAAATGAC 2340
 CAAATCAGTA TTTTATTA TGAATATTA TTGCTGGAGG CGTCCCAGGC AAGCCTGGCT 2400
 GTAGTAGCGA GTGATCTGGC GGGGGGCGTC TCAGCACCTC CCCCAGGGGG TGCATCTCAG 2460
 CCCCCTCTTT CGTCTCTCC CGTCCAGCCC CAGCCCTGGG CCTGGGCTGC CGACACCTGG 2520
 CGCAGAGCCC CTGCTGTGAT TGGTGTCTCC TGGGCTCTCC GGGTGGATGA AGCCAGGCGT 2580
 CGCCCCCTCC GGGAGCCGCG GGGTGAAGCG CCGGGGCCCC CCGTCTGCCA GCCTCCCCCG 2640
 TCCCCAATCT GCATCTCACT CTGGGTGTCT TGGTCTTTTA TTTTGTGTA GTGTCAATTG 2700
 TATAACTCTA AACGCCCATG ATAGTAGCTT CAAACTGGAA ATAGCGAAAT AAAATAACTC 2760
 AGTCTGC

Seq ID NO: 341 Protein sequence
 Protein Accession #: NP_003079

1 11 21 31 41 51
 MTANGTAEAV QIQFGLINCG NKYLTAFAFG FKNVASASSL KKKQIWTLEQ PPDEAGSAAV 60
 CLRSHLGRYL AADKGNVTC EREVPGPDCR FLIVAHDDGR WSLQSEAHRR YPGGTEDRLS 120
 CFAQTVSPA E KWSVHIAMHP QVNIYSVTRK RYAHLSARPA DEIAVDRDVP WGVDSLITLA 180
 FQDQRYSVQT ADHRFLRHG RLVARPEPAT GYTFLEFRSGK VAFRDCGGRY LAPSPSGTL 240
 KAGKATKVGK DELFALEQSC AQVVLQAANE RNVSTRQGM DLSANQDEETD QETFQLEIDR 300
 DTKKCAPRTH KGYWTLTAT GGVQSTASSK NASCYFDIEW RDRRITLRAS NGKFVTSKN 360
 GQLAASVETA GSELEFLMKL INRPIIVFRG EHGFIGCRKV TGTLDANRSS YDVFQLEFND 420
 GAYNIKDSTG KYWTGSDSA VTSSGDTFVD FFFPEPCDYNK VAIKVGGRYL KGDHAGVLKA 480
 SAETVDPASL WEY

Seq ID NO: 342 DNA sequence
 Nucleic Acid Accession #: FGENESH predicted
 Coding sequence: 660..1705

1 11 21 31 41 51
 CGCTCCGCAC ACATTTCCTG TCGCGGCCTA AGGGAAGCTG TTGGCCGCTG GGGCCGCGGG 60
 GGGATTCTTG GCAGTTGGGG GGTCCGTCGG GAGCGAGGGC GAGAGGGGAA GAGAGGGGAA 120
 CCGGGTGGG GAAGCCAGCT GTAGAGGGCG GTGACCGCGC TCCAGACACA GCTCTGCGTC 180
 CTCGAGCGGG ACAGATCCAA GTTGGGAGCA GCTCTGCGTG CCGGGCCCTCA GAGAATGAGG 240
 CCGGCGTTCG CCTGTGCTCT CCTCTGGCAG GCGCTCTGGC CCGGGCCGGG CGGCGGCGAA 300
 CACCCCACTG CCGAGCCGTC TGGCTGCTCG GCGCTCGGGG CCTGCTACAG CCTGCAACC 360
 GCTACCATGA AGCGCGAGG GCGCGAGGAG GCCTGCATCC TGCGAGGTGG GCGGCTCAGC 420
 ACCGTGCGTG CCGGAGCGCA GTGCTCGCGT TCGTCCGCGC TCGTCCGCGC AGGCCAGGG 480
 CCGGAGGGGG GCTCCAAAGA CCTGCTGTTC TGGGTGCGAC TGGAGCGCAG CGGTTCCAC 540
 TGCACCTCTG AGAAGCAGCC TTTGCGGGGT TTTCTCTGGC TGTCCTCCGA CCGCGCGGGT 600
 CTCGAAAGCG ACACGCTGCA GTGGGTGGAG GAGCCCCAAC GCTCCTGCAC CCGCGGAGAG 660
 TGCGCGGTAG TCCAGGCCAC CGGTGGGGTC GAGCCCGCAG CTGGAAGGAG ATGCGATGCC 720
 ACCCTGCGGC CAAAGCGCTT CTGTGCAAGT ACCAGTTTGA GGTCTTGTGT CCGCGCGCGC 780
 GCGCCGGGGC CGCTCTAAC TTGAGCTATC GCGCGCCCTT CCAAGCTGAC AGCGCGGCTC 840
 TGGACTTCAG TCCACTCTGG ACCGAGGTGA GTGCGCTCTG CCGGGGACAG CTCCCGATCT 900
 CAGTTACTTG CATCGCGGAC GAAATCGGCG CTCGCTGGGA CAAACTCTCG GCGATGTGT 960
 TGTGTCCCTG CCGCGGAGG TACCTCCGTG CTGGCAATG CGCAGAGCTC CCTAAGTGCC 1020
 TAGACGACTT GGGAGGCTTT GCCTGCGAAT GTGCTACGGG CTTGAGCTG GGGAGGAGG 1080
 GCGGCTCTTG TGTGACCACT GGGGAAGGAC AGCCGACCTT TGGGGGAGC GGGGTGCCCA 1140
 CCAGGCGCCC GCGGCGCACT GCAACAGGCC CCGTGCCGCA GAGAACATGG CCAATCAGGG 1200
 TCGACGAGAA GCTGGGAGAG ACACCACTG TCCCTGAACA AGACAATTCA GTAACATCTA 1260
 TTCTTGAGAT TCTCTGATGG GGATCACAGA GCACGATGTC TACCTTCAA ATGTCCCTTC 1320
 AAGCCGAGTC AAAGGCCACT ATCACCCTAT CAGGGAGCGT GATTTCCAAG TTTAATTCTA 1380
 CGACTTCTCT TGCACTCTCT CAGGCTTTCT ACTCCTCTCT TGCGTGGTCT TTTAATTCTG 1440
 TGAGCACAGC AGTAGTAGTG TTGGTGTATCT TGACCATGAC AGTACTGGGG CTTGTCAAGC 1500
 TCTGCTTTCA CGAAAGCCCC TCTTCCAGC CAAGGAAGGA GTCTATGGGC CCGCGGGGCC 1560
 TGGAGAGTGA TCTGAGCCC GCTGCTTTGG GCTCCAGTTC TGACCATGTC ACAAACAATG 1620
 GGGTGAAAGT CCGGGAAGT GATCTGCGGG ACAGAGCAGA GGGTGCCTTG CTGGCGGAGT 1680
 CCCCCTCTTG CTCTAGTGAT GCATAG

Seq ID NO: 343 Protein sequence
 Protein Accession #: FGENESH predicted

1 11 21 31 41 51
 MGKDFMTKTP KAPATKAKID KWDLIKLSKF CTAKETIIRV NSQPTDWQKT FAIYPSDKGV 60
 IARIYKELEQ IYKKKKPTKT LRTHFLSRPK GNCWPLGPRG DSWQLGGPSG ARAEGKGGGT 120
 GLGKPAVEGG DRAPDTALRP RAGQIQVGSS SACGASENEA GVRPVPLAG ALARAGRRT 180
 PHCRPCWLLG LGGLLQAPAP YHEAAGRG G LHPARWGAQH RACGRRAARC ARAPAGRPR 240
 RRGQLRPAVL GRTGAQAPPL HPGERAFAGF LLAVLRFRRS RKRHAAVGGG APTLLHRAEM 300
 RGTGPHRWGR ARSWKEMRCH LRANGYLCKY QFVLCAPAP PGAASNLVSR APFQLHSAAL 360
 DFSPPGTEVS ALCRGQLPIS VTICADEIGA RWDKLSGDVL CPCPGRYLRA GKCAELPNCL 420
 DDLGGFACCE ATGFELGKDG RSCVTSGBGQ PTLGGTGVPT RRPATATSP VPQRTWPIRV 480
 DEKLGETPLV PEDDNSVTSI PEIPRWGSQS TMSLTQMSLQ AESKATITPS GSVISKFNST 540
 TSSATPAQFD SSSAVVFIFV STAVVVLVIL TMTVLGLVKL CFHESPSSQP RKESMGPFGL 600
 ESDPEPAALG SSSAHCTNNG VKVGDCLRD RAEALLAES PLGSSDA

Seq ID NO: 344 DNA sequence
Nucleic Acid Accession #: NM_012072
Coding sequence: 149-2107

5
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85

```

1      11      21      31      41      51
|      |      |      |      |      |
AAAGCCCTCA GCCTTTGTGT CCTTCTCTGC GCCGAGTGG CTGCAGCTCA CCCCTCAGCT 60
CCCCTTGGGG CCCAGCTGGG AGCCGAGATA GAAGCTCCTG TCGCGCTGG GCTTCTCGCC 120
TCCCGCAGAG GGCACACAG AGACCGGAT GGCCACCTCC ATGGGCTGCT TGCTGCTGCT 180
GCTGCTGCTC CTGACCCAGC CCGGGGCGGG GACGGGAGCT GACACGGAG CGGTGGTCTG 240
CGTGGGGACC GCCTGTCTACA CGGCCCACTC GGGCAAGCTG AGCGCTGCC AGGCCAGAA 300
CCACTGCAAC CAGAACGGGG GCAACCTGGC CACTGTGAAG AGCAAGGAG AGGCCAGCA 360
CGTCCAGCGA GTACTGGCCC AGCTCCTGAG GCGGGAGGCA GCCCTGACGG CGAGGATGAG 420
CAAGTTCTGG ATTGGGCTCC AGCGAGAGAA GGGCAAGTGC CTGGACCCCTA GTCTGCGGCT 480
GAAGGGCTTC AGCTGGGTGG GCGGGGGGGA GGACACGCCT TACTCTAACT GGCACAAGGA 540
GCTCCGGAAC TCGTGCATCT CCAAGCGCTG TGTGTCTCTG CTGTGGACC TGTCCAGCC 600
GCTCCTTCCC AACCGCTGCG CCAAGTGGTC TGAGGGCCCC TGTGGAGCC CAGGCTCCCC 660
CGGAAGTAAC ATTGAGGGCT TCGTGTGCAA GTTCAGCTTC AAAGGCATGT GCCGGCCTCT 720
GGCCCTGGGG GGCCCGAGTC AGGTGACCTA CACCACCCCT TTCCAGACCA CCAGTTCTCT 780
CTTGGAGGCT GTGCCCTTTG CCTCTGCGGC CAATGTAGCC TGTGGGGAAG GTGACAAGGA 840
CGAGACTCAG AGTCATTATT TCCTGTGCAA GGAGAAGGCC CCCGATGTGT TCGACTGGGG 900
CAGCTCGGGC CCCCTCTGTG TCAGCCCCAA GTATGGCTGC AACTTCAACA ATGGGGGCTG 960
CCACCAGGAC TGCTTTGAAG GGGGGGATGG CTCCTTCTCT TCGCGCTGCC GACCAGGATT 1020
CCGGCTGCTG GATGACCTGG TGACCTGTGC CTCTCGAAAC CCTTGCAGCT CCAGCCCATG 1080
TCGTGGGGGG ACCCTGCTGG TCCTGGGACC CCATGGGAAA AACTACACGT GCCGCTGCC 1140
CCAAGGGTAC CAGCTGGACT CGAGTCAGCT GGACTGTGTG GACGTGGATG AATGCCAGGA 1200
CTCCCCCTGT GCCCAGGAGT GTGTCAACAC CCCTGGGGGC TTCGCTGCG AATGCTGGGT 1260
TGGCTATGAG CCGGCGGCTC CTGGAGAGGG GGCCTGTGAG GATGTGGATG AGTGTGCTCT 1320
GGGTGCGCTG CCTTGGCCCC AGGCGTGCAC CAACACAGAT GGCTCATTTT ACTGCTCCTG 1380
TGAGGAGGGG TACGTCTCTG CCGGGGAGGA CCGGACTCAG TGCCAGGACG TGGATGAGTG 1440
TGTGGGCCCC GGGGGCCCCC TCTGCGACAG CTGTGCTTTC AACACACAAG GGTCTTCCA 1500
CTGTGGCTGC CTGCCAGGCT GGGTGTCTGC CCCAAATGGG GTCTCTTGCA CCATGGGGCC 1560
TGTGTCTCTG GGACCAACAT CTGGGCCCCC CGATGAGGAG GACAAAGGAG AGAAGAAGG 1620
GAGCAGCGTG CCCCAGCTG CAACAGCCAG TCCCAACAAG GGGCCCCGAG GCACCCCAAA 1680
GGCTACACCC ACCCTGCTGG GACCTTCTGT GTCATCTGAC GCCCCCATCA CATCTGCC 1740
ACTCAAGATG CTGGCCCCCA GTGGGTCTCT AGGCGTCTGG AGGGAGCCCA GCATCCATCA 1800
CGCCACAGCT GCCTCTGGCC CCCAGGAGCC TGCAAGTGGG GACTCTCCG TGGCCACACA 1860
AAACAACGAT GGCACCTGAC GGCAAAAGCT GCTTTATTTC TACATCTAG GCACCGTGGT 1920
GGCCATCCTA CTCTGTCTGG CCCTGGCTCT GGGGCTACTG GTCTATCGCA AGCGGAGAGC 1980
GAAGAGGGAG TACCTGAAGT AGAAGAAGCC CCAGAATGCG GCAGACAGTT ACTCCTGGGT 2040
TCCAGAGCGA GCTGAGAGCA GGGCCATGGA GAACCACTAC AGTCCGACAC CTGGGACAGA 2100
CTGCTGAAGG TGAGGTGGCC CTAGAGACAC TAGAGTCACC AGCCACCATC CTCAGAGCTT 2160
TGAACTCCCC ATTCCAAAGG GGCACCCACA TTTTGTGAA AGACTGGACT GGAATCTTAG 2220
CAACAATTG TAACTCTCTC CCTTAAAGGC CCCTTGGAA ATGCAAGTAT TTTCTACGGG 2280
TGTTTGATGT TCTGGAATG GAAGCTGTGT GTTGGCGTGC CACGGTGGGG ATTTCTGTAG 2340
TCTATAATGA TTGTACTCTC CCCTCCCTTT TCAAATTTCA ATGTGACCAA TTCCGGATCA 2400
GGGTGTGAGG AGGCTGGGGC TAAGGGGCTC CCCTGAATAT CTCTCTGCT CACTTCCACC 2460
ATCTAAGAGG AAAAGGTGAG TTGCTCATGC TGATTAGGAT TGAATGATT TGTTTCTCTT 2520
CCTAGGATGA AAATAAATC AATTAATAT TCAATTAGGT AAGAAGATCT GGTTTTTTGG 2580
TCAAAGGGAA CATGTTGCGA CTGGAACAT TTCTTTACAT TTGCATTCT CCATTTCGCC 2640
AGCAACAGTC TTGCTAAATG TGATACTGT GACATCTCTC AGAATGGCCA GAAGTGCAAT 2700
TAACCTCTTA GGTGGCAAGG AGGCAGGAAG TGCTCTTTA GTTCTTACAT TTCTAATAGC 2760
CTTGGGTTTA TTTGCAAAAG AAGCTTGAAA AATATGAGAA AAGTTGCTTG AAGTGCAAT 2820
CAGGTGTTTG TGAAGTCACA TAATCTACGG GGCTAGGGCG AGAGAGGCCA GGGATTGTTT 2880
CACAGATACT TGAATTAAT CATCCAAATG TACTGAGGTT ACCACACACT TGACTACGGA 2940
TGTGATCAAC ACTAACAGG AAACAAATC AAGGACAACC TGCTTTTGG CCAGGGCAGG 3000
CCTCAGACAC CCTGCTCTGT GCGCCGCTC CACTTCATCC TGCCCGGAAT GCCAGTGCTC 3060
CGAGCTCAGA CAGAGGAAGC CCTGCAGAAA GTTCCATCAG GCTGTTTCTT AAAGGATGTG 3120
TGAACGGGAG ATGATGCACT GTGTTTGAAG AGTTGTCTATT TTAAGCAAT TTAGCACAGT 3180
TCATAGTCCA CAGTTGATGC AGCATCTGGA GATTTTAAAT CCTGAAAGTG GGGTGGCGCA 3240
CACACCAAGT AGGGAGCTAG TCAGGCAGTT TGCTTAAGGA ACTTTTGTTC TCTGTCTCTT 3300
TTCTTAAAA TGGGGGTAA GGAGGGGAGG AAGAGGGAAA GAGATGACTA ACTAAAAATCA 3360
TTTTTACAGC AAAAAGTCTC CAAAGCCATT TAAATTATAT CCTCATTTTA AAGTTTACAT 3420
TTGCAAAATAT TTCTCCTAT GATAATGACG TCGATAGTGT GCACTCTTTC TCTCTCTCTC 3480
TCTCTCTCAC ACACACACAC ACACACACAC ACACACACAC AGAGACACGG CACCATTCTG 3540
CCTGGGGCAC TGGAACACAT TCCTGGGGGT CACCGATGGT CAGAGTCACT AGAAGTTACC 3600
TGATGATCTC TGGGAGGCTC CATGTCTCCT GTGGGCTTTT TACCACCACT GTGCAGGAGA 3660
ACAGACAGAG GAAATGTGTC TCCTCCAAG GCCCCAAAGC CTCAGAGAAA GGGTGTCTCT 3720
GGTTTTGCTC TAGCAATGCA TCGGTCTCTG AGGTGACACT CTGGAGTGGT TGAAGGGCCA 3780
CAAGGTGCAG GGTAAATACT CTTGCCAGTT TTGAAATATA GATGCTATGG TTCAGATTGT 3840
TTTTAATAGA AAATAAAGG GGCAGGGGAA GTGAAAGGAA AGATGGAGGT TTTGTGCGGC 3900
TCGATGGGGC ATTTGGAAC TCTTTTAAA GTCATCTCAT GGTCTCCAGT TTTCAAGTTG 3960
AACTCTGTGT TTTAACAATT AAGGGAGACA AAGGCTGTGT CCATTTGGCA AAACCTCTCT 4020
GGCCACGAGA CTCTAGGTGA TGTGTGAAGC TGGGAGTCT GTGGTGTGGA GAGCAGCCAT 4080
CTGTCTGGCC ATTCAGAGGA TTCTAAAGAC ATGGCTGGAT GCGCTGCTGA CCAACATCAG 4140
CACTTAAATA AATGCAAAAT CAACATTTCT CCCTCTGGGC CTTGAAAATC CTTGCCCTTA 4200
TCATTTGGGG TGAAGGAGAC ATTTCTGTCC TTGGCTTCCC ACAGCCCCAA CGCAGTCTGT 4260
GTATGATCCC TGGGATCCAA CGAGCCCTCC TATTTTCACA GTGTTCTGAT TGCTCTCACA 4320
GCCCCAGCCC ATCGTCTGTT CTCTGAATGC AGCCCTGTTC TCAACAACAG GGAGGTCATG 4380
GAACCCCTCT GTGGAACCCA CAAGGGGAGA AATGGGTGAT AAAGAATCCA GTTCTCTCAA 4440
ACCTTCCCTG GCAGGCTGGG TCCTCTCTCT GCTGGGTGGT GCTTCTCTT GCACACCAT 4500
CCACACAGGG GGGGAGAGCC AGCAACCCAA CCAGACAGCT CAGGTTGTGT ATCTGATGGA 4560
AACCCTGGG CTCAAACACG TGCTTTATTC TCCTGTTTAT TTTTGTGTT ACTTTGAAGC 4620
ATGGAATATC TTGTTTGGGG GATCTTGGGG CTACAGTAGT GGGTAAACAA ATGCCACCG 4680
GCCAAGAGGC CATTAAACAA TCGTCTTGT CCTGAGGGGC CCCAGCTTGC TCGGGCGTGG 4740
CACAGTGGGG AATCCAAGGG TCACAGTATG GGGAGAGGTG CACCTGCCA CCTGCTAACT 4800

```

5
10
15
20
25
30
35

TCTGCTAGA CACAGTGTTC CTGCCAGGT GACCTGTTCA GCAGCAGAAC AAGCCAGGGC 4860
CATGGGGACG GGGGAAGTTT TCACCTGGAG ATGGACACCA AGACAATGAA GATTGTGTGT 4920
CCAAATAGGT CAATAATCTT GGGAGACTCT TGGAAAAAAC TGAATATATT CAGGACCAAC 4980
TCTCTCCCTC CCCTCATCCC ACATCTCAAA GCAGACAATG TAAAGAGAGA ACATCTCACA 5040
CACCCAGCTC GCCATGCCTA CTCATTCTCT AATTTTCAGGT GCCATCACTG CTCTTTCTTT 5100
CTTCTTTGTC ATTTGAGAAA GGATGCAGGA GGACAATTCC CACAGATAAT CTGAGGAATG 5160
CAGAAAAACC AGGGCAGGAC AGTTATCGAC AATGCATTAG AACTTGGTGA GCATCCTCTG 5220
TAGAGGGACT CCACCCTGTC TCAACAGCTT GGCTTCCAGG CAAGACCAAC CACATCTGGT 5280
CTCTGCCCTT GGTGGCCAC ACACCTAAGC GTCATCGTCA TTGCCATAGC ATCATGATGC 5340
AACAATCTA CGTGTAGCAC TACGACGTTA TGTTTGGGTA ATGTGGGGAT GAACTGCATG 5400
AGGCTCTGAT TAAGGATGTG GGAAGTGGG CTGCGGTAC TGTCGGCCTT GCAAGGCCAC 5460
CTGGAGGCTT GTCTGTTAGC CAGTGGTGGG GGAGCAAGGC TTCAGGAAGG GCCAGCCACA 5520
TGCCATCTTC CTGCGATCA GGCAAAAAAG TGGAAATAAA AAGTCAAACC TTTATATGCA 5580
TGTGTTATGT CCATTTTGA GGATGAACTG AGTTTAAAAA AATTTTITTT TCTCTTCAAG 5640
TTGCTTTGTC TTTTCCATCC TCATCACAAG CCTTGTGTTG AGTGTCTTAT CCCTGAGCAA 5700
TCTTTGATG GATGATGATG ACTTTTGTGTT CAACCTTTAT TCCTGTAAAT 5760
ATTTCTGTGA AAACCTAGGAG AACAGAGATG AGATTTGACA AAAAAAATTT GAATTAATAA 5820
TAACACAGTC TTTTAAAAAC TAACATAGGA AAGCCTTTCC TATTATTCTT CTTCCTAGCT 5880
TCTCCATTGT CTAAATCAGG AAAACAGGAA AACACAGCTT TCTAGCAGCT GCAAAATGGT 5940
TTAATGCCCC CTACATATTT CCATCACCTT GAACAATAGC TTAGCTTGGT GAACTCTGAGA 6000
TTATGATCCA GAAGAGATCT GTCTCTACTT CGGCTGCAAA ACCCATGGTT TAAATCTATA 6060
TGGTTTGTGC ATTTTCTCAA CTAAAAATAG AGATGATAAT CCGAATTCTC CATATATCA 6120
CTAATCAAAG ACATATTTT CATACTAGAT TCCTGAGACA AATACTCACT GAAGGGCTTG 6180
TTTAAAAATA AATTGTGTTT TGGTCTGTTT TTGTAGATAA TGCCCTTCTA TTTTAGGTAG 6240
AAGCTCTGGA ATCCCTTTAT TGTGCTGTTG CTCTTATCTG CAAGGTGGCA AGCAGTTCTT 6300
TTGACAGAT TTTGCCCACT ATTCCTCTGA GCTGAAGTTC TTTGCATAGA TTTGGCTTAA 6360
GCTTGAATTA GATCCCTGCA AAGGCTTGCT CTGTGATGTC AGATGTAATT GTAAATGTCA 6420
GTAATCACTT CATGAATGCT AAATGAGAAT GTAAGTATTT TTAATGTGT GTATTTCAAA 6480
TTTGTGTTGAC TAAATCTGGA ATTACAAGAT TTCTATGCAG GATTTACCTT CATCTGTGC 6540
ATGTTTCCCA AACTGTGAGG AGGGAAGGCT CAGAGATCGA GCTTCTCCTC TGAGTTCTAA 6600
CAAAATGGTG CTTTGAAGGT CAGCCTTTAG GAAGGTGCAG CTTTGTGTGC CTTTGAGCTT 6660
TCTGTTATGT GCCTATCCTA ATAACTCTT AAACACATT

Seq ID NO: 345 Protein sequence
Protein Accession #: NP_036204

40
45
50

1 11 21 31 41 51
| | | | |
MATSMGLLLL LLLLLTPQGA GTGADTEAVV CVGTACYTAH SGKLSAAEAQ NHCNQNGGNL 60
ATVRSKEEAA HVQRVLAQLL RREAAALTARM SKFWIGLQRE KGKCLDPSLP LKGFWSVWGG 120
EDTPYSNWHK ELRNSICISKR CVALLDLSQ PLLPNRLPKW SEQPCGSPGS PGSNIEGFVC 180
KFSFKGMCPR LALGGPGQVT YTPFQTSS SLEAVPFASA ANVACGEGDK DETQSHYPLC 240
KEKAPDFVFD GSSGLPLCVSP KYGCNFNNGG CHQDCPEGGD GSFLCGCRPG FRLLDDLVTG 300
ASRNPCCSSP CRGGATCVLG PHGKNYTCRC PQGYQLDSSQ LDCVDVDEQD DSPCAQECVN 360
TPGGFRCEBW VGYEPGGPGE GACQDVDECA LGRSFPQAQC TMTDGSFHCS CEEGYVLAGE 420
DGTQCQDVDE CVGPGGPLCD SLCFNTQGSF HCGCLPGWVL APNGVSCIMG PVSLLGPPSGP 480
DEEDKEGEKE GSTVPRAAAT SPTRGPEGTP KATPTTSRPS LSSDAPITSA PLKMLAPSGS 540
SGVWREPSIH HATAASGPQE PAGGDSSVAT QNNDGTDGQK LLLFYILGTV VAILLLALA 600
LGLLVYRRRR AKREEKKEKK PQNAADSYSW VPERAESRAM ENQYSPTPGT DC

Seq ID NO: 346 DNA sequence
Nucleic Acid Accession #: Z31560
Coding sequence: <1-966

55
60
65
70
75

1 11 21 31 41 51
| | | | |
CACAGCGCCC GCATGTACAA CATGATGGAG ACGGAGCTGA AGCCGCGCGG CCGCGAGCAA 60
ACTTCGGGGG GCGGCGGCGG CAACTCCACC GCGGCGGCGG CCGGCGGCAA CCAGAAAAAC 120
AGCCCGGACC GCCTCAAGCG GCCCATGAAT GCCTTCATGG TGTGGTCCCG CGGGCAGCGG 180
CGCAAGATGG CCCAGAGAGG CCCCAGATG CACAACCTCG AGATCAGCAA CGGCCTGGCG 240
GCCGAGTGGG AACTTTTGTG GGAGACGGAG AAGCGGCGGT TCATCGACGA GGCTAAGCGG 300
CTGCGAGCGC TGACATGAA GGAGCACCCG GATTATAAAT ACCGCGCCCG GCGGAAAAAC 360
AAGACGCTCA TGAAGAAGGA TAAGTACACG CTGCCCGGCG GGCTGCTGGC CCGGCGGCGG 420
AATAGCATGG CGAGCGGGGT CGGGGTGGGC GCGGCGCTGG GCGCGGCGGT GAACCAAGCGC 480
ATGGACAGTT ACGCGCACAT GAACGCGCTG AGCAACGGCA GCTACAGCAT GATGCAGGAC 540
CAGCTGGGCT ACCCGCAGCA CCGGGGCTC AATGCGCACG GCGCAGCGCA GATGCAGCCC 600
ATGCACCGCT ACGACGTGAG CGCCCTGCAG TACAACCTCA TGACCACTC CGACACCTAC 660
ATGAACGGCT CGCCACCTA CAGCATGTCC TACTCGCAGC AGGGCACCCC TGGCATGGCT 720
CTTGGCTCCA TGGGTTCCGT GGTCAAGTCC GAGGCCAGCT CCAGCCCCCT TGTGGTTACC 780
TCTTCTCCCG ACTCCAGGGC GCCCTGCCAG GCCGGGGACC TCCGGGACAT GATCAGCATG 840
TATCTCCCGG GCGCCGAGGT GCCGGAACCC GCGGCCCCCA GCAGACTTCA CATGTCCAG 900
CACTACCAGA CGGGCCCGGT GCCCGGCACG GCCATTAAAC GCACACTGCC CCTCTCACAC 960
ATGTGAGGGC CGGACAGCGA ACTGGAGGGG GGAGAAATTT TCAAGAAAAA ACGAGGGAAA 1020
TGGGAGGGGT GCAAAAGAGG AGAGTAAGAA ACAGCATGGA GAAACCCCGG TACGCTCAAA 1080
AAAAA

Seq ID NO: 347 Protein sequence
Protein Accession #: CAA83435

80
85

1 11 21 31 41 51
| | | | |
HSARMYNMME TELKPPQPQ TSAGGGGNST AAAAGGNQKN SPDRVKRPMN AFMVWSRGQR 60
RKMAQENPKM HNSEISKRLG AEWKLLSETE KRPFIDEAKR LRALHMKHEP DYKYRPRRKT 120
KTLMKKDKYT LPGGLLAPFG NSMASGVGVG AGLGAGVNQR MDSYAHMNGW SNGYSYMMQD 180
QLGYPQHFGI NAHGAAQMQP MHRYDVSALQ YNSMTSSQTY MNGSPYYSMS YSQQGTGMA 240
LGSMGSVVK SASSPPFVVT SSSHSRAPCQ AGDLRDMISM YLPGAIEVPEP AAPSRLLHMSQ 300
HYQSGPVPGT AINGTLPLSH M

Seq ID NO: 348 DNA sequence
Nucleotide Accession #: NM_002638
Coding sequence: 120-473

```
5      1      11      21      31      41      51
      |      |      |      |      |      |
      CAATACAGCT AAGGAATTAT CCCTTGTAAG TACCACAGAC CCGCCCTGGA GCCAGGCCAA 60
10     GCTGGACTGC ATAAAGATTG GTATGGCCTT AGCTCTTAGC CAAACACCTT CCTGACACCA 120
      TGAGGGCCAG CAGCTTCTTG ATCGTGGTGG TGTTCCTCAT CGCTGGGACG CTGGTCTTAG 180
      AGGCAGCTGT CACGGGAGTT CCTGTTAAAG GTCAAGACAC TGTCAAAGGC CGTGTTCAT 240
      TCAATGGACA AGATCCCGTT AAAGGACAAG TTTCAGTTAA AGGTCAAGAT AAAGTCAAAG 300
      CGCAAGAGCC AGTCAAAGGT CCAGTCTCCA CTAAGCCTGG CTCTGCCCC ATTATCTTGA 360
15     TCCGGTGGGC CATGTTGAAT CCCCTAACC GCTGCTTGAA AGATACTGAC TGCCACAGGAA 420
      TCAAGAAATG CTGTGAAGGC TCTTGGCGGA TGGCCTGTTT CGTTCGCCAG TGAAGGGAGC 480
      CGGTCTCTTG TGACCTGTGT CCGTCCCCAG AGCTACAGGC CCCATCTGGT CCTAAGTCCC 540
      TGCTGCCCTT CCCCTTCCCA CACTGTCCAT TCTTCTCCCC ATTCAGGATG CCCACGGCTG 600
      GAGCTGCCTC TCTCATCCAC TTTCGAATAA A
```

Seq ID NO: 349 Protein sequence:
Protein Accession #: NP_002629

```
25     1      11      21      31      41      51
      |      |      |      |      |      |
      MRASSFLIVV VFLIAGTLVL EAAVTGVFVK GQDTVKGKRP FNGQDPVKQV VSVKGQDKVK 60
      AQEPVKGPVS TKPGSCPILL IRCAMLNPPN RCLKDTCFPG IKKCEGSCG MACFVPQ
```

Seq ID NO: 350 DNA sequence
Nucleic Acid Accession #: NM_007183
Coding sequence: 75-2468

```
35     1      11      21      31      41      51
      |      |      |      |      |      |
      GAATTCGGGA CAGGACGTGA AGATAGTTGG GTTTGGAGGC GGCCCGCCAG CCCAGGCCCG 60
      GTGGACCTGC CGCATGCAG GACGGTAAC TCTGTCTGTC GGCCCTGCAG CCTGAGGCCG 120
      GCGTGTGCTC CCTGGCGCTG CCCTCTGACC TGCAGCTGGA CCGCCGGGGC GCCGAGGGGC 180
      CGGAGGCCGA GCGGCTGCGG GCAGCCCGCG TCCAGGAGCA GGTCGCGCGC CGCCTCTTGC 240
40     AGCTGGGACA GCACCCGCGG CACAACGGGG CCGCTGAGCC CGAGCCTGAG GCCGAGACTG 300
      CCAGAGGCAC ATCAGGGGGG CAGTACCACA CCCTGCAGGC TGGCTTCAGC TCTCGCTCTC 360
      AGGGCTGAGT TGGGGAAGA ACCTCGGGCT TCCGGCCCAT GCCTACAGCC GCCTACAGCC 420
      CAGCCTCTCTG TCCCTCCCGC TCCGCGGTGG ATCTGAGCTG CAGTCGGAGG CTGAGTTCAG 480
      CCCACAATGG GGGCAGCGCC TTTGGGGCCG CTGGGTACGG GGGTGCCCG CCCACCCCTC 540
      CCATGCCAC CAGGCCCGTG TCCTTCCATG AGCGCGGTGG GGTGGGAGC CGGGCGGACT 600
45     ATGACACACT CTCCTCGGCG TCGCTGCGGC TGGGGCCCGG GGGCCTGGAC GACCGCTACA 660
      GCGTGGTGTG TGAGCAAGCT GAGCCCGCGG CCACCTCCAC CTACAGGGGC TTTGCTAGC 720
      AGCGCCAGGC CAGCTCCAGC TCCAGCCGGG CAGGGGGGCT GGAATGGCCC GAGGCCACTG 780
      AGGTTTCCCC GAGCCGAGCC ATCCGTGCCC CTGCGCTGCG GACCCTGCAG CGATTCCAGA 840
      GCAGCCACCG GAGCCCGGGG GTAGGCGGGG CAGTGCCCGG GCGCGTCCCT GAGCCAGTGG 900
50     CTCGAGCGCC ATCTGTGCGC AGCCTCAGCC TCAGCCTGGC TGAATCGGGC CACCTGCGCG 960
      ACGTGCATGG GTTCAAGAGC TACGGTAGCC ACCGAACCTT GCAGAGACTC AGCAGCGGTT 1020
      TTGATGACAT TGACCTGCCC TCAGCAGTCA AGTACCTCAT GGCTTCAGAC CCCAAGCTGC 1080
      AGGTGCTGGG AGCGGCTTAC ATCCAGCACA AGTGCTACAG CGATGCAGCC GCCAAGAAGC 1140
      AGGCCCGCAG CTTTCAGGCC GTGCCTAGGC TGGTGAAGCT TTCAACACG GCCAACCAGG 1200
55     AAGTGACAGC CCATGCCACA GGTGCCATGC GCAACCTCAT CTAGCACAAC GCTGACACA 1260
      AGCTGGCCCT GGTGAGGAGG AACGGGATCT TCGAGCTGCT CGGCAACTG CGGGAGCAGG 1320
      ATGATGAGCT TCGCAAAATG GTCAAGGGA TCTGTGGAA CCTTTCATCC AGCGACCAAC 1380
      TGAAGGACCG CTTGGCCAGA GACACGCTGG AGCAGCTCAC GGAACCTGGT TTGAGCCCCC 1440
      TGTCGGGGGC TGGGGGTCCC CCCCTCATCC AGCAGAACGC CTCGGAGGCG GAGATCTTCT 1500
60     ACAACGCCAC CGGCTTCTCT AGGAACCTCA GCTCAGCCTC TCAGGCCACT CGCCAGAAGA 1560
      TGCGGGAGTG CCACGGGCTG GTGGACGCCC TGGTCACTTC TATCAACCA GCCCTGGACG 1620
      CGGGCAATG CGAGGACAAG AGCGTGGAGA ACGCGGTGTG CGTCTGCGG AACCTGTCTC 1680
      ACCGCTCTA CGACGAGATG CCGCGTCCG CGCTGCAGCG GCTGGAGGGT CGCGGCCGCA 1740
      GGGACCTGGC GGGGGCGCGG CCGGGAGAGG TCGTGGGCTG CTTACGCGG CAGAGCCGCG 1800
65     GGCTGCGCGA GCTGCCCTCT GCCGCCGATG CGCTCACCTT CGCGGAGGTG TCCAGGAGCC 1860
      CCAAGGGCCT CGATGGCTG TGGAGCCCCC AGATCGTGGG GCTGTACAAC CGGCTGCTCG 1920
      AGCGCTGCGA GCTCAACCGG CACACGACGG AGGCGGCCGC CGGGGCGCTG CAGAACATCA 1980
      CGGCAGGCGA CCGCAGGTGG GCGGGGGTGC TGAGCCGCTT GGCCTGGAG CAGGAGCGTA 2040
      TTCTGAACCC CCTGCTAGAC CGTGTGAGGA CCGCCGACCA CCACAGCTG CGCTCACTGA 2100
70     CTGGCCTCAT CCGAAACCTG TCTCGGAACG CTAGGAACAA GGACGAGATG TCCACGAAGG 2160
      TGGTGAGCCA CCGTATCGAG AAGCTGCCAG GCAGCGTGGG TGAGAAGTCG CCCCAGCCG 2220
      AGGTGCTGGT CAACATCATA GCTGTGCTCA ACAACCTGGT GGTGGCCAGC CCCATCGCTG 2280
      CCCGAGACCT GCTGATTTT GACGAGCTCC GAAAGCTCAT CTTTCATCAAG AAGAAGCGGG 2340
75     ACAGCCCCGA CAGTGAGAAG TCCTCCCGGG CAGCATCCAG CCTCTGGCC AACCTGTGGC 2400
      AGTACAACAA GCTCCACCGT GACTTTCGGG CGAAGGGCTA TCGGAAGGAG GACTTCTGG 2460
      GCCCATAGGT GAAGCTTCTT GGAGGAGAAG GTGACGTGGC CCAGGTCCA AGGGACAGAC 2520
      TCAGTCTCAG GCTGCTTGGC AGCCAGCCTT GGAGGAGAAG GCTAATGACG GAGGGGCCCC 2580
      TCGTGGGGC CCGTGTGTGC ATCTTTGAGG GTCTGGGGCC ACCAGGAGGG GCAGGGTCTT 2640
80     ATAGCTGGGG ACTTGGCTTC CGCAGGGCAG GGGGTGGGGC AGGGCTCAAG GCTGCTCTGG 2700
      TGTATGGGGT GGTGACCCAG TCACATTGGC AGAGGTGGGG GTTGGCTGTG GCCTGGCAGT 2760
      ATCTTGGGAT AGCCAGCACT GGGGAATAAG ATGGCCATGA ACAGTCAACA AAAAAAAAAA 2820
      AAAAGGAATT C
```

Seq ID NO: 351 Protein sequence
Protein Accession #: NP_009114.1

```
85     1      11      21      31      41      51
```

5 MQDGNFLLSA LQPEAGVCSL ALPSDLQLDR RGAEGPEAER LRAARVQEQV RARLLQLGQQ 60
 PRHNGAAEPE PEAEARTGTS RGQYHTLQAG FSSRSQGLSG DKTSGFRPIA KPAYSASWS 120
 SRSAVDLSGS RRLSSAHNGG SAFQAAAGYGG AQPTPPMPTR PVSFHERGGV GSRADYDTLS 180
 LRSRLGPGG LDDRYSLVSE QLEPAATSTY RAFAYERQAS SSSSRAGGLD WPEATEVSPS 240
 RTIRAPAVRT LQRFQSSHSR RGVGGA VPGA VLEPVARAPS VRSLSLSLAD SGHLPDVHGF 300
 NSYGSHTRLQ RLSSGFDDID LPSAVKYLMA SDPNLQVLGA AYIQHKCYSD AAACKQARSL 360
 QAVPRLVKLF NHANQEVQRH ATGAMRNLIY DNADNKLALV EENGIFELLR TLRQDDELRL 420
 10 KNVGTILWNL SSSDHLKDR LARDTLEQLTD LVLSPLSGAG GPPLIQNAS EAEIFYNATG 480
 FLRNLSASQ ATRQKMRECH GLVDALVTSI NHALDAGKCE DKSVENAVCV LRNLRYRLYD 540
 EMPPSALQRL EGRGRRLDLAG APPGEVVGCF TPQSRRLREL PLAADALTFA EVSKDPKGLE 600
 WLNSPQIVGL YNRLLRCEL NRHTTEAAAG ALQNTAGADR RWAGVLSRLA LEQERILNPL 660
 LDRVRTADHH QLRSLTGLIR NLSRNARNKD EMSTKVVS HL IEKLPGSVGE KSPPAEVLVN 720
 15 IIAVLNNLVV ASPIAARDLL YFDGLRLKLI IKKKRDSFDS EKSSRAASSL LANLWQYNKL 780
 HRDFRAGYR KEDFLGP

Seq ID NO: 352 DNA sequence
 Nucleic Acid Accession #: M31469
 Coding sequence: 1-651

20 1 11 21 31 41 51
 25 ATGGCTGCGC AGGAGAGGCC CCAGGTCCAG TTCAAACCTG TATTGGTTGG TGATGGTGGT 60
 ACTGGAAAAA CGACCTTCGT GAAACGTCAT TTGACTGGTG AATTTGAGAA GAAGTATGTA 120
 GCCACCTTGG GTGTTGAGGT TCATCCCTCA GTGTTCACCA CCAACAGAGG ACCTATTAGA 180
 TTCAATGTAT GGGACACAGC CGGCCAGGAG AAATTCGGTG GACTGAGAGA TGGCTATTAT 240
 ATCCAAGCCC AGTGTGCCAT CATAATGTTT GATGTAACAT CGAGAGTTAC TTACAAGAAT 300
 30 GTGCCTAACT GGCATAGAGA TCTGGTACGA GTGTGTGAAA ACATCCCAT TGTGTTGTGT 360
 GGCACAAAG TGGATTATTA GGACAGGAAA GTGAAGGCGA AATCCATTGT CTTCACCGA 420
 AAGAAGAATC TTCAGTACTA GCACATTTCT GCCAAAAGTA ACTACAACCT TGAAAAGCCC 480
 TTCCTCTGGC TTGCTAGGAA GCTCATTGGA GACCCTAACT TGGAAATTGT TGCCATGCCT 540
 GCTCTCGCCC CACCAAGAGT TGTCTAGGAC CCAGCTTTGG CAGCAGATG TGAGCAGGAC 600
 35 TTAGAGGTG CTGAGCAAC TGCTCTCCG GATGAGGATG ATGACCTGTG A

Seq ID NO: 353 Protein sequence
 Protein Accession #: AAA36546

40 1 11 21 31 41 51
 MAAQGEPOVQ FKLVLVGDGG TGKTFVKRHH LTGEFEKKYV ATLGVEVHPL VFHTNRGPIK 60
 FNVWDTAGQE KFGGLRDGYI IQAQCAIMF DVTSRVTYKN VFNWHRDLVR VCENIPIVLC 120
 GNKVDIKDRK VKAKSIVFHR KKNLQYYDIS AKSNYNFEKP FLWLARKLIG DPNLEFVAMP 180
 45 ALAPPEVMD PALAAQYEH DEDDDL

Seq ID NO: 354 DNA sequence
 Nucleic Acid Accession #: NM_002820
 Coding sequence: 304-831

50 1 11 21 31 41 51
 55 CCGGTTGCGA AAGAAGCTGA CTTGAGAGGG GGAAACTTTC TTCTTTTAGG AGGCGGTTAG 60
 CCTGTTTCCA CGAACCCAGG AGAACTGCTG GCCAGATTAA TTAGACATTG CTATGGGAGA 120
 CGTGTAACAA CACTACTTAT CATTGATGCA TATATAAAAC CATTTTATTT TCGCTATTAT 180
 TTCAGAGGAA GCGCCTCTGA TTGTTTCTT TTTCCCTTT TTGCTCTTTC TGGCTGTGTG 240
 GTTTGGAGAA AGCACAGTTG GAGTAGCCGG TTGCTAAATA AGTCCCGAGC GCGAGCGGAG 300
 ACGATGACAG CGAGACTGGT TCAGCAGTGG AGCGTCCGGG TGTTCTGCTG GAGCTACGCG 360
 60 GTGCCCTCCT GCGGGCGCTC GGTGGAGGGT CTCAGCCGCC GCCTCAAAAG AGCTGTGTCT 420
 GAACATCAGC TCCTCCATGA CAAGGGGAA GCTCATCAAG ATTTACGGCG ACGATTCTTC 480
 CTTCAACATC TGATCGCAGA AATCCACACA GCTGAAATCA GAGCTACCTC GGAGGTGTCC 540
 CCTAACTCCA AGCCCTCTCC CAACACAAAG AACCACCCCG TCCGATTGGT GTCTGATGAT 600
 GAGGGCAGAT ACCTAACTCA GGAAGCTAAC AAGGTGGAGA CGTACAAAGA GCAGCCGCTC 660
 65 AAGACACCTG GGAAGAAAAA GAAAGGCAAG CCCGGGAAAC GCAAGGAGCA GGAAGAGAAA 720
 AAACGGCGAA CTCGCTCTGC CTGGTTAGAC TCTGGAGTGA CTGGGAGTGG GCTAGAAGGG 780
 GACCACTGTG CTGACACCTC CACAACGTCG CTGGAGCTCG ATTCACGGTA ACAGGCTTCT 840
 CTGGCCCGTA GCCTCAGCGG GGTGCTCTCA GCTGGGTTT GGAGCCTCCC TTCTGCCTTG 900
 GCTTGGACAA ACCTAGAATT TTCTCCCTTT ATGTATCTCT ATCGATTGTG TAGCAATTGA 960
 70 CAGAGAATAA CTCAGAATAT TGTCTGCCIT AAAGCAGTAC CCCCCTACCA CACACACCCC 1020
 TGTCTCCAG CACCATAGAG AGGCCTAGA GCCCATTCCT CTTTCTCCAC CGTCACCCAA 1080
 CATCAATCCT TTACCACTCT ACCAAATAAT TTCATATTCA AGCTTCAGAA GCTAGTGACC 1140
 ATCTTCATAA TTTGCTGGAG AAGTGATTTT CTCTCCCTTA CTCTCACACC TGGGCAAACT 1200
 TTCTTCAGTG TTTTTCATTT CTTACGTTCT TTCACTTCAA GGGAGAATAT AGAAGCATTT 1260
 75 GATATTATCT ACAACACTG CAGAACAGCA TCATGTCATA AACGATTCTG AGCCATTAC 1320
 ACTTTTATT TAATTAATG TATTTAATTA AATCTCAAAT TTATTTTAAT GTAAAGAACT 1380
 TAAATTATGT TTTAAACACA TGCCCTTAAAT TTGTTTAATT AAATTTAACT CTGTTTCTA 1440
 CCAGCTCATA CAAATAAAT GGTTCCTGAA AATGTTTAA GATTAACTTA CAAGGATATA 1500
 80 GGTTCCTCCT ATGTATCTTT TTGTTTATG GCAAGATGAA ATAATTTTTC TAGGGTAATG 1560
 CCGTAGGAAA AATAAACTT CACATTAAAA AAAAA

Seq ID NO: 355 Protein sequence
 Protein Accession #: NM_002820

85 1 11 21 31 41 51
 MQRRLVQQWS VAVFLLSYAV PSCGRSVEGL SRRLKRAVSE HQLLHDKGKS IQDLRRRFFL 60
 HHLIAETHTA EIRATSEVSE NSKPSFNTKN HPVRFSGSDE GRYLTQETNK VETYKEQPLK 120

TPGKKKKGKP GKRKEQEKKK RRTSRAWLDS GVTGSGLEGD HLSDTSTTSL ELSDR

Seq ID NO: 356 DNA sequence
Nucleic Acid Accession #: NM_017522
Coding sequence: 1-2100

5
10
15
20
25
30
35
40
45
50

1	11	21	31	41	51	
ATGGGCTCC	CCGAGCCGG	CCCTCTCCG	CTTCTGGCG	TGCTGCTGCT	GCTGCTGCTG	60
CTGCTGCTGC	TGCGGCTCCA	GCATCTTGCG	GCGGCAGCG	CTGATCCGCT	GCTCGGCGGC	120
CAAGGGCCGG	CCAAGGAGTG	CGAAAAGGAC	CAATTCAGT	GCCGGAACGA	GCGCTGCATC	180
CCCTCTGTGT	GGAGATGCGA	CGAGGACGAT	GACTGCTTAG	ACCACAGCGA	CGAGGACGAC	240
TGCCCCAAGA	AGACCTGTGC	AGACAGTGAC	TTCACTGTG	ACAACGGCCA	CTGCATCCAC	300
GAACGCTGGA	AGTGTGACGG	CGAGGAGGAG	TGTCCTGATG	GCTCCGATGA	GTCCGAGGCC	360
ACTTGACCA	AGCAGGTGTG	TCCTGCAGAG	AAGCTGAGCT	GTGGACCCAC	CAGCCACAAG	420
TGTTGACTCT	CCTCGTGGCG	CTCGACGGG	GAGAAGGACT	GCGAGGGTGG	AGCGGATGAG	480
GCCGGCTGTG	CTACCTCACT	GGGCACCTGC	CGTGGGACG	AGTTCAGATG	TGGGGATGGG	540
ACATGTGTCC	TTGCAATCAA	GCATGCAAC	CAGGAGCAG	ACTGTCCAG	TGGGATGAT	600
GAAGCTGGCT	GGCTACAGGG	GCTGAACGAG	TGTCGACACA	ACAATGGCG	CTGCTCACAC	660
ATCTGCACTG	ACCTCAAGAT	TGGCTTTGAA	TGCACGTGCC	CAGCAGGCTT	CCAGCTCCTG	720
GACCAGAAGA	CTTGTGGCGA	CATTGATGAG	TGCAAGGACC	CAGATGCCTG	CAGCCAGATC	780
TGTGTCAATT	ACAAGGGCTA	TTTTAAGTGT	GAGTGTCTACC	CTGGCTGCGA	GATGGACCTA	840
CTGACCAAGA	ATGCAAGGC	TGCTGCTGGC	AAGAGCCCAT	CCCTAATCTT	CACCAACCGC	900
ACGAGTGGG	AGGTACGACC	TGTGAAGCGG	AACCTATTAC	GCCTCATCCC	CATGCTCAAG	960
AATGTCGTGG	ACCTAGATGT	GGAAAGTGCC	ACCAATCGCA	TCTACTGGTG	TGACCTCTCC	1020
TACGCTAAGA	TCTATAGCGC	CTACATGGAC	AAGGCCAGTG	ACCCGAAAGA	GCGGGAGGTC	1080
CTCATTGACG	AGCAGTTGCA	CTCTCCAGAG	GGCCTGGCAG	TGGACTGGGT	CCACAAGCAC	1140
ATCTACTGGA	CTGACTCGGG	CAATAAGACC	ATCTCAGTGG	CCACAGTTGA	TGGTGGCCCG	1200
CGAGCGACTC	TCTTCAGCGG	TAACCTCAGT	GAACCCCGGG	CCATCGCTGT	TGACCCCTCG	1260
CGAGGGTTCA	TGTATTGGTC	TGACTGGGGG	GACCAGGCCA	AGATTGAGAA	ATCTGGGCTC	1320
AACGGTGTGG	ACCGGCAAA	ACTGGTGTCA	GACAATATTG	AATGGCCCAA	CGGAATCACC	1380
CTGGATCTGC	TGAGCCAGCG	CTTGTACTGG	GTAGACTCCA	AGCTACACCA	ACTGTCCAGC	1440
ATTGACTTCA	GTGGAGGCAA	CAGAAAGACG	CTGATCTCCT	CCACTGACTT	CCTGAGCCAC	1500
CCTTTGGGA	TAGCTGTGTT	TGAGGACAAG	GTGTTCTGGA	CAGACCTGGA	GAACGAGGCC	1560
ATTTTCACTG	CAAATCGGCT	CAATGGCCTG	GAATCTCCA	TCTTGCTGTA	GAACCTCAAG	1620
AACCCACATG	ACATTGTCTAT	CTTCCATGAG	CTGAAGCAGC	CAAGAGCTCC	AGATGCCTGT	1680
GAGCTGAGTG	TCCAGCCTAA	TGGAGGCTGT	GAATACCTGT	GCCTTCCTGC	TCCTCAGATC	1740
TCCAGCCACT	CTCCCAAGTA	CACATGTGCC	TGTCCTGACA	CAATGTGGCT	GGGTCCAGAC	1800
ATGAAGAGGT	GCTACCGAGA	TGCAAAATGAA	GACAGTAAGA	TGGGCTCAAC	AGTCACTGCC	1860
GCTGTTATCG	GGATCATCGT	GCCCATAGTG	GTGATAGCCC	TCTGTGTCAT	GAGTGGATAC	1920
CTGATCTGGA	GAAACTGGAA	CGGGAAGAAC	ACCAAAAGCA	TGAATTTTGA	CAACCCAGTC	1980
TACAGGAAAA	CAACAGAAGA	AGAAGATGAA	GATGAGCTCC	ATATAGGGAG	AACCTGCTCAG	2040
ATTGGCCATG	TCTATCCTGC	ACGAGTGGCA	TTAAGCCTTG	AAGATGATGG	ACTACCTGTA	2100
GGATGGGATC	ACCCCTCTCG	TGCCCTCATG	AATTCAGTCC	CATGCACTAC	ACTCCGGATG	2160
GTGATGACT	GGATGAATGG	GTCTCTATAT	ATGGGTCTGT	GTGAGTGTAT	GTGTGTGTGT	2220
GATTTTPTTT	TTTAAATGAG	TTTGGCGGAA	AGGTAACCAC	AAAGTTATGA	TGAACCTGCA	2280
ACATCCAAAG	GATGTGAGAG	TTTTCTATAT	TATAATGTTT	TATACACTTT	TTAACTGGTT	2340
GCACTACCCA	TGAGGCAATC	GTGGAAATGG	TACTGCTGAC	TAACATGATG	CACATAACCA	2400
AATGGGGGCC	AATGGGCACG	TACCTTACTC	ATCATTTAAA	AACTATATTT	ACAGAAGATG	2460
TTTGGTGTCT	GGGGGGCTTT	TTTAGGTTT	GGGCATTGTT	TTTTTGTA	TAAGATGATT	2520
ATGCTTTGTG	GCTATCCATC	AACATAAGT				

Seq ID NO: 357 Protein sequence
Protein Accession #: NP_059992

55
60
65
70

1	11	21	31	41	51	
MGLPEPGLR	LLALLLLLLL	LLLLRLQHLA	AAAADPLLGG	QGPKECEKD	QFQCRNERCI	60
PSVWRCEDD	DCLDHSDEDD	CPKKTCAUSD	FTCDNGHCII	ERWKCDEBEE	CPDGSDESEA	120
TCTKQVCPAE	KLSCGPTSHK	CVPASWRCDG	EKDCGGGADE	AGCATSLGTC	RGDEFCQDGG	180
TCVLAIKHCN	QEQDCPDGSD	EAGCLQGLNE	CLHNNGGCSH	ICTDLKIGFE	CTCPAGFQLL	240
DQKTCGDIDE	CKDPDACSQI	CUNYKGYFKC	ECYPGCEMDL	LTNKNCAAAG	KSPSLIFTNR	300
TSABDRPVKR	NYSRLIFMLK	NVVALDVEVA	TNRIYWCDSL	YRKIYSAYMD	KASDPKEREV	360
LIDBQLHSPE	GLAVDWHVHK	IYWTDSGNKT	ISVATVDGGR	RRTLEFRNLG	EPRAIADVPL	420
RGFMYSWDWG	DQAKIEKSLG	NGVDRQTLVS	DNIEWPNGIT	LDLLSRLYLW	VDSKLHQLSS	480
IDFSGGNRKT	LISSTDFLSH	PFGLAVFEDK	VFWTDLENEA	IFSANRLNGL	EISILAENLN	540
NPHDIVIFHE	LKQPRAPDAC	ELSVQPNGGC	EYLCCLPAPQI	SSHSPKYTCA	CPDTMWLGPD	600
MKRCYRDANE	DSKMGSTVTA	AVIGIIVPIV	VIALLCMSGY	LIWRNWKRNK	TKSMNFDNFP	660
YRKTEEED	DELHIGRTAQ	IGHVYPARVA	LSLEDDGLP			

Seq ID NO: 358 DNA sequence
Nucleic Acid Accession #: M27826
Coding sequence: <1-503

75
80
85

1	11	21	31	41	51	
AGCCCAAGAA	ACATCTCACC	AATTTCAAAT	CTGATCTATT	CGGCTTAGCG	ACTGAAGATT	60
GACGCTGCC	GATCGCTCTG	GAAGTCCCTT	GGACCATCAC	AGAAGCCGAG	CTTCGGGTAA	120
CTCTCACAGT	GGAGGGTAAG	TCCATCCCTT	GTTTAAATCGA	TACGGGGGCT	ACCCACTCCA	180
CGTTCCTTTC	TTTTCAAGGG	CCTGTTTCCC	TGCCCCCAT	AACGTGTTGT	GGTATTGACG	240
GCCAAGCTTC	AAAACCCCTG	AAAACCTCCC	CACCTCTGGT	CCAACCTTGA	CAACACTCTT	300
TTATGCACTC	TTTTTTAGTT	ATCCCCACCT	GCCCCACTTC	CTTATTAGGC	CGAAATATTT	360
TAACCAAAAT	ATCTGCTTCC	CTGACTATT	CTGGAGTACA	GCTACATCTC	ATTGCTGCCC	420
TTCTTCCCAA	TCCAAAGCCT	CCTTTGTGTC	CTCTAACATC	CCCAACATAT	CAGCCCTTAC	480
CACAAGACCT	CCCTCAGCT	TAATCTCTCC	CACCTTAGGT	TCCCACGCGG	CCCCTAATCC	540
CACCTGAAGC	AGCCCTGAGA	AACATCGCCC	ATCTCTCTCT	CATACCAACC	CCCAAAATT	600
TTCCGCGCTC	CAACACTTCA	ACACTATTTT	GTTTTATTTG	TCTTATTAA	ATCAGAAGGC	660

AGGAATGTCA GGCCTCTGAG CCCAGGCCAG GCCATCGCAT CCCCTGTGAC TTGCACGTAT 720
 ACATCCAGAT GGCCTGAAGT AACTGAAGAT CCACAAAAGA AGTAAAAACA GCCTTAACGT 780
 ATGACATTCC ACCATTGTGA TTTGTTCTCG CCCACCCCTA ACTGATCAAT GTACTTTGTA 840
 ATCTCCCCCA CCTTAAAGAA GGTTCCTTGT AATTCTCCCC ACCCTTGAGA ATGTACTTTG 900
 TGAGATCCAC CCTGCCCCAC CAGAGAACAA CCCCTTTTGA TTGTAATTTT TTATTACCTT 960
 CCCAAATCCT ATAAACACAG CCCACCCCTA TCTTCCTTCA CTGACTCTCT TTTGCGACTC 1020
 AGCCACCGGC ACCCAGGTGA AATAAACAGC TTTATTGCTC AC

Seq ID NO: 359 Protein sequence
 Protein Accession #: AAA65999

1 11 21 31 41 51
 PKKHLTNFKS DLFGLATEDW RCPIASEVFW TITEAELRVT LTVEGKSIPC LIDTGATHST 60
 LPSPQGFVSL APITVVGIDG QASKPLKTPP LWCQLGQHSF MHSFLVPTC FLPLLGRNII 120
 TKLSASLTIP GVQLHLIAL LFPNKPPLCP LTSPQYQPLP QDLPSA

Seq ID NO: 360 DNA sequence
 Nucleic Acid Accession #: NM_001854
 Coding sequence: 162-5582

1 11 21 31 41 51
 AACCATCAAA TTTAGAAGAA AAAGCCCTTT GACTTTTTC CCTCTCCCT CCCCAATGGC 60
 TGTGTAGCAA ACATCCCTGG CGATACCTTG GAAAGGACGA AGTTGGTCTG CAGTCGCAAT 120
 TTCTGGTGGTT GAGTTCACAG TGTGAGTGC GGGGCTCGGA GATGGAGCCG TGGTCTCTTA 180
 GGTGGAAGAAC GAAACGGTGG CTCTGGGATT TCACCGTAAC AACCTCGCA TTGACCTTCC 240
 TCTTCCAAGC TAGAGAGCTG AGAGGAGCTG CTCCAGTTGA TGTACTAAAA GCCTAGATT 300
 TTCACAATTC TCCAGAGGGA ATATCAAAAA CAACGGGATT TTGCACAAAC AGAAAGAAAT 360
 CTAAGAGCTC AGATACCTGT TACAGAGTTT CAAAGCAAGC ACAACTCAGT GCCCAACAA 420
 AACAGTTATT TCCAGTGGAG ACTTTCCCGA AAGACTTTTC AATACTATT ACAGTAAAA 480
 CAAAAAAGG AATTCACTCT TCCCTTTTAT CTATATATA TGAGCATGGT ATTCAGCAA 540
 TTGGTGTGTA GGTGGGAGA TCACCTGTTT TCTGTGTTGA AGACCACACT GGAACACCTG 600
 CCCCAGAAGA CTATCCCTC TCCAGAACTG TTAACATCGC TGACGGGAAG TGGCATCGGG 660
 TAGCAATCAG CGTGGAGAAG AAAACTGTGA CAATGATTGT TGATTGTAAG AAGAAAACCA 720
 CGAAACCACT TGATAGAAGT GAGAGAGCAA TTGTGTATAC CAATGGAAATC ACGGTTTTTG 780
 GAACAAGGAT TTTGGATGAA GAAGTTTTTG AGGGGGACAT TCAGCAGTTT TTGATCAGAG 840
 GTGATCCCAA GGCAGCATAT GACTACTGTG AGCATTATAG TCCAGACTGT GACTCTTCAG 900
 CACCAAGGC TGCTCAAGCT CAGGAACCTC AGATAGATGA GTATGCACCA GAGGATATA 960
 TCGAATATGA CTATGAGTAT GGGGAAGCAG AGTATAAAGA GGCTGAAAGT GTAACAGAGG 1020
 GACCCACTGT AACTGAGGAG ACAATAGCAC AGACGGAGGC AAACATCGTT GATGATTTTC 1080
 AAGAATACAA CTATGGAACA ATGGAAGATT ACCAGACAGA AGCTCCTAGG CATGTTTCTG 1140
 GGACAAATGA GCCAAATCCA GTTGAAGAAA TATTTACTGA AGAATATCTA ACGGGAGAGG 1200
 ATTATGATTC CCAGAGGAAA AATTCTGAGG ATACACTATA TGAACACAA GAAATAGACG 1260
 GCAGGGATTC TGATCTTCTG GTAGATGGAG ATTTAGGCGA ATATGATTTT TATGAATATA 1320
 AAGAATATGA AGATAAACCA ACAAGCCCC CTAAATGAAGA ATTTGGTCCA GGTGTACAG 1380
 CAGAACTCGA TATTACAGAA ACAAGCATAA ATGGCCATGG TCATATGGA GAGAAAGGAC 1440
 AGAAAGGAGA ACCAGCAGTG GTTGAGCCTG GTATGCTTGT CGAAGGACCA CCAGGACCA 1500
 CAGGACCTGC AGGTATTATG GGTCTCTCCG GTCTACAAGG CCCACTGGA CCCCTGGTG 1560
 ACCCTGGCGA TAGGGGCCCC CCAGGACGCT CTGGCTTACC AGGGGCTGAT GGTCTACCTG 1620
 GTCTCTCTGG TACTGTGTTG ATGTTACCGT TCCGTTATGG TGGTGTGGT TCCAAAGGAC 1680
 CAACCATCTC TGCTCAGGAA GCTCAGGCTC AAGCTATTCT TCAGCAGGCT CGGATTGCTC 1740
 TGAGAGGCCC ACTTGGCCCA ATGGGTCTAA CTGGAAGACC AGGTCTGTG GGGGGGCTG 1800
 GTTCATCTGG GGCACAAAGT GAGAGTGGTG ATCCAGGTCC TCAGGGCCCT CGAGGCGTCC 1860
 AGGGTCCCC TGCTCAAGC GGAACACCTG GAAAAGGGG TCGTCCAGGT GCAGATGGAG 1920
 GAAGAGGAAT GCCAGAGAA CTTGGGGCAA AGGAGATCG AGGGTTGAT GGACTTCCG 1980
 CTCTGCCAGG TGACAAAGGT CACAGGGGTG AACGAGGTCC TCAAGTCTCT CCAGGTCTCT 2040
 CTGGTGATGA CTGCTGAGG GAGAAAGATG GAGAAATTGG ACCAAGAGGT CTTCCAGGTG 2100
 AAGCTGGCCC ACGAGGTTTG CTGGGTCCAA GGGGAATCC AGGAGCTCCA GGGCAGCTG 2160
 GTATGCGAGG TGATAGTGGC CCCCAGGAC CAAAAGGGAA CATGGGTCCC CAAGGGGAGC 2220
 CTGGGCTCTC AGGTCAACAA GGGAAATCCG GACCTCAGGG TCTTCTGCT CCACAAGGTC 2280
 CAATTGCTCC TCTTGGTGAA AAAGGACCAC AAGGAAACCC AGGACTTGCT GGACTTCTG 2340
 GTGCTGATGG GCCTCTGGT CATCTGGGA AAGAAGGCCA GTCTGGAGAA AAGGGGGCTC 2400
 TGGTCCCCC TGCTCCACAA GGTCTATTG GATNNCCGG CCCCGGGGA GTAAAGGGAG 2460
 CAGATGGTGT CAGAGGTCTC AAGGATCTA AAGGTGAAA GGTGAAAGT GGTTTTCCAG 2520
 GATTCAAAGG TGACATGGGT CTAAGAGGTG ACAGAGGAGA AGTTGGTCAA ATTGGCCCAA 2580
 GAGGGNAGA TGCCCTTGAA GGACCCAAAG GTGAGCAGG CCCAAGTGA GACCCAGGTC 2640
 CTTCAAGTCA AGCAGAGAA AAGGGAAAC TTGGAGTTCC AGGATTACCA GGATATCCAG 2700
 GAAGACAAGG TCCAAGGGT TCCACTGGAT TCCCTGGGTT TCCAGGTGCC AATGGAGAGA 2760
 AAGGTGCACG GGGAGTAGCT GGCACACAG GCCCTCGGG TCAGCGTGGT CCAACGGGTC 2820
 CTCGAGGTTT AAGAGGTGCA AGAGGTCCCA CTGGGAAACC TGGGCCAAG GGCCTTCAG 2880
 GTGGCGATGG CCTCTCTGGC CCTCCAGGTG AAAGAGGTCC TCAAGGACCT CAGGTCAGG 2940
 TTGGATTCCC TGGACCAAAA GGCCCTCTCT GACCACAGG AAGGATGGGC TGCCAGGAC 3000
 ACCCTGGGCA ACGTGGGGAG ACTGGATTTC AAGGCAAGAC CGGCCCTCT GGGCCAGGGG 3060
 GAGTGGTTGG ACCACAGGGA CCAACCGGTG AGACTGGTCC AATAGGGGAA CGTGGGTATC 3120
 CTGGTCTCTC TGGCCCTCTT GGTGAGCAAG GTCTTCTG TGCTGCAGGA AAAGAAGGTG 3180
 CAAAGGGTGA TCCAGTCTCT CAAGGTATCT CAGGGAAGAA TGGACCAAGG GATTACGTG 3240
 GATTCTCAGG GAAGAAAGGT CTCTCTGAG CTCAAGGTGC ACCTGGACTG AAAGGAGGGG 3300
 AAGGTCCCCA GGGCCACCAA GGTCCAGTTG GCTCACCAGG AGAACGTGGG TCAGCAGGTA 3360
 CAGCTGGCCC AATTGGTTTA CGAGGGCGCC CGGACCTCA GGTCTCTCT GGTCCAGCTG 3420
 GAGAGAAAGG TGCTCTTGA GAAAAGGTC CCCAAGGGCC TGCAGGGAGA GATGAGTTT 3480
 AAGGTCTCTG TGGTCTCCCA GGGCCAGCTG GTCTTGGCG CTCCTCTGGG GAAGACGGAG 3540
 ACAGGGTGTA AATTGTGTAG CCGGACAAA AAGGCAGCAA GGTGGCAAG GGAGAAATG 3600
 GCCCTCCCCG TCCCCAGGT CTTCAAGGAC CAGTTGGTGC CCTGGAATT GCTGGAGGTG 3660
 ATGGTGAACC AGGTCTTAGA GGCAGCAGG GATGTTTGG GCACAAAGGT GATGAGGGTG 3720
 CCAGAGGCTT CCTTGGACCT CTTGGTCCAA TAGGTCTTCA GGTCTGCCA GGCCACCTG 3780
 GTGAAAAGG TGAAAATGGG GATGTTGGTC CATGGGGGCC ACCTGGTCTT CCAGGCCCAA 3840

	GAGGCCCTCA	AGGTCCCAAT	GGAGCTGATG	GACCACAAGG	ACCCCCAGGT	TCTGTTGGTT	3900
	CAGTTGGTGG	TGTTGGAGAA	AAGGGTGAAC	CTGGAGAAGC	AGGAAACCCA	GGGCCTCCTG	3960
	GGGAAGCAGG	TGTAGGCGGT	CCCAAGAGAG	AAAGAGGAGA	GAAAGGGGAA	GCTGGTCCAC	4020
5	CTGGAGCTGC	TGGAGCTCCA	GGTGCCAAGG	GGCCGCCAGG	TGATGATGGC	CCTAAGGGTA	4080
	ACCCGGGTCC	TGTTGGTTTT	CCTGGAGATC	CTGGTCTCTC	TGGGGAACCT	GGCCCTGCAG	4140
	GTCAGATGG	TGTTGGTGGT	GACAAGGGTG	AAGATGGAGA	TCCTGGTCAA	CCGGGTCTCT	4200
	CTGGCCCATC	TGGTGAGGCT	GGCCCCCAGG	GTCTCTCTGG	AAAACGAGGT	CCTCTCTGGAG	4260
	CTGCAGGTGC	AGAGGGAAGA	CAAGGTGAAA	AAGTGTCTAA	GGGGGAAGCA	GGTGCAGAAAG	4320
10	GTCCTCTCTG	AAAAACCGGC	CCAGTCCGTC	CTCAGGGACC	TGCAGGAAAG	CCTGGTCCAG	4380
	AAGGTCTTCG	GGGCATCCCT	GGTCTGTGG	GAGAACAAGG	TCTCCCTGGA	GCTGCAGGCC	4440
	AAGATGGACC	ACCTGGTCTT	ATGGGACCTC	CTGGCTTACC	TGGTCTCAAA	GGTGACCCTG	4500
	GCTCCAAGGG	TGAAAAGGGA	CATCTGGT	TAATTGGCCT	GATTGGTCTT	CCAGGAGAAG	4560
	AAGGGGAAAA	AGGTGACCGA	GGGCTCCCTG	GAATCTCAAG	ATCTCCAGGA	GCAAAAGGGG	4620
15	ATGGGGGAAT	TCTTGTCTCT	GCTGGTCCCT	TAGGTCCACC	TGGTCTCTCA	GGCTTACCAG	4680
	GTCCTCAAGG	CCCAAAGGGT	AACAAAGGCT	CTACTGGACC	CGCTGGCCAG	AAAGGTGACA	4740
	GTGGTCTTCC	AGGGCTCTCT	GGGCTCCAG	GTCCACCTGG	TGAAGTCATT	CAGCCTTTAC	4800
	CAATCTTGTG	CTCCAAAAAA	AGAGAGAAGC	ATACTGAAGG	CATGCAAGCA	GATGCAGATG	4860
	ATAATATTCT	TGATTACTCG	GATGGAATGG	AAGAAATATT	TGTTTCCCTC	AATTCCCTGA	4920
20	AACAAGACAT	CGAGCATATG	AAATTTCCAA	TGGGTACTCA	GACCAATCCA	GCCCGAAGCT	4980
	GTAAGAGCCT	GCAACTCAGC	CATCTGACT	TCCAGATGG	TGAATATTGG	ATTGATCCTA	5040
	ACCAAGGTTG	CTCAGGAGAT	TCCTTCAAAG	TTTACTGTAA	TTTCACATCT	GGTGGTGAGA	5100
	CTTGCATTTA	TCAGACAAAA	AAATCTGAGG	GAGTAAGAAT	TTTCATCATG	CCAAAGGAGA	5160
	AACCAGGAAG	TTGGTTTATG	GAATTTAAGA	GGGGAAAGCT	GCTTTCATAC	TTAGATGTTG	5220
25	AAGGAAATTC	TCTCAATATG	GTGCAATGA	CATTCTTGAA	ACTTCTGACT	GCCTCTGCTC	5280
	GGCAAAATTT	CACCTACCAC	TGTCTCAGT	CAGCAGCCCTG	GTATGATGTG	TCATCAGGAA	5340
	GTTATGACAA	AGCACTTCGC	TTCTGGGAT	CAATGTATGA	GGAGATGTCC	TATGACATA	5400
	ATCCTTTTAT	AAAAACACTG	TATGATGGTT	GTACGTCCAG	AAAAGGCTAT	GAAAAAACTG	5460
	TCATTTGAAT	CATATACACCA	AAAATTGATC	AAGTACCTAT	TGTTGATGTC	ATGATCAGTG	5520
30	ACTTTGGTGA	TCAGAACTAG	AAGTTCGGAT	TGGAAGTTGG	TCCTGTTTGT	TTTCTTGGCT	5580
	AAGATTGAAG	CAAGAAGCAT	ATCAAAATCA	CAGAAAAATG	ACCTTGGTGC	CACCAACCCA	5640
	TTTTGTGCCA	TGTCAAGATT	TGGAATAAGG	ATGTATGGAA	AACAACGCTG	CATATACAGG	5700
	TACCATTTAG	GAAATACCGA	TGCCTTTGTG	GGGGCAGAAAT	CACAGACAAA	AGCTTTGAAA	5760
	ATCATAAAGA	TATAAGTTGG	TGTGGCTAAG	ATGGAAACAG	GGCTGATTCT	TGATTTCCCAA	5820
35	TTCTCACTC	TCCTTTTCTT	ATTGAATTT	CTTTGGTGTG	GTAGAAAAACA	AAAAAAGAAA	5880
	AATATATATT	CATAAAAAAT	ATGGTGCTCA	TTCTCATCCA	TCCAGGATGT	ACTAAAACAG	5940
	TGTGTTTAAT	AAATTGTAAT	TATTTTGTGT	ACAGTTCTAT	ACTGTTATCT	GTGTCCATT	6000
	CCAAAACCTG	CACGTGTCCC	TGAATTCGCG	TGACTCTAAT	TTATGAGGAT	GCCGAAGCTC	6060
40	GATGGCAATA	ATATATGTAT	TATGAAAATG	AAGTTATGAT	TTCCGATGAC	CCTAAGTCCC	6120
	TTTCTTTGGT	TAATGATGAA	ATTCTTTTGT	GTGTGTTT			

Seq ID NO: 361 Protein sequence
Protein Accession #: NP_001845

45	1	11	21	31	41	51	
	MEPWSSRWKT	KRWLWDFTVT	TLALTFLFQA	REVRGAAPVD	VLKALDFHNS	PEGISKTTGF	60
	CTNRKNSKGS	DTAYRVSKQA	QLSAPTQKLF	PGGTFFPEDFS	ILFTVFKPKG	IQSFLLSIYN	120
	EHGIQIQIGVE	VGRSPVFLFE	DHTGKPAPED	YPLFRVTNIA	DGKWHRVVIA	VEKKTVTMIV	180
50	DCKKKTTKPL	DRSERAIVD	NGITVFGTRI	LDBEVFEGDI	QQFLITGDPK	AAYDYCEHYV	240
	PDCSSAPFKA	AQAQEPQIDE	YAPEDIIEYD	YBYGEAEYKE	AESVTETGPTV	TEETIAQTEA	300
	NIVDDFQYEN	YGTMESYQTE	APRHVSGTNE	PNFVEEIFTE	EYLTGEDYDS	QRKNSEDTLY	360
	ENKEIDGRDS	DLVVDGLDGE	YDFYKEYEYK	DKPTSPPNEE	FGPGVPAETD	ITETSINGHG	420
	AYGEKGQKGE	PAVVEPQMLV	EGPFGPAGPA	GIMGPPGLQG	PTGPPGDPGD	RGPFGPRPGL	480
55	GADGLPGPPG	TMLMLPFRYG	GDGSKGPTIS	AQEAQAQAIL	QQAIRIALRG	PGPMGLTRFP	540
	GFVGGPGSSG	AKGESGDPGP	QGPFGVQGGP	GPTGKPGKRG	RPGADGGRGM	PGEPGAKGDR	600
	GFDFGLPLPG	DKHGRGERGP	QGPFGPPGDD	GMRGEDGEIG	PRGLPGEAGP	RGLLGPRTGP	660
	GAPGQPGMAG	VDGPPGPKGN	MGPQGEFPGP	QQQGNFPGQG	LPFGPQGPFG	PGKGPQGGK	720
	GLAGLPGADG	PPGHFPGKEG	SGEKGALGPP	GPQGPIGXPG	PRGVKADGV	RGLKGSKGKE	780
60	GEDGPPGPKG	DMGLKGRDGE	VQIGPRGXG	GPBGPKGRAG	PTGDPGPGSQ	AGEKGLGVFP	840
	GLPGYFGRQG	PKGSTGFFGF	PGANGKGRAR	GVAGKPGPRG	QRGPTGPRGS	RGARGFTGKP	900
	GPKGTSGDDG	PPGPPGGRGP	QGPQGPVGGP	GPKGPVGGPP	RMGCPGHPGQ	RGETGFQGGT	960
	GPPGPGGVVG	PQGPPTGTGP	IGERGYPGPF	GPPGQGLPFG	AAGKEGAKGD	PGPQGISGKD	1020
	GPAGLRGFFG	ERGLPGAQGA	PGLKGGEGPQ	GPPGVPVGSFG	ERGSAGTAGP	IGLRGRPGFP	1080
65	GPPGPAGEKG	APGEGKPGQP	AGRDGVQGPV	GLPGVPAGPAG	SPGEDGDKGE	IGEPGQKGSK	1140
	GGKGENGPPG	PPGLQGPVGA	PGIAGGDGEP	GPRGQGMFG	QKGDGARGF	PGPPGPIGLQ	1200
	GLPGPPGEGK	ENGDVGPWGP	PGPPGPRGPG	GPNGADGPGQ	PPGSGVSGVG	VGEKGEPEGA	1260
	GNPFGPPGAG	VGGPKGERGE	KGEAGPPGAA	GPPGAKGPPG	DDGPKGNPGP	VGFPDGPDPG	1320
	GELGPAGQDG	VGGDKGEDGD	PGQGPFGPGS	GEAGFPFGPG	KRGFPGAAGA	EGRQGEKGA	1380
70	GEAGAEPPFG	KTGPVGPQGP	AGKPGPEGLR	GIPGVPGEQG	LPGAAGQDGP	PGPMGPPGLP	1440
	QLKGDPPGSK	EKGHPGLIGL	IGPPGEQGEK	GDRGLPGTQG	SPGAKGDGGI	PGPAGPLGFP	1500
	GPPGLPGPQG	PKGNKSGTGP	AGQKGDGSLP	GPPGPPGPPG	EVIQPLPILS	SKKTRRRHTEG	1560
	MQADADDNII	DYSDGMEBIF	GSLNSLKQDI	EHMFPMTGTQ	TNPARTCKDL	QLSHDPFDDG	1620
	EYWIDPNQGC	SGDSFKVYCN	FTSGGETCIY	PDKKSEGVRI	SSWPKEKPGS	WFSEFKRGKL	1680
75	LSYLDVEGNS	INMVQMTFLK	LLTASARQNF	TYHCHQSAAM	YDVSSGSYDK	ALRFLGSNDE	1740
	EMSYDNNPFI	KTYLDGCTSR	KGYEKTIVBI	NTPKIDQVPI	VDVMISDFGD	QNRKFGFEVG	1800
	PVCFLG						

Seq ID NO: 362 DNA sequence
Nucleic Acid Accession #: NM_003107
Coding sequence: 351-1775

85	1	11	21	31	41	51	
	TTCCCCAGCA	TTCCGAGAAAC	TCCTCTCTAC	TTAGACACGG	TCTCCAGACT	CAGCCGAGAG	60
	ACAGCAAAC	GCAGCGCGGT	GAGAGAGCGA	GAGAGAGGGA	GAGAGAGACT	CTCCAGCCTG	120
	GGAACTATAA	CTCCTCTGCG	AGAGGCGGAG	AACCTCTTCC	CCAAATCTTT	TGGGGACTTT	180

TCTCTCTTTA CCCACCTCCG CCCCTGCGAG GAGTTGAGGG GCGAGTTCGG CCGCCGCGCG 240
 CGTCTTCCCG TTCGGCGTGT GCTTGGCCCG GGAACCGGG AGGGCCCGGC GATCGCGCGG 300
 CGGCGCGCGC GAGGGTGTGA GCGCGCGTGG GCGCCCGCGC AGCCGAGGCC ATGGTGCGAG 360
 AAACCAACAA TGCCGAGAAC AGGGAAGCGC TGCTGGCCGG CGAGAGCTCG GACTCGGGCG 420
 CCGGCGCTCGA GCTGGGAATC GCCTCCTCCC CCACGCCCGG CTCACCGCGC TCCACGGGCG 480
 GCAAGGCCGA CGACCCGAGC TGGTGCAAGA CCGCGAGTGG GCACATCAAG CGACCCATGA 540
 ACGCCTTCAT GGTGTGTCG CAGATCGAGC GCGCAAGAT CATGGAGCAG TCGCCCGACA 600
 TGCACAACGC CGAGATCTCC AAGCGGCTGG GCAAACGCTG GAAGCTGCTC AAAGACAGCG 660
 ACAAGATCCG TTTCAATCGA GAGGCGGAGC GGCTGCGCCT CAAGCACATG GCTGACTACC 720
 CCGACTACAA GTACCGGCCG AGGAAGAAGG TGAAGTCCGG CAACGCCAAC TCCAGCTCCT 780
 CCGCGCGCGC CTCTCCAAAG CCGGGGAGAG AGGGAGACAA GGTGCTGGC AGTGGCGGG 840
 GCGGCCATGG GGGCGGCGGC GCGCGCGGGA GCAGCAACGC GGGGGAGGGA GCGCGCGGTG 900
 CGAGTGGCGG CGGCGCCAAC TCCAAACCGG CGCAGAAAAA GAGCTGCGGC TCCAAAGTGG 960
 CGGGCGCGCG GGGCGGTGGG GTTAGCAAAAC CGCACGCCAA GCTCATCTG GCAGGCGGG 1020
 GCGGCGCGCG GAAAGCAGCG GCTGCGCGCG CCGCCTCCTT CGCCGCGGAA CAGGCGGGGG 1080
 CCGCGCGCCT GCTGCCCTCG GCGGCGCGCG CGACACCA CTGCTGTAC AAGGCGCGGA 1140
 CTCACAGCGC CTGCGCCTCC GCCTCCTCGG CAGCCTCGGC CTCGCGAGCG CTCGCGCGCC 1200
 CCGGCAAGCA CCTGGCGGAG AAGAAGGTGA AGCGCGTCTA CTGTTCGGC GGCTGGGGCA 1260
 CGTCTGCTGC GCGCGTGGCG GTTAGCAAAAC CGGAGCGGAG CCCCAGCGAC CCCCTGGGCG 1320
 TGTACGAGGA GAGGCGCGCG GGCTGCTCGC CCGACGCGCC CAGCCTGAGC GCGCGCAGCA 1380
 GCGCGCGCCT GCTCCCGCGC CGCGCGCGCT CGCCCGCGGA CCACCGCGGC TACGCCAGCC 1440
 TGCAGCGCGC CTGCGCGCGC CCGTCCAGCG CGCCTCGCA CGCGTCTCC TCGGCTCTGT 1500
 CCCACTCTCT CTCTCTCTCC TCCTCGGCT CTCTGCTCTC CGACGACGAG TTCGAAGACG 1560
 ACCTGCTCGA CCTGAACCCC AGCTCAAACT TTGAGAGCAT GTCCCTGGGC AGCTTCAGTT 1620
 CGTCTGCGCG GCTCGACCGG GACCTGAGTT TTAACCTCGA GCGCGGCTCC GGCTCGCACT 1680
 TCGAGTTCCC GAGTACTCG AGCCCGAGG TGAGCGAGAT GACTCTGGGA GACTGGCTCG 1740
 AGTCCAGCAT CTCCAACCTG GTTTTCACTT ACTGAAGGCG GCGCAGCGAG GGAGAAGGGC 1800
 CCGGGGGGGT AGGAGAGGAG AAAAAAAGG TGAAGAAAG AAACGAAAG GACAGACGAA 1860
 GAGTTTAAAG AGAAAAAGGA AAAAAAGTAA CAGGGCTCGT TCGCCCGCGT 1920
 TCTGCTGCTC GGATCAAGGA GCGCGCGCGC GTTTTGGACC CGCGCTCCCA TCCCCACCT 1980
 TCCCGGCGCG GGGACCCACT CTGCCAGCC GGAGGAGCGC GGAGGAGGAA GAGGGTAGAC 2040
 AGGGGCGACC TGTGATTGTT GTTATTGATG TTGTTGTGA TGGCAAAAAA AAAAAGCGAC 2100
 TTCAGTTTGG CTCCTCTTGG CTTGAAGAGA CCCCTCCCCC CTTCAACGAG GCTTCCGGAC 2160
 TTGTTGTCAC CCCCAGCAAG AAGCGAGTT AGTTTCTAG AGACTTGAAG GAGTCTCCCC 2220
 CTTCTGTCAT CACCACCTTG GTTTTGTGTT ATTTTGTCTC TTGGTCAAGA AAGGAGGGGA 2280
 GAACCCAGCG CAGCCTCTCC CCCCTTTT TAAACGCGTG ATGAAGACAG AAGGCTCCGG 2340
 GGTGACGAAT TTGGCGGATG GCAGATGTTT TGGGGGAACG CCGGAGCTGA GAGACTCCAC 2400
 GCAGGCGAAT TCCCGTTTGG GGCCTTTTTC TCCTCCCTCT TTTCCCTTG CCCCTCTGCG 2460
 AGCGGAGGGA AGAGATGTTG AGGGGAGGAG GCCAGCCAGT GTGACCGGCG CTAGGAAATG 2520
 ACCCGAGAAC CCGGTTGGAA GCGCAGCAGC GGGAGCTAGG GCGGGGGCGG GAGGAGGACA 2580
 CGAACTCGAA GGGGTTTAC GTTCAAACTG AAATGGATTG GCACGTGGGG GAGCTGGCGG 2640
 CCGCGGCTGC TGGGCTCTCG CCTTCTTTC TACGTGAAAT CAGTGAGGTG AGACTTCCCA 2700
 GACCCCGGAG CCGTGGAGGA GAGGAGACTG TTTGATGTGG TACAGGGGCA GTCAGTGGAG 2760
 GCGAGTGGT TTCGGAAAAA AAAAAAGAAA AAAAGGG

Seq ID NO: 363 Protein sequence
 Protein Accession #: NP_003098

1 11 21 31 41 51
 MVQQTNNAE TEALLAGESS DSGAGLELGI ASSPTPGSTA STGGKADDPs WCKTPSGHIK 60
 RPMNAFMVWS QIBRRKIMEQ SPDMHNABIS KRLGKRWKLL KDSDKIPFIR EAERLRKHKM 120
 ADYDPYKYRP RKIKVKSNNAN SSSSAAASSK PGEKGDKVGG SGGGGHGGGG GGGSSNAGGG 180
 GGGASGGGAN SKPAQKKSCG SKVAGGAGGG VSKPHAKLIL AGGGGGGKAA AAAAAFAAE 240
 QAGAAALLPL GAGADHHSLY KARTPSASAS ASSAASASAA LAAPGKHLAE KVKRVYLFPG 300
 GLGTSSSPVG GVAGADPSD PLGLYEEBGA GCSPPDAPSL GRSSAASSPA AGRSPADHRG 360
 YASLRAASPA PSSAPSHASS SASSHSSSSS SSGSSSSDDE FEDDLLDLNP SSNFESMSLG 420
 SFSSSSALDR DLDFNFPBGS GSHFEPDYC TPEVSEMISS DWLESSISNL VFY

Seq ID NO: 364 DNA sequence
 Nucleic Acid Accession #: U10860
 Coding sequence: 123-2204

1 11 21 31 41 51
 TGCGCGGTGC TCCTCGACCA GGCCTCCTTC TCAACCTCAG CCGCGGCGCG CGACCTTCC 60
 GGCACCTTCC CGCCCGCTCT CGTACTGTGG CCGTCACCGC CGCGGCTCCG GCGCTGGCCC 120
 CGATGGCTCT GTGCAACGGA GACTCCAAGC TGGAGAATGC TGGAGGAGAC CTTAAGGATG 180
 GCCACACCA CTATGAAGGA GCTGTTGTCA TTCTGGATGC TGGTGTCTAG TACGGGAAAG 240
 TCATAGACCG AAGAGTGAGG GAACGTGTCG TGCACTCTGA AATTTTCCCC TTGGAAACAC 300
 CAGCATTGCG TATAAAGGAA CAAGGATTCC GTGCTATTAT CATCTCTGGA GGACCTAATT 360
 CTGTGTATGC TGAAGATGCT CCCTGGTTTG ATCCAGCAAT ATTCACTATT GGCAAGCCTG 420
 TTCTTGAAT TTGCTATGGT ATGCAGATGA TGAATAAGGT ATTGGAGGT ACTGTGCACA 480
 AAAAAAGTGT CAGAGAAGAT GGAGTTTCA ACATTAGTGT GGATAATACA TGTTCATTAT 540
 TCAGGGGCTT TCAGAAGGAA GAAGTTGTTT TGCTTACACA TGGAGATAGT GTAGACAAAG 600
 TAGCTGATGG ATTCAAGGTT GTGGCAGGTT CTGGAAACAT AGTAGCAGGC ATAGCAAAATG 660
 AATCAAAAAA GTTATATGGA GCACAGTCC ACCCTGAAGT TGGCCTTACA GAAATGGAA 720
 AAGTAATACT GAAGAATTTC CTTTATGATA TAGCTGGATG CAGTGGAAAC TTCACCGTGC 780
 AGAACAGAGA ACTTGTAGTGT ATTCGAGAGA TCAAGAGAG AGTAGGCACG TCAAAAGTTT 840
 TGTTTTACT CAGTGGTGGG GTAGACTCAA CAGTTTGTAC AGCTTTGCTA AATCGTCTT 900
 TGAACCAAGA ACAAGTCATT CTCTGTCACA TTGATAATGG CTTTATGAGA AAACGAGAAA 960
 GCCAGTCTGT TGAAGAGGCC CTCAAAAAGC TTGGAATTCA GGTCAAAGTG ATAAATGCTG 1020
 CTCATTCTTT CTACAATGGA ACAACAACCC TACCAATATC AGATGAAGAT AGAACCCAC 1080
 GGAAAAAGAT TAGCAAAACG TTAATATGTA CCACAAGTCC TGAAGAGAAA AGAAAAATCA 1140
 TTGGGGATAC TTTTGTAAAG ATTGCCAATG AAGTAATGG AGAAATGAAC TTGAAACCG 1200
 AGGAGGTTTT CCTTGGCCAA GGTACTTTAC GGCCTGATCT AATTGAAAGT GCATCCCTTG 1260

TTGCAAGTGG CAAAGCTGAA CTCATCAAAA CCCATCAGAA TGACACAGAG CTCATCAGAA 1320
 AGTTGAGAGA GGAGGGAAAA GTAATAGAAC CTCTGAAAGA TTTTCATAAA GATGAAGTGA 1380
 GAATTTTGGG CAGAGAACTT GGACTTCCAG AAGAGTTAGT TTCCAGGCAT CCATTTCCAG 1440
 5 GTCCCTGGCCT GGCAATCAGA GTAATATGTG CTGAAGAACC TTATATTGTG AAGGACTTTC 1500
 CTGAAACCAA CAATATTTTG AAAATAGTAG CTGATTTTTC TGCAAGTGTT AAAAAGCCAC 1560
 ATACCCTATT ACAGAGAGTC AAAGCCTGCA CAACAGAAGA GGATCAGGAG AAGCTGATGC 1620
 AAATTACCAG TCTGCATTCA CTGAATGCCT TCTTGCTGCC AATTAATACT GTAGGTGTGC 1680
 AGGGTGACTG TCGTTCTCTAC AGTTACGTGT GTGGAATCTC CAGTAAAGAT GAACCTGACT 1740
 10 GGAATCACT TATTTTCTG GCTAGGCTTA TACCTCGCAT GTGTCACAAC GTTAACAGAG 1800
 TTGTTTATAT ATTTGGCCCA CCAGTTAAAG AACCTCCTAC AGATGTTACT CCCACTTTCT 1860
 TGACAACAGG GGTGCTCAGT ACTTTACGCC AAGCTGATTG TGAGGCCCAT AACATTCTCA 1920
 GGGAGTCTGG GTATGCTGGG AAAATCAGCC AGATGCCGGT GATTTTGACA CCATTACATT 1980
 TTGATCGGGA CCCACTTCAA AAGCAGCCTT CATGCCAGAG ATCTGTGGTT ATTCGAACCT 2040
 15 TTATTACTAG TGACTTCATG ACTGGTATAC CTGCAACACC TGGCAATGAG ATCCCTGTAG 2100
 AGGTGGTATT AAGATGGTC ACTGAGATTA AGAAGATTCC TGGTATTCT CGAATTATGT 2160
 ATGACTTAAC ATCAAAGCCC CCAGGAACCTA CTGAGTGGGA GTAATAAACT TC

Seq ID NO: 365 Protein sequence

Protein Accession #: AAA60331

1 11 21 31 41 51
 | | | | |
 MALCNGDSKL ENAGGDLKDG HHYEGAVVI LDAGAQQYGV IDRRVRELFP QSEIPPLETP 60
 25 AFAIKEQGFPR AIIISGGPNS VVAEDAPWFD PAIFTIGKPV LGICYGMQMM NKVFGTGHK 120
 KSVREDGVFN ISVDNCTSLF RGLQKEEVL LTHGDSVDKV ADGFKVVAR SGNIVAGIANE 180
 SKKLYGAQFH PEVGLTENGL VILKNFLYDI AGCSGTFTVQ NRELECIREI KERVGTSKVL 240
 VLLSGGVDST VCTALLNRAL NQEQVIAVHI DNGFMRKRES QSVEEALKKL GIQVKVINAA 300
 HSPYNGTTTL PISDEDRTPR KRISKLTNMT TSPEEKRII GDTFVKIANE VIGEMNLKPE 360
 30 EVFLAQTGLR PDLIESASLV ASGKAELIKT HNDTELIRK LRBEKGIVIE LKDPFHKDEVR 420
 ILGRELGLPE ELVSRHFPFG PGLAIRVICA EEPYICKDFP ETNNILKIVA DFSASVKKPH 480
 TLLQRVKACT TEEDQEKLMQ ITSLHSLNLF LLPIKTVGVQ GDCRSYSYVC GISSKDEPDW 540
 BSLIFLARLI PRMCHNVNRV VYIFGPPVKE PFTDVTPTFL TTGVLSLTLRQ ADFEAHNILR 600
 ESGYAGKISQ MPVILTPHF DRDPLQKQPS QRSVVIRTF ITSDFMGTIP ATPGNEIPVE 660
 35 VVLKMTVEIK KIPGISRIMY DLTSKPPGTT EWE

Seq ID NO: 366 DNA sequence

Nucleic Acid Accession #: NM_004219

Coding sequence: 46-654

1 11 21 31 41 51
 | | | | |
 GCGGCCTCAG ATGAATGCGG CTGTTAAGAC CTGCAATAAT CCAGAAATGGC TACTCTGATC 60
 45 TATGTTGATA AGGAAAATGG AGAACCAGGC ACCCGTGTGG TTGCTAAGGA TGGGCTGAAG 120
 CTGGGGTCTG GACCTTCAAT CAAAGCCTTA GATGGGAGAT CTCAAGTTTC AACACCACGT 180
 TTTGGCAAAA CGTTCGATGC CCAACCAAGC TTACCTAAAG CTACTAGAAA GGCTTTGGGA 240
 ACTGTCAACA GAGCTACAGA AAGTCTGTA AAGACCAAGG GACCCCTCAA ACAAAAACAG 300
 CCAAGCTTTT CTGCCAAAAA GATGACTGAG AAGACTGTTA AAGCAAAAAG CTCTGTTCCT 360
 50 GCCTCAGATG ATGCCCTATCC AGAAATAGAA AAATCTTTTC CCTTCAATCC TCTAGACTTT 420
 GAGAGTTTTG ACCTGCCTGA AGAGCACCAG ATTGCGCACC TCCCTTGTAG TGGAGTGCCT 480
 CTATGATCTG TTGACGAGCT GAGAGAGCTT GAAAAGCTGT TTCAGCTGGG CCCCCTTCA 540
 CCTGTGAAGA TGCCCTCTCC ACCATGGGAA TCCAATCTGT TGCAGTCTCC TTCAAGCATT 600
 CTGTGCGACC TGGATGTTGA ATTGCCACCT GTTGTCTGTG ACATAGATAT TTAAATTCT 660
 55 TAGTGCTTCA GAGTTTGTGT GTATTGTGAT TAATAAAGCA TTCTTCAACA GAAAAAATA 720
 AAAAAA

Seq ID NO: 367 Protein sequence

Protein Accession #: NP_004210

1 11 21 31 41 51
 | | | | |
 MATLIYVDKE NGEPTGTRVVA KDGLKLGSGP SIKALDGRSQ VSTPRFGKTF DAPPALPKAT 60
 65 RKALGTVNRA TEKSVKTKGP LKQKQPSFSA KMTTEKTVKA KSSVPASDDA YPEIEKFFFP 120
 NPLDFESFDL PEHQIAHLP LSGVPLMILD EERELEKLFQ LGPPSPVKMP SPPWESNLLQ 180
 SPSSILSTLD VELPPVCCDI DI

Seq ID NO: 368 DNA sequence

Nucleic Acid Accession #: NM_000597

Coding sequence: 118-1104

1 11 21 31 41 51
 | | | | |
 75 ATTCGGGGCG AGGGAGGAGG AAGAAGCGGA GGAGGGCGCT CCCGCTCGCA GGGCCGTGCA 60
 CCTGCCCCGC CGCCCGCTCG CTGCTCGGCC CGCCGCGCCG CGCTGCCGAC CGCCAGCATG 120
 CTGCCGAGAG TGGGCTGCCC CGCGCTGCGG CTGCCGCGCG CGCGCTGTCT GCGCGTGTCT 180
 CGCTGTCTGC TGCTGCTACT GGGCGCGAGT GGC CGCGCGCG CGCGGGCGCG CGCGGAGGTG 240
 CTGTTCCGCT GCCCGCCCTG CACACCCGAG CGCCTGGCCG CCTGCGGGCC CCGCGCGGTG 300
 80 GCGCCGCGCG CGCGGCTGGC CGCAGTGGCC GGAGGCGCCC GCATGCCATG CGCGGAGCTC 360
 GTCCGGGAGC CGGGCTGCGG CTGCTGCTCG GTGTGCGCCC GCTGTGGAGG CGAGGCGTGC 420
 GGCGTCTACA CCCCGCGCTG CGGCCAGGGG CTGCGCTGCT ATCCCCACCC GGGCTCCGAG 480
 CTGCCCTTGC AGGCGCTGGT CATGGGCGAG GGCACCTGTG AGAAGCGCGG GGACGCGGAG 540
 TATGGCGCCA GCCCGCGCTG GGTTCAGAGC AATGGCGATG ACCACTCAGA AGGAGGCGCT 600
 85 GTGGAGAACC ACGTGGACAG CACCATGAAC ATGTGGGCGG GGGGAGGCGG TGCTGGCCGG 660
 AAGCCCTTCA AGTGGGTAT GAAGGAGCTG GCCGTGTTCG GGGAGAAGGT CACTGAGCAG 720
 CACCGGCAGA TGGCAAGGG TGGCAAGCAT CACCTTGGCC TGGAGGAGCC CAAGAAGCTG 780
 CGACCACCCC CTGCCAGGAC TCCTTGCCAA CAGGAACCTG ACCAGGTCTT GGAGCGGATC 840

TCCACCATGC GCCTTCCGGA TGAGCGGGGC CCTCTGGAGC ACCTCTACTC CCTGCACATC 900
 CCCAAGTGTG ACAAGCATGG CCTGTACAAC CTCAAACAGT GCAAGATGTC TCTGAACGGG 960
 CAGCGTGGGG AGTGCTGGTG TGTGAACCCC AACACCGGGA AGCTGATCCA GGGAGCCCCC 1020
 ACCATCCGGG GGGACCCCGA GTGTCACTCT TTCTACAATG AGCAGCAGGA GGCTTGCCGG 1080
 GTGCACACCC AGCGGATGCA GTAGACGCGA GCCAGCCGGT GCCTGGCCGC CCTGCCCCCC 1140
 GCCCTCTCC AAACACCGGC AGAAAACGGA GAGTGCTTGG GTGGTGGGTG CTGGAGGATT 1200
 TTCCAGTTCT GACACACGTA TTTATATTGG GAAAGAGACC AGCACCAGAG TCGCACCTCT 1260
 CCCGCCCTCT CTCTTCCGAC CTGCAGATGC CACACCTGCT CTTTCTTGCT TCCCCCGGG 1320
 GAGGAAGGGG GTTGTGGTGG GGGAGCTGGG GTACAGGTTT GGGGAGGGGG AAGAGAAATT 1380
 TTTATTTTGG AACCCCTGTG TCCCTTTTGC ATAAGATTAA AGGAGAGAAA AGT

Seq ID NO: 369 Protein sequence
Protein Accession #: NP_000588

1 11 21 31 41 51
 MLPRVGCPL PLPPPLLLPL LPLLLLGLLA SGGGGGARAE VLFRCPPTCT ERLAACGPPP 60
 VAPPAVAAV AGGARMPCAE LVREPGCGCC SVCARLEGEA CGVYTPRCGQ GLRCYPHFGS 120
 ELPLQALVMG EGTCEKRRDA EYGASPEQVA DNGDDHSEGG LVENHVDSTM NMLGGGGSAG 180
 RKPLKSGMKE LAVFREKVTE QHRQMGKGGK HHLGLEBPKK LRPPPARTPC QBELDQVLER 240
 ISTMLRPDER GPLEHLYSLH IPNCDKHGLY NLKQCKMSLN GQRGECWCVN PNTGKLIQGA 300
 PTIRGDPECH LFINQQEAC GVHTQRMQ

Seq ID NO: 370 DNA sequence
Nucleic Acid Accession #: NM_004264
Coding sequence: 6-440

1 11 21 31 41 51
 GGAACATGGC GGATCGGCTC ACGCAGCTTC AGGACGCTGT GAATTCGCTT GCAGATCAGT 60
 TTTGTAATGC CATTTGGAGTA TTGCAGCAAT TTGGTCTCTC TGCTCTTTTC AATAATATTC 120
 AGACAGCAAT TAACAAGAC CAGCCAGCTA ACCCTACAGA AGAGTATGCC CAGCTTTTTC 180
 CAGCAGTGTG TGCAAGACA GCAAAAGACA TTGATGTTTT GATAGATTCC TTACCCAGTG 240
 AAGAATCTAC AGCTGCTTTA CAGGCTGCTA GCTTGATATA GCTAGAAGAA GAAAACCATG 300
 AAGCTGCTAC ATGTGTGGAG GATGTTGTTT ATCGAGGAGA CATGCTTCTG GAGAAGATAC 360
 AAAGCGCACT TGCTGATATT GCACAGTCAC AGCTGAAGAC AAGAAGTGGT ACCCATAGCC 420
 AGTCTCTTCC AGACTCATAG CATCAGTGGG TACCATGTGG CTGAGAAAAG AACTGTTTGA 480
 GTGCCATTAA GAATCTGCA CTAGACTTAG ATACAAGCCT TACCAACATA TACAGAAACA 540
 TTAACACTA TGACACATTA CCTTTTTCAG TATTTTAAAT AGTCTTCTAT TTTCACTCTT 600
 GATAAGCTTA TAAATCATGA TTGAATCAGC TTTAAAGCAT CATACCATCA TTTTAACT 660
 GAGTGAATTT AATGAAGCAT GTAATACATT AATGAACATA ATATAAGGAA ACATATGTAA 720
 AATTCTGTGA TGACATAATT TATGTCTCCA TTTGTTGTA TTGGCCAGTA CTTTACAAAT 780
 C

Seq ID NO: 371 Protein sequence
Protein Accession #: NP_004255

1 11 21 31 41 51
 MADRLTQLQD AVNSLADQFC NAIGVLQCCG PPASFNNIQT AINKDQFANP TEEYAQLFAA 60
 LIARTAKDID VLIDSLPSEE STAALQAASL YKLEENHEA ATCVEDVVYR GDMLEKIQS 120
 ALADIAQSQL KTRSGTHSQS LPDS

Seq ID NO: 372 DNA sequence
Nucleic Acid Accession #: AJ271091
Coding sequence: 1-1113

1 11 21 31 41 51
 ATGGAGAATC AGGTGTTGAC GCCGCATGTC TACTGGGCTC AGCGACACCG CGAGCTATAT 60
 CTGCGCGTGG AGCTGAGTGA CBTACAGAAC CCTGCCATCA GCATCACTGA AAACGTGCTG 120
 CATTTCAAAG CTCAAGGACA TGGTGCCAAA GGAGACAATG TCTATGAATT TCACCTGGAG 180
 TTCTTAGACC TTGTGAAACC AGAGCCTGTT TACAACTGA CCCAGAGGCA GGTAAACATT 240
 ACAGTACAGA AGAAAGTGAG TCAGTGGTGG GAGAGACTCA CAAAGCAGGA AAAGCGACCA 300
 CTGTTTTTGG CTCTGACTT TGATCGTTGG CTGGATGAAT CTGATCGGGA AATGGAGCTC 360
 AGAGCTAAGG AAGAAGAGCG CCTAAATAAA CTCCGACTGG AAAGCGAAGG CTCTCTGAA 420
 ACTCTTACAA ACTTAAGGAA AGGATACCTG TTTATGTATA ATCTTGTCGA ATTCTTGGGA 480
 TTCTCCTGGA TCTTTGTCAA CCTGACTGTG CGATTCTGTA TCTTGGGAAA AGAGTCTCTT 540
 TATGACACAT TCCATACTGT GGCTGACATG ATGTATTCTT GCCAGATGCT GGCAGTTGTG 600
 GAAACTATCA ATGCAGCAAT TGGAGTCACT ACGTCACCGG TGCTGCCTTC TCTGATCCAG 660
 CTTCTTGGA GAAATTTTAT TTTGTTTATC ATCTTTGGCA CCATGGAAGA AATGCAGAAC 720
 AAAGCTGTGG TTTCTTTTGT GTTTTATTTG TGGAGTGCAA TTGAAATTTT CAGGTACTCT 780
 TTCTACATGC TGACGTGCAT TGACATGGAT TGGAAAGTGC TCACATGGCT TCGTTACACT 840
 CTGTGGATT CTTTATATCC ACTGGGATGT TTGGCGGAAG CTGTCTCAGT GATTCACTCC 900
 ATTTCAATAT TCAATGAGAC CGGACGATTC AGTTTCACAT TGCCATATCC AGTGAAATC 960
 AAAGTTAGAT TTTCTTTTTC TCTTCAGATT TATCTTATAA TGATATTTTT AGGTTTATAC 1020
 ATAAATTTTC GTCACTTTTA TAAACAGCGC AGACTGAAAA TGAGGCGCAG CGCAGTGGCT 1080
 CATGCCTGTG ATCCACGCGC TTTGGGAGGC TGA

Seq ID NO: 373 Protein sequence
Protein Accession #: CAB69070

1 11 21 31 41 51
 MENQVLTPHV YWAQRHRELY LRVELSDVQN PAISITENVL HFKAQGHGAK GDNVYEFHLE 60
 FLDLVKPEPV YKLTQRQVNI TVQKKVSQWW ERLTKQEKRP LFLAPDFDRW LDESDAEMEL 120
 RAKEBERLNK LRLESBGSPE TLTNLRKGYL FMYNLVQFLG FSWIFVNLTV RFCILGKESF 180

YDTFHTVADM MYPCQMLAVV ETINAAIGVT TSPVLPBLSIQ LLGRNFILFI IPGTMEEQN 240
 KAVVFFVFFYL WSAIEIFRYS FYMLTCIDMD WKVLTWLRYS LWIPLYPLGC LAEAVSVIQS 300
 IPIFNETGRF SFTLPYPVKI KVRFSFPLQI YLIMIFLGLY INFRHLYKQR RLKMRAGAVA 360
 HACDPSALGG

Seq ID NO: 374 DNA sequence
 Nucleic Acid Accession #: NM_016395
 Coding sequence: 1-1113

1 11 21 31 41 51
 | | | | |
 ATGGAGAATC AGTGTGTGAC GCCGCATGTC TACTGGGCTC AGCGACACCG CGAGCTATAT 60
 CTGCGCGTGG AGCTGAGTGA CGTACAGAAC CCTGCCATCA GCATCACTGA AAACGTGCTG 120
 CATTTCAAAG CTCAAGGACA TGGTGCCAAA GGAGACAATG TCTATGAATT TCACCTGGAG 180
 TTCTTAGACC TTGTGA AAC AGAGCCTGTT TACAACTGA CCCAGAGGCA GGTAAACATT 240
 ACAGTACAGA AGAAAGTGAG TCAGTGGTGG GAGAGACTCA CAAAGCAGGA AAAGCGACCA 300
 CTGTTTTTGG CTCTGACTT TGATCGTTGG CTGGATGAAT CTGATGCGGA AATGGAGCTC 360
 AGAGCTAAGG AAGAAGAGCG CCTAAATAAA CTCCGACTGG AAAGCGAAGG CTCTCCTGAA 420
 ACTCTTACAA ACTTAAGGAA AGGATACCTG TTTATGTATA ATCTTGTGCA ATTCTTGGGA 480
 TTCTCTCGGA TCTTTGTCAA CCTGACTGTG CGATTCTGTA TCTTGGGAAA AGAGTCTTTT 540
 TATGACACAT TCCATACTGT GGCTGACATG ATGTATTCTT GCCAGATGCT GGCAGTTGTG 600
 GAAACTATCA ATGCAGCAAT TGGAGTCACT ACCTCACCAG TGCTGCCTTC TCTGATCCAG 660
 CTTCTTGGAA GAAATTTTAT TTGTTTTATC ATCTTTGGCA CCATGGAAGA AATGCAGAAC 720
 AAAGCTGTGG TTTTCTTTGT GTTTTATTTG TGGAGTGCAA TTGAAATTTT CAGGTACTCT 780
 TTCTCATGTC TGACGTGCAT TGACATGGAT TGGAAAGTGC TCACATGGCT TCGTTAAGT 840
 CTGTGGATTC CCTTATATCC ACTGGGATGT TTGGCGGAAG CTGTCTCAGT GATTCACTCC 900
 ATTCCAATAT TCAATGAGAC CGGACGATTC AGTTTCACAT TGCCATATCC AGTGAAATC 960
 AAAAGTTAGT TTTCTCTTTT TCTTCAGATT TATCTTATAA TGATATTTT AGGTTTATAC 1020
 ATAAATTTTC GTACCTTTA TAAACAGCGC AGACTGAAAA TGAGGCGCAG CGCAGTGGCT 1080
 CATGCCGTG ATCCAGCGC TTTGGGAGC TGA

Seq ID NO: 375 Protein sequence
 Protein Accession #: NP_057479

1 11 21 31 41 51
 | | | | |
 MENQVLTPHV YWAQRHRELY LRVELSDVQN PAISITENVL HFKAQGHGAK GDNVYEFHLE 60
 FLDLVKPEPV YKLTQRQVNI TVQKKVSQW ERLTKQEKRP LPLAPDFDRN LDESDAEMEL 120
 RAKEERLNK LRLESRSPE TLNLRKGYL FMYNLVQFLG FSWIFVNLTV RFCILGKESF 180
 YDTFHTVADM MYPCQMLAVV ETINAAIGVT TSPVLPBLSIQ LLGRNFILFI IPGTMEEQN 240
 KAVVFFVFFYL WSAIEIFRYS FYMLTCIDMD WKVLTWLRYS LWIPLYPLGC LVEAVSVIQS 300
 IPIFNETGRF SFTLPYPVKI KVRFSFPLQI YLIMIFLGLY INFRHLYKQR RRRYKGRKR 360
 STKKKDLDF LPV

Seq ID NO: 376 DNA sequence
 Nucleic Acid Accession #: NM_005987
 Coding sequence: 1-270

1 11 21 31 41 51
 | | | | |
 ATGAATTCCTC AGCAGCAGAA GCAGCCTTGC ACCCCACCCC CTCAGCCTCA GCAGCAGCAG 60
 GTGAAACAAC CTTGCCAGCC TCCACCCGAG GAACCATGCA TCCCCAAAC CAAGGAGCCC 120
 TGCCAAACCA AGGTGCTCTGA GCCCTGCCAC CCCAAAGTGC CTGAGCCCTG CCAGCCCAAG 180
 ATTCCAGAGC CCGGCCAGCC CAAGGTGCCT GAGCCCTGCC CTTCAACGGT CACTCCAGCA 240
 CCAGCCCAAGC AGAAGACCAA GCAGAAGTAA

Seq ID NO: 377 Protein sequence
 Protein Accession #: NP_005978

1 11 21 31 41 51
 | | | | |
 MNSQQQKQPC TPPPQPQQQ VKQPCQPPQ EPCIPKTKEP CQPKVPEPCH PKVPBPCQPK 60
 IPEPCQPKVP EPCPSTVTPA PAQQTQKQK

Seq ID NO: 378 DNA sequence
 Nucleic Acid Accession #: NM_002105
 Coding sequence: 74-505

1 11 21 31 41 51
 | | | | |
 ACAGCAGTTA CACTGCGGCG GCGCTCTGTT CTAGTGTGTT AGCCGTCGTG CTTACCCGGT 60
 CTACCTCGCT AGCATGTCGG GCGCGGCGCA GACTGGCGGC AAGGCCGCGG CCAAGGCCAA 120
 GTCGCGCTCG TCGCGCGCGG GCCTCCAGTT CCCAGTGGGC CGGTATACAC GGCTGCTCGG 180
 GAAGGGCCAC TACCGCGAGC GCGTTGGCGC CGGCGCGCCA GTGTACCTGG CGGCAGTGCT 240
 GGAGTACCTC ACCGCTGAGA TCTTGGAGCT GCGCGGCAAT GCGGCCGCGG ACAACAAGAA 300
 GACGCGAATC ATCCCCGCC ACCTGCAGCT GGCCATCCGC AACGACGAGG AGCTCAACAA 360
 GCTGCTGGGC GCGGTGACGA TCGCCAGGG AGGCGTCTGT CCAACATCC AGGCGTGCT 420
 GCTGCCAAG AAGACCAGCG CCACCTGGG GCCGAAGGCG CCCTCGGGCG GCAAGAAGGC 480
 CACCCAGGCC TCCAGGAGT ACTAAGAGGG CCCGCGCGCG GCGCGGCGCG CCCAGCTCCC 540
 CATGCCACCA CAAAGGCCCT TTTAAGGGCC ACCACCGCC TCAATGGAAG AGCTGAGCGC 600
 CTTCAAGCTG CGGGGCAAGC GGGCGCGGCG TCCCTTCCCC TCCCTCCCC TCGCCCGGCT 660
 TCGCCGCGCG GCCTCGAGTC CCGCCCGGCC CCGCTCCCG TCCCGCACCG CCGTCCCGGT 720
 CGGCTCGGG CCGCTCGGT CCGCCGCTCG CCCTCCGTA GGGTTCGGGC CTTCCGGATG 780
 CGGCTTGGGC GCTCTCGGG GACCTCCGTG GCGCGGAAGA CCCGAGCCTG CCGGGGGGAG 840

GCCGGCGGGC CGCACCTGCG CCGCCTCGGC GTTCGTGACT CAGCCGCCCC ATCCCAGAGTC 900
 GCTAAGGGGC TGGCGGGGAGG COGCAGCACC TTCTGGAAGA CTGGCCCTTC CGCTCTGACG 960
 CAGGGCCGAG GTGGGCGAGTC CAGGCCGAGA GCCGGCGGCC CTGAAGGTGA GTGAGGCCCT 1020
 CGGCAGCTGC AGCCGGGGTG TCTGGTACCC CCCCGGCGTG GTGCTTAGCC CAGGACTTTC 1080
 AGACGCGCGC TGGCGGGGAG GCTTTGGTGG GAGAGACGCG ATCGCGGATT TCGGTCTGGC 1140
 GCCCCTTCTG CGGCCGGGAC CCAGGCCTTT CACATCAGCT CTCCTCCATC CTTTCATTCAT 1200
 AGGTCTGCGC TGGGGCCGGG ACGAAGCACT TGGTAACAGG CACATCTTCC TCCGAGTGA 1260
 CTGCTCTCTA GGAGGACATT TAGGGGAGGG CAGAGGCCTG CAGTTTGGCT TCACGGCTGG 1320
 CTATGTGGAC AGCAAGAGTC GTTTTGGCGA ACGCGACTGG CAGCCAGGCC TGTCGGGCCC 1380
 CCGACGCCGC CCAATTTCCT TTCCAGCAA CTCAACTCGG CAATCCAAGC ACCTAGATAC 1440
 CAGCAACAAGT CGGTAAATCC CTGTCTGGAC TGAGCCTCGG TTGGCTTCTG AACTGGAATT 1500
 CTGCAGCTAA CCCTTCCACG ACTAGAACCT TAGGCATTGG GGAGTTTATG ATGACTAAT 1560
 TTTATTAAAG GATTGTTTTT TTTT

Seq ID NO: 379 Protein sequence
Protein Accession #: NP_002096

1 11 21 31 41 51
 | | | | |
 MSGRGKTGGK ARAKAKSRSS RAGLQFPVGR VHRLLRKGHY AERVGAGAPV YLAADVLEYLT 60
 AEILELAGNA ARDNKKTII PRHLQLAIRN DEELNKLGG VTIAGGGVLP NIQAVLLPRK 120
 TSATVGPAPK SGGKKATQAS QEY

Seq ID NO: 380 DNA sequence
Nucleic Acid Accession #: AL136942
Coding sequence: 184-864

1 11 21 31 41 51
 | | | | |
 ACGCGTCCGG CAGAAGCTCG GAGCTCTCGG GGTATCGAGG AGGCAGGCCG CGCGGGCGCAC 60
 GGGCGAGCGG GCCCGGAGCC GGAGCGCGCG AGGAGCCGCG AGCAGCGCGG CGGCGGGCTC 120
 CAGGCGAGGC GGTGACGCTC CCTGAAAAC TGCAGCGCGG CTGCGCCAC TGCGCCCGGA 180
 GCGATGAAGA TGGTGGCGCC CTGGACGCGG TTCTACTCCA ACAGCTGCTG CTTGTGCTGC 240
 CATGTCGCGA CCGGCACCAT CCTGCTCGCG GTCTGCTATC TGATCATCAA TGCTGTGGTA 300
 CTGTTGATTT TATTGAGTGC CTTGGCTGAT CGGGACTAGT ATAACCTTTC AAGTTCTGAA 360
 CTGGGAGGTG ACTTTGAGTT CATGGATGAT GCCAACATGT GCATTGCCAT TGGGATTCT 420
 CTCTCATGA TCCTGATATG TGCTATGGCT ACTTACGGAG CGTACAAGCA ACGCGCAGCC 480
 TGGATCATCC CATTCTCTCG TTACCAGATC TTTGACTTTG CCCTGAACAT GTTGGTTGCA 540
 ATCACTGTGC TTATTATCC AAATCCATT CAGGAATACA TACGGCAACT GCCTCCTAAT 600
 TTTCCCTACA GAGATGATGT CATGTCACTG AATCCTACCT GTTTGGTCCT TATTATTCTT 660
 CTGTTTATTA GCATTATCTT GACTTTTAA GGTACTTGA TTAGCTGTGT TTGGAAGTGC 720
 TACCGATACA TCAATGGTAG GAATCCTCT GATGTCTCGG TTTATGTTAC CAGCAATGAC 780
 ACTACGGTGC TGCTACCCCG GTATGATGAT GCCACTGTGA ATGGTCTGTC CAAGGAGCCA 840
 CCGCCACCTT ACGTGTCTGC CTAAGCCTTC AAGTGGCGCG AGCTGAGGGC AGCAGCTTGA 900
 CTTTGCAGAC ATCTGAGCAA TAGTTCTGTT ATTCTACTTT TGCCATGAGC CTCTCTGAGC 960
 TTGTTTGTG CTGAATGCT ACTTTTAAA ATTATAGATG TAGATTGAAA ACTGTAGTTT 1020
 TCAACATATG CTTTGTCTGA ACATGTGAT AGATTAAGT TAGAATTCCT CTTGTACGAT 1080
 TGGGGATATA ACGGGCTTCA CTAACCTTCC CTAGGCATTG AAATTTCCCT CAAATCTGAT 1140
 GGACCTAGAA GTCTGCTTTT GTACCTGCTG GGGCCCAAAG TTGGGCATTT TTCTCTCTGT 1200
 TCCCTCTCTT TTGAAAATGT AAAATAAAAC CAAAAATAGA CAATTTTTC TTGAGCCATT 1260
 CCAGCATAGA GAACAAAACC TTATGGAAAC AGGAATGTCA ATTGTGTAAT CATGTGTCTA 1320
 ATTAGGTAAA TAGAAGTCTT TATGTATGTG TTACAAGAAT TTCCCCCA ACATCCTTTA 1380
 TGAATGAAGT TCAATGACAG TTTGTGTTTG GTGGTAAAGG ATTTTCTCCA TGGCCTGAAT 1440
 TAAGACCAT AGAAAGCACC AGGCGGTGGG AGCAGTGACC ATCTACTGAC TGTCTCTGTG 1500
 GATCTGTGT CAGGGACAT GGGGTGACAT GCCTCGTATG TGTTAGAGGG TGGAAATGGAT 1560
 GTGTTTGGCG CTGCAATGGG TCTGGTCCCC CTCTCTCCTT GGATTTCATC CCCCACCCAG 1620
 GGGCCGCTGT CTTCTAGTGT TCTGCCCTAG ATTGGTTCAA GGAGGTCATC CAATGACTTT 1680
 TATCAAGTGG AATTGGGATA TATTGATAT ACTTCTGCTT AACACATGG AAAAGGGTTT 1740
 TCTTTTCCCT GCAAGCTACA TCCTACTGCT TTGAACCTCC AAGTATGTCT AGTACAGTTT 1800
 TAAATGTAA ACATTTTCAG AAAAATGAGG ATTGCCCTCC TTGTATGCGC TTTTACCTT 1860
 GACTACCTGA ATTGCAAGGG ATTTTATAT ATTATATAT TACAAAGTCA GCAACTCTCC 1920
 TGTGTGTTCA TTATTGAATG TGCTGTAAAT TAAGTCGTTT GCAATTAATA CAAGGTTTGC 1980
 CCACATCCAA AAAAAAAAAA AAAAA

Seq ID NO: 381 Protein sequence
Protein Accession #: CAB66876

1 11 21 31 41 51
 | | | | |
 MKMVPWTRF YNSNCLCCH VRTGTLILGV WYLIINAVVL LILLSALADP DQYNFSSSEL 60
 GGDFFEMDDA NMCIAIAISL LMILICAMAT YGAYKQRAAW IIPFFCYQIF DPAIINMLVAI 120
 TVLIYPNSIQ EYIRQLPPNF PYRDDVMSVN PTCVLVLIIL FISIIITFKG YLISCVWNCY 180
 RYINGRNSSD VLIVVYSNDT TVLLEPPYDDA TVNGAAKEPP PPYVSA

Seq ID NO: 382 DNA sequence
Nucleic Acid Accession #: NM_002510
Coding sequence: 92-1774

1 11 21 31 41 51
 | | | | |
 CAGATGCCAG AAGAACTCTG TTGCTCTTGG TGGACGGGCC CAGAGGAATT CAGAGTTAAA 60
 CCTTGAGTGC CTGCGTCCGT GAGAAATCAG CATGGAATGT CTCTACTATT TCCTGGGATT 120
 TCTGCTCTG CTGCAAGAT TTGCCACTGA TGCCGCCAAA CGATTTCATG ATGTGCTGGG 180
 CAATGAAAGA CCTTCTGCTT ACATGAGGGA GCACAATCAA TTAATGGCT GGTCTTCTGA 240
 TGAATATGAC TGAATGAAA AACTCTACCC AGTGTGGAAG CCGGGAGACA TGAGGTGGAA 300
 AAATCTCTGG AAGGGAGGCC GTGTGCAGGC GGTCTGTACC AGTGACTCAC CAGCCCTCGT 360

	GGGCTCAAA	ATAACATTG	CGGTGAACCT	GATATTCCCT	AGATGCCAAA	AGGAAGATGC	420
	CAATGGCAAC	ATAGTCTATG	AGAAGAAGCTG	CAGAAATGAG	GCTGGTTTAT	CTGCTGATCC	480
	ATATGTTTAC	AACCTGGACAG	CATGGTCAGA	GGACAGTGAC	GGGGAAAAATG	GCACCGGCCA	540
5	AAGCCATCAT	AACGCTCTCC	CTGATGGGAA	ACCTTTCTCT	CACCAACCCG	GATGGAGAAG	600
	ATGGAATTTC	ATCTACGCTC	TCCACACACT	TGGTCAGTAT	TTCCAGAAAT	TGGGACGATG	660
	TTCACTGAGA	GTTTCTGTGA	ACACAGCCAA	TGTGACACTT	GGGCTCAAC	TCATGGAAGT	720
	GACTGTCTAC	AGAAGACATG	GACGGGCATA	TGTTCCCATC	GCACAAGTGA	AAGATGTGTA	780
	CGTGGTAACA	GATCAGATTTC	CTGTGTTTGT	GACTATGTTC	CAGAGAAGCG	ATCGAAATTC	840
10	ATCCGACGAA	ACCTTCCTCA	AAGATCTCCC	CATTATGTTT	GATGTCCTGA	TTCATGATCC	900
	TAGCCACTTC	CTCAATTATT	CTACCATTA	CTACAAGTGG	AGCTTCGGGG	ATAATACTGG	960
	CCTGTTTGT	TCCACCAATC	ATACTGTGAA	TCACACGTAT	GTGCTCAATG	GAACCTTCAG	1020
	CCTTAACCTC	ACTGTGAAAG	CTGCAGCACC	AGGACCTTGT	CGCCACCCG	CACCAACCAC	1080
	CAGACCTTCA	AAACCCACCC	CTTCTTTAGG	ACCTGCTGGT	GACAAACCCC	TGGAGCTGAG	1140
	TAGGATTCTC	GATGAAAACT	GCCAGATTAA	CAGATATGGC	CACITTCAG	CCACCATCAC	1200
15	AATTGTAGAG	GGAACTCTAG	AGGTTAATAT	CATCCAGATG	ACAGACGTCC	TGATGCCGGT	1260
	GCCATGGCCT	GAAAGCTCCC	TAATAGACTT	TGTCGTGACC	TGCCAAGGGA	GCATTCCCAC	1320
	GGAGGTCTGT	ACCATCATTT	CTGACCCAC	CTGCGATATC	ACCCAGAAC	CAGTCTGCAG	1380
	CCCTGTGGAT	GTGGATGAGA	TGTGCTGCT	GACTGTGAGA	CGAACCTTCA	ATGGGTCTGG	1440
20	GAGTACTGT	GTGAACCTCA	CCCTGGGGGA	TGACACAAGC	CTGGCTCTCA	CGAGCACCCCT	1500
	GATTTCTGTT	CCTGACAGAG	ACCCAGCCTC	GCCTTTAAGG	ATGGCAAAAC	GTGCCCCGAT	1560
	CTCGTTGGC	TGCTTTGGCA	TATTTGTCAC	TGTGATCTCC	CTCTTGGTGT	ACAAAAAACA	1620
	CAAGGAATAC	AACCCAATAG	AAAATAGTCC	TGGGAATGTG	GTGAGAAGCA	AAGGCTGTAG	1680
	TGCTTTTCTC	AACCGTGCAA	AAGCCGTGTT	CTTCCCGGGA	AACCAAGAAA	AGGATCCGCT	1740
25	ACTCAAAAAC	CAGAATAATT	AAGGAGTTTC	TTAAATTTTC	ACCTTGTTC	TGAAGCTCAC	1800
	TTTTCACTGT	CATTGATGTG	AGATGTGCTG	GAGTGGCTAT	TAACCTTTTT	TTCTTAAAGA	1860
	TTATTGTTAA	GATGATGATT	TGGTTTGGGG	AAGTTGAATT	TTTTATAGGT	TAAATGTCT	1920
	TTTAGAGATG	GGGAGAGGGA	TTATACTGCA	GGCAGCTTCA	GCCATGTTGT	GAAACTGATA	1980
	AAAGCAACTT	AGCAAGGCTT	CTTTTCATTA	TTTTTTATGT	TTCACTTATA	AAGTCTTAGG	2040
30	TAACTAGTAG	CATGAAACAA	CTGTGTCCCG	AGAGTAAGGA	GAGAAGCTAC	TATGTATTAG	2100
	AGCCTAACCC	AGGTTAACTG	CAAGAAGAGG	CGGGATACTT	TCAGCTTTCC	ATGTAACCTG	2160
	ATGCATAAAG	CAAGTGTATG	CCAGTTTCTA	AGATCATGTT	CCAAGCTAAC	TGAATCCCAC	2220
	TTCAATACAC	ACTCATGAAC	TCCTGATGGA	ACAATAACAG	GCCCAAGCCT	GTGATATGAT	2280
	GTGCACACTT	GCTAGACTCA	GAATAAATAC	TACTCTCATA	AATGGGTGGG	AGTATTTTGG	2340
35	TGACAACTTA	CTTTGCTTGG	CTGAGTGAAG	GAATGATATT	CATATATTCA	TTTATTCCAT	2400
	GGACATTTAG	TTAGTGCTTT	TTATATACCA	GGCATGATGC	TGAGTGACAC	TCTTGTGAT	2460
	ATTTCCAAAT	TTTTGTATAG	TGCTGCACAC	TATTTGAAAT	CATATATTAA	GACTTTCCAA	2520
	AGATGAGGTC	CCTGTTTTTT	CATGGCAACT	TGATCAGTAA	GGATTTCACC	TCTGTTTGTA	2580
	ACTAAACCA	TCTACTATAT	GTTAGACATG	ACATTCTTTT	TCTCTCCTTC	CTGAAAAATA	2640
40	AAGTGTGGGA	AGAGACAAAA	AAAAAATAA				

Seq ID NO: 383 Protein sequence
Protein Accession #: NP_002501

	1	11	21	31	41	51	
45	MECLYYFLGF	LLLAARLPLD	AAKRFHDVLG	NERPSAYMRE	HNQLNGWSSD	ENDWNEKLYP	60
	VWKRGMNRWK	NSWKGGRVQA	VLTSDSPALV	GSNITFAVNL	IPPRCQKEDA	NGNIVYEKNC	120
	RNEAGLSADP	YVYNWTANSE	DSGDENGTGO	SHHNVPDGGK	PPPHHPGWR	WNFIYVFHTL	180
50	GQYFQKLGR	SVRVSVNTAN	VTLGPQLMEV	TVYRRHGRAY	VPLAQKVDVY	VVTDQIPVTV	240
	TMFQKNDNR	SDTEFLKDLF	IMFDVLHDP	SHFLNYSTIN	YKWSFGDNTG	LFVSTNHTVN	300
	HTYVLNGTFS	LNLITVKAAP	GPCPPPPPPP	RPSKPTPSLG	PAGDNPLELS	RIPDENQVIN	360
	RYGHFQATIT	IVEGLELVNI	IQMTDVLMPV	PWPESSLIID	VVTCQGSIPT	EVCTIISDPT	420
	CEITQNTVCS	PVDVDEMCLL	TVRRTFNGSG	TYCVNLTLGD	DTSLALTSTL	ISVDFRDPAS	480
55	PLRMANSALI	SVGCLAIFVT	VISLLVYKXH	KEYNPIENSP	GNVVRSGKLS	VPLNRKAVF	540
	FPGNQEKDPL	LKNQEFKGV					

Seq ID NO: 384 DNA sequence
Nucleic Acid Accession #: NM_001134
Coding sequence: 48-1877

	1	11	21	31	41	51	
60	TCCATATTGT	GCTTCCACCA	CTGCCAATAA	CAAAATAACT	AGCAACCATG	AAGTGGGTGG	60
	AATCAATTTT	TTTAATTTTC	CTACTAAATT	TTACTGAATC	CAGAACACTG	CATAGAAATG	120
65	AATATGGAAT	AGCTTCCATA	TTGGATTCTT	ACCAATGTAC	TGCAGAGATA	AGTTTAGCTG	180
	ACCTGGCTAC	CATATTTTTT	GCCAGTTTGG	TTCAAGAAAGC	CACITTCAG	GAAGTAAGCA	240
	AAATGTGTA	AGATGCAATG	ACTGCAATTG	AGAAACCCAC	TGGAGATGAA	CAGTCTTCAG	300
	GGTGTTTAGA	AAACGAGCTA	CCTGCCTTTC	TGGAAGAACT	TTGCCATGAG	AAAGAAATTT	360
70	TGGAGAAAGTA	CGGACATTCA	GACTGCTGCA	GCCAAAGTGA	AGAGGGAAGA	CATAACTGTT	420
	TTCTTGACCA	CAAAAAGCCC	ACTCCAGCAT	CGATCCCACT	TTTCCAAGTT	CCAGAACCTG	480
	TCACAAGCTG	TGAAGCATAT	GAAGAAGACA	GGGAGACATT	CATGAACAAA	TTCAATTTATG	540
	AGATAGCAAG	AAGGCATCCC	TTCTGTATG	CACCTACAAT	TCTTCTTTGG	GCTGCTCGCT	600
	ATGACAAAAT	AATTCCATCT	TGCTGCAAG	CTGAAATATG	AGTTGAATGC	TTCCAAACAA	660
75	AGGCAGCAAC	AGATTACAAA	GAATTAAGAG	AAAGCAGCTT	GTTAAATCAA	CATGCAATGTG	720
	CAGTAATGAA	AAATTTTGGG	ACCGAACTT	TCCAAGCCAT	AACTGTTACT	AAACTGAGTC	780
	AGAAAGTTTAC	CAAAGTTAAT	TTTACTGAAA	TCCAGAAACT	AGTCTGTGAT	GTGGCCCATG	840
	TACATGAGCA	CTGTTGCGAG	GGAGATGTGC	TGGATTGTCT	GCAGGATGGG	GAAAAAATCA	900
	TGTCCTACAT	ATGTTCTCAA	CAAGACACTC	GTCAACACAA	AATAACAGAA	TGCTGCAAAC	960
80	TGACCAAGCT	GGAAAGCTGT	CAATGTATAA	TTTATGCAGA	AAATGATGAA	AAACCTGAAG	1020
	GTCTATCTCC	AAATCTAAAC	AGGTTTTTAG	GAGATAGAGA	TTTTAACCAA	TTTTCTTCAG	1080
	GGGAAAAAAA	TATCTTCTTG	GCAAGTTTTG	TTTATGAAAT	TTCAAGAGAA	CATCCTCAGC	1140
	TTGCTGTCTC	AGTAATTTCTA	AGAGTTGCTA	AAGGATACCA	GGAGTTATTG	GAGAAGTGTT	1200
	TTCCAGACTGA	AAACCTCTT	GAATGCCAAG	ATAAAGGAGA	AGAAGAATTA	CAGAAATACA	1260
85	TCCAGGAGAG	CCAAGCATTTG	GCAAGGCGAA	GCTGCGGCTT	CTTCCAGAAA	CTAGGAGAAAT	1320
	ATTACTTACA	AAATCGGTTT	CTCGTTGCTT	ACACAAGGAA	AGCCCCCAG	CTGACCTCGT	1380
	CGGAGCTGAT	GGCCATCACC	AGAAAAATGG	CAGCCACAGC	AGCCACTTGT	TGCCAACTCA	1440
	GTGAGGACAA	ACTATTGGCC	TGTGGCGAGG	GAGCGGCTGA	CATTATTATC	GGACACTTAT	1500

GTATCAGACA TGAAATGACT CCAAGTAAACC CTGGTGTGG CCAGTGCTGC ACTTCTTCAT 1560
 ATGCCAACAG GAGGCCATGC TTCAGCAGCT TGGTGGTGA TGAACATAT GTCCCTCTCG 1620
 CATTCTCTGA TGACAAGTTC ATTTTCCATA AGGATCTGTG CCAAGCTCAG GGTGTAGCGC 1680
 TGAAAACGAT GAAGCAAGAG TTTTTCATTA ACCTTGTGAA GCAAAAGCCA CAAATAACAG 1740
 AGGAACAAC TGAAGCTGTC ATTGCAGATT TCTCAGGCCT GTTGGAGAAA TGCTGCCAAG 1800
 GCCAGGAACA GGAAGTCTGC TTTGCTGAAG AGGGACAAAA ACTGATTTC AAAACTCGTG 1860
 CTGCTTTGGG AGTTTAAATT ACTTCAGGGG AAGAGAAGAC AAAACGAGTC TTTCATTGCG 1920
 TGTGAACCTT TCTCTTAAAT TTTAACTGAT TTAACACTTT TTGTGAATTA ATGAATGAT 1980
 AAAGACTTTT ATGTGAGATT TCCTATCAC AGAAATAAAA TATCTCCAAA TG

Seq ID NO: 385 Protein sequence
 Protein Accession #: NP_001125

1 11 21 31 41 51
 MKWVESIFLI FLLNFESRT LHRNEYGIAS ILDSYQCTAE ISLADLATIF FAQFVQEATY 60
 KEVSKMVKDA LTAIEKPTGD EQSSGCLENO LPAPLEELCH EKEILEKYGH SDCCSQSEEG 120
 RHNCFLAHKK PTPASIFLFG VPEPVTSCEA YEEDRETFMN KFIYBIARRH PPLYAPTILL 180
 WAARYDKIIP SCCKAENAVE CFQTKAATVT KELRESSLLN QHACAVMKNF GTRTFQAITV 240
 TKLSQKFTKV NFTEIQKLVL DVAHVHEHCC RODVLDCLQD GEKIMSYICS QQDTLSNKIT 300
 ECCKLTTLER GQCIHAEND EKEPGLSPNL NRFLGDRDFN QFSSGEKNIF LASFVHEYSR 360
 RHPQLAVSVI LRVAQGYQEL LEKCFQTENP LECQDKGEE LQYIQESQA LAKRSCGLFQ 420
 KLGEYLLQNA FLVAYTKKAP QLTSSSELMAI TRKMAATAAT CQQLSEDKLL ACGEAADI 480
 IGHLCIRHEM TPNVPGVGQC CTSYANRRP CFSLLVDET YVPPAFSDDK FIFHKDLCA 540
 QGVALQTMKQ EPLINLVKQK POITEEQLEA VIADFSGLLE KCCQGGQEV CFABEGQKLI 600
 SKTRALGV

Seq ID NO: 386 DNA sequence
 Nucleic Acid Accession #: NM_002205.1
 Coding sequence: 1..3149

1 11 21 31 41 51
 ATGGGGAGCC GGACGCCAGA GTCCCCCTCTC CACGCCGTGC AGCTGCGCTG GGGCCCCCGG 60
 CGCCGACCCC CGCTSSBTGCC GCTGCTGTGTG CTGCTSSBTGC CGCCGCCACC CAGGGTCGGG 120
 GGCTTCAACT TAGACGCGGA GCGCCACGCA GTACTCTCGG GCGCCCGCGG CTCCTTCTTC 180
 GGATTCTCAG TGGAGTTTAA CCGCCCGGGA ACAGACGGGG TCAGTGTGCT GGTGGGAGCA 240
 CCCAAGGCTA ATACCAAGCA GCCAGAGTGT CTGCAGGGTG GTGCTGTCTA CCTCTGTCTC 300
 TGGGGTGCCA GCCCCACACA GTGCACCCCC ATTGAATTGG ACAGCAAAGG CTCTCGGCTC 360
 CTGGAGTCTT CACTGTCCAG CTCAGAGGGA GAGGAGCCGT TGGAGTACAA GTCTTGCAG 420
 TGGTTCGGGG CACACAGTTG AGCCCATGGC TCCTCCATCT TGGCATGCGC TCCACTGTAC 480
 AGCTGGCCCA CACAGAAGGA GCCACTGAGC GACCCCGTGG GCACCTGCTA CCTCTCCACA 540
 GATAACTTCA CCGCAATTCT GGAGTATGCA CCCTGCCGCT CAGATTTCAG CTGGGCAGCA 600
 GGACAGGGTT ACTGCCAAGG AGGCTTCAGT GCCGAGTTCA CCAAGACTGG CCGTGTGGTT 660
 TTAGTGGGAC CAGGAAGCTA TTTCTGGCAA GGCCAGATCC TGCTGTCCAC TCAGGAGCAG 720
 ATTGCAGAA TCTATTACCC CAGTATCCCT ATCAACCTGG TTCAAGGGGA GCTGCAGACT 780
 CGCCAGGCGA GTTCCATCTA TGATGACAGC TACCTAGGAT ACTCTGTGGC TGTGGTGAA 840
 TTCAGTGGTG ATGACACAGA AGACTTTGTT GCTGGTGTGC CCAAGGGGAA CCTCACTTAC 900
 GGCTATGTCA CCATCTTAA TGGCTCAGAC ATTCGATCCC TCTACAACCT CTCAGGGGAA 960
 CAGATGGGCT CCTACTTTGG CTATGCAGTG GCCGCCACAG ACCTCAATGG GGACGGGGAG 1020
 GATGACTTGC TGTGTTGGGG ACCCTGCTCT ATGGATCGGA CCCCTGACGG GCGGCTCTAG 1080
 GAGGTGGGCA GGGTCTACGT CTACCTGCAG CACCAGCCCG GCATAGAGCC CACGCCCAACC 1140
 CTTACCTTCA CTGGCCATGA TGAGTTTGGC GCTCCTTGAC CCCCTGGGG 1200
 GACCTGGACC AGGATGGCTA CAATGATGTG GCCATCGGGG CTCCCTTTGG TGGGGAGACC 1260
 CAGCAGGGAG TAGTGTGTGT ATTTCTTGGG GGCCAGGAG GGCTGGGGCT TAAGCCTTCC 1320
 CAGGTTCGCG AGCCCTGTGT GCGAGCCAGC CACACCCAG ACTTCTTTGG CTCTGCCCTT 1380
 CGAGGAGGCC GAGACCTGGA TGGCAATGGA TATCCTGATC TGATTGTGGG GTCCCTTGGT 1440
 GTGGAACAAG CTGTGGTATA CAGGGGCCGC CCCATCGTGT CCGCTAGTGC CTCCTCACC 1500
 ATCTTCCCCG CCATGTTCAA CCCAGAGGAG CGGAGCTGCA GCTTAGAGGG GAACCTGTG 1560
 GCCTGCATCA ACCTTAGCTT CTGCCCTCAAT GCTTCTGGAA AACACGTTGC TGACTCCATT 1620
 GGTTCACAG TGAACCTTCA GCTGGACTGG CAGAAGCAGA AGGGAGGGGT ACGGCGGGCA 1680
 CTGTCTCTGG CCTCCAGGCA GGCAACCCCTG ACCCAGACCC TGCTCATCCA GAATGGGGCT 1740
 CGAGAGGATT GCAGAGAGAT AGAGATCTAC CTCAGGAACG AGTCAGAATT TCGAGACAAA 1800
 CTCTCGCCGA TTCACATCGC TCTCAACTTC TCCTTGGACC CCAAGCCCC AGTGGACAGC 1860
 CACGGCTTCA GGCAGCCCT ACATTATCAG AGCAAGAGCC GGATAGAGGA CAAGGCTCAG 1920
 ATCTTGTCTG ACTGTGGAGA AGACAACATC TGTGTGCTG ACCTGCAGCT GGAAGTGT 1980
 GGGGAGCAGA ACCATGTGTA CCTGGGTGAC AAGAATGCC TGAACCTCAC TTTCCATGCC 2040
 CAGAATGTGG GTGAGGGTGG CGCCTATGAG GCTGAGCTTC GGGTCACCGC CCCTCCAGAG 2100
 GCTGAGTACT CAGGACTCGT CAGACACCCA GGGAACTTCT CCAGCCTGAG CTGTGACTAC 2160
 TTTGCCGTGA ACCAGAGCCG CCGCTGGTGT TGTGACCTGG GCAACCCCAT GAAGGCAGGA 2220
 GCCAGTCTGT GGGGTGGCCT TCGGTTTACA GTCCCTCATC TCGGGACAC TAAGAAAACC 2280
 ATCCAGTTTG ACTTCCAGAT CCTCAGCAAG AATCTCAACA ACTCGCAAG CGACGTGGTT 2340
 TCCTTTCCGC TCTCCGTGGA GGCTCAGGCC CAGGTCAACC TGAACGGTGT CTCCAAGCCT 2400
 GAGGCAGTGC TATTCCAGT AAGCGACTGG CATCCCCGAG ACCAGCTCA GAAGGAGGAG 2460
 GACCTGGGAC TCTCTGTCCA CCATGTCTAT GAGCTCATCA ACCAAGGCCC CAGCTCCATT 2520
 AGCCAGGTG TGCTGGAAC TCACTGCACC ACCAATCACC CCATTAAACC AAAGGGCTG 2580
 GTGACCAAG TTACGGGACT CCGTCAACC CAGCAAAAAC GGGAAAGCTC AAGCCGAGC 2640
 GAGTTGGATC CCGGACCTCA GATCCTGAAA TGCCCGGAGG CTGAGTGT 2700
 TCTGCTCTCT CCGGACCTCA GATCCTGAAA TGCCCGGAGG CTGAGTGT 2760
 TGTGAGCTCG GCGCCCTGCA CCAACAAGAG AGCCAAAGTC TGCAATGTGA TTTCCGAGTC 2820
 TGGGCCAAGA CTTTCTTGCA GCGGGAGCAC CAGCCATTGA GCCTGCAGTG TGAGGCTGTG 2880
 TACAAAGCCC TGAAGATGCC CTACCGAATC CTGCTCGGC AGCTGCCCCA AAAAGAGCGT 2940
 CAGGTGGGCA ACTGATGTGA ATGGACCAAG GCAGAAGGCA GCTATGGCGT CCCACTGTG 3000
 ATCATCATCC TAGCCATCCT GTTTGGCCTC CTGCTCCTAG GTCTACTCAT CTACATCCTC 3060
 TACAAAGCTTG GATTCTTCAA ACGCTCCCTC CCATATGSCA CCGCCATGGA AAAAGCTCAG 3120
 CTCAAGCCTC CAGCCACCTC TGATGCCTGA

Seq ID NO: 387 Protein sequence
Protein Accession #: NP_002196.1

```

5      1      11      21      31      41      51
      |      |      |      |      |      |
MGSRTPEPPL HAVQLRWGPR RRPPLPLPLL LLLPPPPRVG GFNLDAEAPA VLSGPPPGSFF 60
GFSVEFYRPG TDGVSVLVGA PKANTSQPGV LQGGAVYLCP WGASPTQCTP IEFDSKGSRL 120
LESSLSSEEG EEPVEYKSLQ WFGATVRAHG SSILACAPLY SWRTEKEPLS DPVGTCTYLS 180
10 DNFTRILEYA PCRSDFSWAA GGGYCQGGFS AEFTKTGRVV LGGPGSYFWQ GQILSATQEQ 240
IAESVYPEYL INLVQQLQT RQASSIYDDS YLGYSVAUGE FSGDDTEDFV AGVPKGNLTY 300
GYVTILNGSD IRSLYNFSGE QMASYFGYAV AATDVNGDGL DDLLVGAPLL MDRTPDGRFQ 360
EVGRVYVYLQ HPAGIEPTPT LTLTGHDHFG RFGSSLTPLG DLDQDGYNDV AIGAPFPGET 420
15 QQGVVVFVPG GPGGLGSKPS QVLQPLWAAS HTPDFFGSAL RGRDLDDNG YPDLVGSPG 480
VDKAVVVRGR PIVSASASLT IFPAMFNPEE RSCSLEGNPV ACINLSFCLN ASGKHVADSI 540
GFTVELQLDW QKQKGGVRRR LPLASRQATL TOTLLIONGA REDCREMKIY LRNESEFRDK 600
LSPIHIALNF SLDPQAPVDS HGLRPLAHYQ SKSRIEDKAQ ILLDCGEDNI CVPDLQLEVF 660
GEQNHVYLG D KNALNLTFFA QNVGEGGAYE AELRVTPAPE AEYSGLVVRHP GNFSSLSCDY 720
20 FAVNQSRLLV CDTGNPMKAG ASLWGLRFT VPHLRDTKKT IQDFQILSK NLNNSQSDV 780
SFRLSVEAQA QVTLNGVSKP EAVLFPVSDW HPRDQPKKEE DLGPAVHHVY ELINQGPSSI 840
SQGVLELSCP QALVQQLLY VTRVTGLNCT TNHPINPKGL ELDPEGLSHH QOKREAPSR 900
SASSGPQILK CPEAECEFLR CELGPLHQOE SQSLQLHFRV WAKTFQLREH QPFLQCEAV 960
YKALMPPYRI LPRQLPQKER QVATAVQWTK AEGSYGVPLW IITLAILFGL LLLGLLIYIL 1020
YKLGFFPKRSL PYGTAMEKAQ LKFPATSDA

```

Seq ID NO: 388 DNA sequence
Nucleic Acid Accession #: NM_002425
Coding sequence: 26..1453

```

30      1      11      21      31      41      51
      |      |      |      |      |      |
AAAGAAGGTA AGGGCAGTGA GAATGATGCA TCTTGCAATC CTTGTGCTGT TGTGTCGCC 60
AGTCTGCTCT GCCTATCCTC TGAGTGGGGC AGCAAAAGAG GAGGACTCCA ACAAGGATCT 120
35 TGCCAGACAA TACCTAGAAA AGTACTACAA CCTCGAAAAG GATGTGAAAC AGTTTAGAAG 180
AAAGGACAGT AATCTCATTT TTAATAAAAT CCAAGGAATG CAGAAGTTC TTGGGTGGA 240
GGTGACAGGG AAGCTAGACA CTGACACTCT GGAGGTGATG CGCAAGCCCA GGTGTGGAGT 300
TCCTGACGTT GGTCACTTCA GCTCCTTTCC TGGCATGCCG AAGTGGAGGA AAACCCACCT 360
TACATACAGG ATTGTGAATT ATACACCAGA TTTGCCAAGA GATGCTGTTG ATTCTGCCAT 420
40 TGAGAAAGCT CTGAAAGTCT GGAAGAGAGT GACTCCACTC ACATTCTCCA GGCTGTATGA 480
AGGAGAGGCT GATATAATGA TCTCTTTCG AGTTAAAGAA CATGGAGACT TTTACTCTTT 540
TGATGGCCCA GGCACAGATT TGGCTCATGC CTACCCACCT GGACCTGGGC TTTATGAGA 600
TATTCACTTT GATGATGATG AAAAATGGAC AGAAGATGCA TCAGGCACCA ATTTATTCTT 660
CGTTGCTGCT CATGAACCTG GCCACTCCCT GGGGCTCTTT CACTCAGCCA ACCTGGAAGC 720
45 TTTGATGTAC CCACCTTACA ACTCATTCAC AGAGCTCGCC CAGTTCGCC TTTGCAAGA 780
TGATGTGAAT GGCATTCAGT CTCTCTACGG ACCTCCCTCT GCCTCTACTG AGGAACCCCT 840
GGTGCCCAAT AATCTGTTC TCTCGGATC TGAGATGCCA GCCAAGTGTG ATCCTGCTTT 900
GTCCTTCGAT GCCATCAGCA CTCTGAGGGG AGAATATCTG TTCTTAAAG ACAGATATT 960
50 TTGGCGAAGA TCCCACTGGA ACCCTGAACC TGAATTTTCA TTGATTTCTG CATTTTGGCC 1020
CTCTCTTCCA TCATATTGG ATGCTGCATA TGAAGTTAAC AGCAGGGACA CCGTTTAT 1080
TTTTAAAGGA AATGATTTCT GGGCCATCAG AGGAAATGAG GTACAAGCAG GTTATCCAAG 1140
AGGCATCCAT AACCTGGGTT TTCTTCCAAC CATAAGGAAA ATTGATGCAG CTGTTTCTGA 1200
CAAGGAAAGG AAGAAACAT ACTTCTTTCG AGCGGACAAA TACTGGAGAT TTGATGAAAA 1260
60 TGCCAGTCC ATGGAGCAAG GCTTCCCTAG ACTAATAGCT GATGACTTTC CAGGAGTTGA 1320
GCCTAAGGTT GATGCTGTAT TACAGGCATT TGGATTTTTC TACTTCTTCA GTGGATCATC 1380
ACAGTTTGAG TTTGACCCCA ATGCCAGGAT GGTGACACAC ATATTAAAGA GTAACAGCTG 1440
GTTACATTGC TAGCCGAGAT AGGGGGAAGA CAGATATGGG TGTTTTAAAT AAATCTAATA 1500
ATTATTATC TAATGTATTA TGAGCCAAAA TGGTTAAATT TTCTGCTGAT TTCTGTGACT 1560
GAAGAAGATG AGCCTTGCAG ATATCTGCAT GTGTCTATGA GAATGTTTCT GGAATTTCTT 1620
ACTTGCTTTT GAATTGCACT GAACAGAAAT AAGAAATACT CATGTGCAAT AGGTGAGAGA 1680
70 ATGTATTTTC ATAGATGTGT TATTACTTCC TCAATAAAAA GTTTTATTTT GGGCCTGTTC 1740
CTT

```

Seq ID NO: 389 Protein sequence
Protein Accession #: NP_002416

```

65      1      11      21      31      41      51
      |      |      |      |      |      |
MHLAFLVLLC LPVCSAYPLS GAAKEEDSNK DLAQQYLEKY YNLEKDVQKF RRDNSNLIVK 60
KIQQMQKFLG LEVTGKLDTD TLEVMRKPRC GVPDVGHFSS FPGMPKWRKT HLTIVRINYT 120
70 PDLPRDAVDS AIEKALKVWE EVTPLTFSRL YEGEADIMIS FAVKEHGDY SFDGPHSLA 180
HAYPPGPGLY GDIHFDDEK WTEDASGTNL FLVAHELGH SLGLFHSANT EALMYPLYNS 240
FTELAQFRLS QDDVNGIQSL YGPPPPASTE PLVPTKSVPS GSEMPAKCDP ALSFDAISTL 300
RGEYLFPPDR YFWRSHWNP EPEFHLISAF WPSLPSYLD AYEVSNSRDTV FIFKGNFEMA 360
75 IRGNEVQAGY PRGHTLGLFP PTIRKIDAAV SDKEKKKTYF FAADKYWRFD ENSQSMEQGF 420
PRLIADDFPG VEPKVDVAVLQ AFGFFYFPGS SSQFEFDPNA RMVTHILKSN SWLHC

```

Seq ID NO: 390 DNA sequence
Nucleic Acid Accession #: NM_002421.2
Coding sequence: 1..1409

```

80      1      11      21      31      41      51
      |      |      |      |      |      |
ATGCACAGCT TTCTCCACT GCTGCTGCTG CTGTTCTGGG GTGTGGTGTC ACACAGCTTC 60
CCAGGCAGCTC TAGAAACACA AGAGCAAGAT GTGGACTTAG TCAGAAAATA CCTGGAAAAA 120
85 TACTACAACC TGAAGAATGA TGGGAGGCAA GTTGAAGAGC GGAGAAATAG TGGCCCACTG 180
GTTGAAAAAT TGAAGCAAAAT GCAGGAATTC TTTGGGCTGA AAGTGAAGTG GAAACAGAT 240
GCTGAAACCC TGAAGGTGAT GAAGCAGCCC AGATGTGGAG TGCTGATGT GGCTCAGTTT 300

```

5
10
15
20

GTCTCTCACTG AGGGGAACCC TCGCTGGGAG CAAACACATC TGACCTACAG GATTGAAAA 360
TACACGCCAG ATTTGCCAAG AGCAGATGTG GACCATGCCA TTGAGAAAGC CTTCCAACCTC 420
TGGAGTAATG TCACACCTCT GACATTACAC AAGGTCTCTG AGGGTCAAGC AGACATCATG 480
ATATCTTTTG TCAGGGGAGA TCATCGGGAC AACTCTCCTT TTGATGGACC TGGAGGAAAT 540
CTTGCTCATG CTTTTCACAC AGGCCCAGGT ATTGGAGGGG ATGCTCATTT TGATGAAGAT 600
GAAAGGTGGA CCAACAATT TACAGAGTAC AACTTACATC GTGTTGCGGC TCATGAACTC 660
GGCCATTCTC TTGGACTCTC CCATTCTACT GATATCGGGG CTTTGATGTA CCCTAGCTAC 720
ACCTTCAGTG GTGATGTTCA GCTAGCTCAG GATGACATTG ATGGCATCCA AGCCATATAT 780
GGACGTTCCC AAAATCCTGT CCAGCCATC GGGCCACAAA CCCCAGAAAGC ATGTGACAGT 840
AAGCTAACCT TTGATGCTAT AACTACGATT CGGGGAGAGG TGATGTTCTT TAAAGACAGA 900
TTCTACATGC GCACAAATCC CTTTACCCG GAAGTTGAGC TCAATTTCAT TTCTGTTTTC 960
TGGCCACAAC TGCCAAATGG GCTTGAAGCT GCTTACGAAT TTGCCGACAG AGATGAAGTC 1020
CGGTTTTTCA AAGGGAATAA GTACTGGGCT GTTCAGGGAC AGAATGTGCT ACACGGATAC 1080
CCCAAGGACA TCTACAGCTC CTTTGGCTTC CTTAGAACTG TGAAGCATAT CGATGCTGCT 1140
CTTTCTGAGG AAAACACTGG AAAAACCTAC TTCTTTGTTG CTAACAAATA CTGGAGGTAT 1200
GATGAATATA AAGATCTAT GATCCAGGT TATCCCAAAA TGATAGCACA TGACTTTTCT 1260
GGAATTGGCC ACAAAGTTGA TGCAGTTTTC ATGAAAGATG GATTTTCTTA TTTCTTTCAT 1320
GGAACAAGAC AATACAAATT TGATCCTAAA ACGAAGAGAA TTTTGACTCT CCAGAAAGCT 1380
AATAGCTGGT TCAACTGCAG GAAAAATTAG

Seq ID NO: 391 Protein sequence
Protein Accession #: NP_002412.1

25
30
35

1 11 21 31 41 51
MHSFPPPLLLL LFWGVVSHSF PATLETQEQD VDLVQKYLEK YYNLKNDGRQ VEKRRNSGPV 60
VEKLKQMKEF FGLKVTGKPD AETLKVMKQP RCGVPDVAQF VLTEGNPRWE QTHLTYRIEN 120
YTPDLPRADV DHAIEKAFQL WSNVTPLTFT KVSEGGQADIM ISFVRGDHRD NSPFDGPGSN 180
LAHAFFQPGF IGGDAHFDED ERWNNFREY NLHRVAHAEL GHSGLGLSHST DIGALMYPST 240
TFSGDVQLAQ DDIDIGIAIY GRSQNPVQPI GPQTPKACDS KLTFDAITTI RGEVMFFKDR 300
FYMRNPFYF EVELNPFISV WPQLPNGLEA AYEFAADRDEV RFFKGNKYWA VQGNVNLHGY 360
PKDIYSSFGF PRTVKHIDAA LSEENTGKTY FFFVANKYWRV DEYKRSMDPG YPKMIAHDFP 420
GIGHKVDVAV MKDGFYFFPH GTRQYKFDPK TKRILTLQKA NSWFNCRKN

Seq ID NO: 392 DNA sequence
Nucleic Acid Accession #: NM_002421.2
Coding sequence: 1..1409

40
45
50
55
60
65

1 11 21 31 41 51
ATGCACAGCT TTCTCTCACT GCTGCTGCTG CTGTTCTGGG GTGTGGTGTC ACACAGCTTC 60
CCAGCGACTC TAGAAACACA AGAGCAAGAT GTGGACTTAG TCCAGAAATA CCTGGAAAAA 120
TACTACAACC TGAAGAATGA TGGGAGGCCA GTTGAAGAGC GGAGAAATAG TGGCCAGTGG 180
GTTGAAAAAT TGAAGCAAT GCAGGAATTC TTTGGGCTGA AAGTGACTGG GAAACAGAT 240
GCTGAAACCC TGAAGGTGAT GAAGCAGCCC AGATGTGGAG TGCTGATGT GGCTCAGTTT 300
GTCTCTCACT AGGGGAACCC TCGCTGGGAG CAAACACATC TGACCTACAG GATTGAAAA 360
TACACGCCAG ATTTGCCAAG AGCAGATGTG GACCATGCCA TTGAGAAAGC CTTCCAACCTC 420
TGGAGTAATG TCACACCTCT GACATTACCC AAGGTCTCTG AGGGTCAAGC AGACATCATG 480
ATATCTTTTG TCAGGGGAGA TCATCGGGAC AACTCTCCTT TTGATGGACC TGGAGGAAAT 540
CTTGCTCATG CTTTTCACAC AGGCCCAGGT ATTGGAGGGG ATGCTCATTT TGATGAAGAT 600
GAAAGGTGGA CCAACAATT TACAGAGTAC AACTTACATC GTGTTGCGGC TCATGCCCTC 660
GGCCATTCTC TTGGACTCTC CCATTCTACT GATATCGGGG CTTTGATGTA CCCTAGCTAC 720
ACCTTCAGTG GTGATGTTCA GCTAGCTCAG GATGACATTG ATGGCATCCA AGCCATATAT 780
GGACGTTCCC AAAATCCTGT CCAGCCATC GGGCCACAAA CCCCAGAAAGC ATGTGACAGT 840
AAGCTAACCT TTGATGCTAT AACTACGATT CGGGGAGAGG TGATGTTCTT TAAAGACAGA 900
TTCTACATGC GCACAAATCC CTTTACCCG GAAGTTGAGC TCAATTTCAT TTCTGTTTTC 960
TGGCCACAAC TGCCAAATGG GCTTGAAGCT GCTTACGAAT TTGCCGACAG AGATGAAGTC 1020
CGGTTTTTCA AAGGGAATAA GTACTGGGCT GTTCAGGGAC AGAATGTGCT ACACGGATAC 1080
CCCAAGGACA TCTACAGCTC CTTTGGCTTC CTTAGAACTG TGAAGCATAT CGATGCTGCT 1140
CTTTCTGAGG AAAACACTGG AAAAACCTAC TTCTTTGTTG CTAACAAATA CTGGAGGTAT 1200
GATGAATATA AAGATCTAT GATCCAGGT TATCCCAAAA TGATAGCACA TGACTTTTCT 1260
GGAATTGGCC ACAAAGTTGA TGCAGTTTTC ATGAAAGATG GATTTTCTTA TTTCTTTCAT 1320
GGAACAAGAC AATACAAATT TGATCCTAAA ACGAAGAGAA TTTTGACTCT CCAGAAAGCT 1380
AATAGCTGGT TCAACTGCAG GAAAAATTAG

Seq ID NO: 393 Protein sequence
Protein Accession #: NP_002412.1

70
75
80

1 11 21 31 41 51
MHSFPPPLLLL LFWGVVSHSF PATLETQEQD VDLVQKYLEK YYNLKNDGRQ VEKRRNSGPV 60
VEKLKQMKEF FGLKVTGKPD AETLKVMKQP RCGVPDVAQF VLTEGNPRWE QTHLTYRIEN 120
YTPDLPRADV DHAIEKAFQL WSNVTPLTFT KVSEGGQADIM ISFVRGDHRD NSPFDGPGSN 180
LAHAFFQPGF IGGDAHFDED ERWNNFREY NLHRVAHAEL GHSGLGLSHST DIGALMYPST 240
TFSGDVQLAQ DDIDIGIAIY GRSQNPVQPI GPQTPKACDS KLTFDAITTI RGEVMFFKDR 300
FYMRNPFYF EVELNPFISV WPQLPNGLEA AYEFAADRDEV RFFKGNKYWA VQGNVNLHGY 360
PKDIYSSFGF PRTVKHIDAA LSEENTGKTY FFFVANKYWRV DEYKRSMDPG YPKMIAHDFP 420
GIGHKVDVAV MKDGFYFFPH GTRQYKFDPK TKRILTLQKA NSWFNCRKN

Seq ID NO: 394 DNA sequence
Nucleic Acid Accession #: NM_014331.2
Coding sequence: 1..1506

85

1 11 21 31 41 51

	ATGGTCAGAA	AGCCTGTGT	GTCCACCATC	TCCAAAGGAG	GTTACCTGCA	GGGAAATGTT	60
	AACGGGAGGC	TGCCTTCCT	GGGCAACAAG	GAGCCACCTG	GGCAGGAGAA	AGTGCAGCTG	120
	AAGAGGAAAG	TCACCTTTACT	GAGGGGAGTC	TCCATTATCA	TTGGCACCAT	CATTGGAGCA	180
5	GGAAATCTTCA	TCTCTCTAA	GGCGGTGCTC	CAGAACACGG	GCAGCGTGGG	CATGTCCTCG	240
	ACCATCTGGA	CGGTGTGTGG	GGTCTGTGCA	CTATTGTGAG	CTTTGTCTTA	TGCTGAATTG	300
	GGAAACAATA	TAAAGAAATC	TGGAGGTCAT	TACACATATA	TTTGGGAAGT	CTTGGTCCA	360
	TTACCAGCTT	TTGTACGAGT	CTGGGTGGAA	CTCCTCATAA	TACGCCCTGC	AGCTACTGCT	420
	GTGATATCCC	TGGCATTGAG	ACGCTACATT	CTGGAACCAT	TTTTTATTCA	ATGTGAAATC	480
10	CCTGAACCTG	CGATCAAGCT	CATTACAGCT	GTGGGCATAA	CTGTAGTGAT	GGTCTTAAT	540
	AGCATGAGTG	TCAGCTGGAG	CGCCCGGATC	CAGATTTTCT	TAACTTTTGG	CAAGCTCACA	600
	GCAATTTCTG	TAATTATAGT	CCCTGGAGTT	ATGCAGCTAA	TAAAGGTCA	AACGCAGAAC	660
	TTTAAAGACG	CGTTTTTCAG	AAGAGATTCA	AGTATTACGC	GGTGGCCACT	GGCTTTTTAT	720
	TATGGAATGT	ATGCATATGC	TGGCTGGTTT	TACCTCAACT	TTGTTACTGA	AGAAGTAGAA	780
15	AACCTTGAA	AAACCATTC	CCTTGCAATA	TGTATATCCA	TGGCCATTGT	CACCATTTGG	840
	TATGTGCTGA	CAATGTGGG	CTACTTTACG	ACCATTAAATG	CTGAGGAGCT	GCTGCTTTCA	900
	AATGCAGTGA	CAGTGTGGCT	TTCTGAGCGG	CTACTGGGAA	ATTCTCTATT	AGCAGTTCGG	960
	ATCTTTGTTG	CCCTCTCTCG	CTTTGGCTCC	ATGAACGGTG	GTGTGTTTGC	TGTCTCCAGG	1020
	TTATTCTATG	TTGCGTCTCG	AGAGGGTCAC	CTTCCAGAAA	TCTCTCCAT	GATTCTATGC	1080
20	CGCAAGCACA	CGCTCTACCC	AGCTGTTATT	GTTTTGCAAC	CTTGACAAT	GATAATGCTC	1140
	TTCTCTGGAG	ACCTCGACAG	TCTTTTGAAT	TTCTCTCAGT	TTGCCAGGTT	GCTTTTATT	1200
	GGGCTGGCAG	TTGCTGGGCT	GATTTATCTT	CGATACAAAT	GCCCAGATAT	GCATCGTCTC	1260
	TTCAAGGTGC	CACGTTCAT	CCCAGCTTTG	TTTTCTTCA	CATGCCCTCT	CATGGTTGCC	1320
	CTTTCCCTCT	ATTCGGACCC	ATTTAGTACA	GGGATTGGCT	TCGTCTATC	TCTGACTGGA	1380
25	GTCCCTGGGT	ATTATCTCTT	TATTATATGG	GACAAGAAAC	CCAGGTGGTT	TAGAATAATG	1440
	TCAGAGAAAA	TAACCAAGAC	ATTACAAATA	ATACTGGAAG	TTGTACCAGA	AGAAGATAAG	1500
	TTATGAACAT	ATGGACTTGA	GATCTTGCCA	ATCTGCCCAA	GGGGAGACAC	AAAATAGGGA	1560
	TTTTTACTTC	ATTTTCTGAA	AGTCTAGAGA	ATTACAACCT	TGGTGATAAA	CAAAAGGAGT	1620
	CAGTTATTTT	TATTATATGA	TTTTCAGATA	TTTCAACTAA	TTTCTAAGAA	ATTTAGTTAT	1680
30	AACCTCATGT	AGTTATGAA	AGTGAATATG	CAGTTATTCT	ATGAGTCGCA	CAATTCTTGA	1740
	GTCTCTGATA	CCTACCTATT	GGGGTTAGGA	GAAGAAGACTA	GACAATTACT	ATGTGGTCAT	1800
	TCTCTACACA	ATGCTTTAGC	ACGGCAAAGA	ACCTTCAAT	TGAAGACTGA	GATTTTCTG	1860
	TATATATGGG	TTTTGTAAAG	ATGGTTTAC	ACACTACAGA	TGTCTATACT	GTGAAAAGTG	1920
	TTTTCAATTC	TGAAAAAAG	CATACATCAT	GATTATGGCA	AAGAGGAGAG	AAAGAAATTT	1980
35	ATTTTACATT	GACATTGCAT	TGCTTCCCTT	TAGATACCAA	TTTAGATAAC	AAACACTCAT	2040
	GCTTTAATGG	ATTATACCCA	GAGCACTTTG	AACAAGAGTC	AGTGGGGATT	GTGTAATACA	2100
	TTAAAGAAGA	TTTCTAGGG	GCTACTGTTT	ATGAGACACA	TCCAGAGAGT	ATGTTTAAGT	2160
	AAAAATCCCT	GAGAAATTAT	TATGTCAGAT	GTTTTTTCAT	TCATTATCAG	GAAGTTTATG	2220
	TTATCTGTCA	TTTTTTTTTT	TCACATCAGT	TTGATCAGGA	AAGTGATATA	CACATCTTAG	2280
40	AGCAAGAGTT	AGTTTGTGAT	TAAATCTCA	TTAGAACAAC	CACCTGTTTC	ACTAATAACT	2340
	TACCCTGAT	GAGTCTATCT	AAACATATGC	ATTTTAAAGCC	TTCAAAATTAC	ATTATCAACA	2400
	TGAGAGAAAT	AACCAACAAA	GAAGATGTTT	AAAAATATAG	TCCCATATCT	GTAATCATAT	2460
	CTACATGCAA	TGTTAGTAAT	TCTGAAGTTT	TTTAAATTTA	TGGCTATTTT	TACACGATGA	2520
	TGAATTTTGA	CAGTTTGTGC	ATTTTCTTTA	TACATTTTAT	ATTCTTCTGT	TAAATATCT	2580
45	CTTCAGATGA	AACGTGTCAG	ATTAATTAGG	AAAAGGCATA	TATTAACATA	AAAATTGCAA	2640
	AAGAAATGTC	GCTGTAAATA	AGATTATCAA	CTGATGTTTC	TAGAAAATTT	CCACTTCTAT	2700
	ATCTAGGCTT	QIFLTFCCLT	AILIIIVPGV	MLIKGQTON	FKDAFSGRDS	SITRLPLAFY	2760
	CTGATAAGAA	GAAATTTGAA	ATGAGAATCT	GTGGATAAGT	GTTTGTGTTC	AGAAGATGTT	2820
	GTTTTGCCAG	TATTAGAAAA	TACTGTGAGC	CGGGCATGGT	GGCTTACATC	TGTAATCCCA	2880
50	GCACCTTGGG	AGGCTGAGGG	GGTGGATCAC	CTGAGGTGGG	GAGTTCCTAG	CCAGCCTGAC	2940
	CAACATGAGG	AAACCCCATC	TCTACTAAAA	ATACAAAATT	AGCTGGGCAT	GGTGGCAGAT	3000
	GCTGTGAATC	TCAGCTATTG	AGGAGGCTGA	GGCAGGAGAA	TTGCTTGAAC	CCGGGAGGCG	3060
	GAGGTTGCAG	TGAGCCAAGA	TTGCACCAC	GTACTCCAGC	CTGGGTGACA	AAGTCAGACT	3120
	CCATCTCCAA	AAAAAAAAAA	AAAA				

Seq ID NO: 395 Protein sequence
Protein Accession #: NP_055146.1

	1	11	21	31	41	51	
60	MVRKPVVSTI	SKGGYVQGNV	NGRLPSLGNK	EPPGQEKVQL	KRKVTLLRGV	SIIIGTIIGA	60
	GIFISPKGV	QNTGSVGM	SLTWTVCGLS	LFGALSYAEL	GTTIKKSGGH	YTYILEVFGP	120
	LPAFVRVWVE	LLIIRPAATA	VISLAFGRYI	LEPFFIQCEI	PELAIKLITA	VGITVVMVLN	180
	SMSVSWASRI	QIFLTFCCLT	AILIIIVPGV	MLIKGQTON	FKDAFSGRDS	SITRLPLAFY	240
65	YGMVYAGWFF	YLNFTVEEVE	NPEKTIPLAI	CISMAITIGV	YVLTNVAYFT	TINAEELLLS	300
	NAVAVTFPSR	LLGNFSLAVP	IFVALSCFPG	MNGGVFAVSR	LPVVASREGH	LPEILSMIHV	360
	RKHTPLPAVI	VLHPLTMIML	PSGDLDSLNL	FLSFARWLFI	GLAVAGLIYL	RYKCPDMHRP	420
	FKVPLFIPAL	FSFTCLFMVA	LSLYSDPFST	GIGFVITLTG	VPAYYLFITW	DKPKRWFIRM	480
	SEKIRTRTQI	ILEVVEEDK	L				

Seq ID NO: 396 DNA sequence
Nucleic Acid Accession #: NM_006528
Coding sequence: 57..764

	1	11	21	31	41	51	
75	GCCGCCAGCG	GCTTTCTCGG	ACGCCCTTGCC	CAGCGGGCCG	CCCGACCCCC	TGCACCATGG	60
	ACCCCGCTCG	CCCTCTGGGG	CTGTGCAATC	TGCTGCTTTT	CCTGACGGAG	GCTGCACTGG	120
80	GCGATGCTGC	TCAGGAGCCA	ACAGGAAATA	ACGCGGAGAT	CTGTCTCCTG	CCCCTAGACT	180
	ACGGACCTCG	CCGGCCCTCA	CTTCTCCGTT	ACTACTACGA	CAGGTACACG	CAGAGCTGCC	240
	GCCAGTTCCT	GTACGGGGGC	TGCGAGGGCA	ACGCCAACAA	TTTCTACACC	TGGGAGGCTT	300
	GCGACGATGC	TTGCTGGAGG	ATAGAAAAAG	TTCCCAAAGT	TTGCCCGCTG	CAAGTGAGTG	360
	TGGACGACCA	GTGTGAGGGG	TCCACAGAAA	AGTATTTCTT	TAATCTAAGT	TCCATGACAT	420
	GTGAAAAATT	CTTTCCCGGT	GGGTGTCAAC	GGAAACCGGAT	TGAGAACAGG	TTTCCAGATG	480
85	AAGCTACTTG	TATGGGCTTC	TGCGACCCAA	AGAAAAATTC	ATCATTTTGC	TACAGTCCAA	540
	AAGATGAGGG	ACTGTGCTCT	GCCATGTGTA	CTCGCTATTA	TTTAAATCCA	AGATACAGAA	600
	CCTGTGATGC	TTTCACTTAT	ACTGGCTGTG	GAGGGAATGA	CAATAACTTT	GTTAGCAGGG	660

WO 02/086443

PCT/US02/12476

AGGATTGCAA ACGTGCATGT GCAAAAGCTT TGA AAAAGAA AAAGAAGATG CCAAAGCTTC 720
 GCTTTGCCAG TAGAATCCGG AAAATTCCGA AGAAGCAATT TTAACATTC TTAATATGTC 780
 ATCTTGTTTG TCTTTATGGC TTATTTGCC TTTATGGTTG ATCTGAAGAA TAATATGACA 840
 GCATGAGGAA ACAATCATT GGTGATTTAT TCACCACTTT TTATTAATAC AAGTCACTTT 900
 TTCAAAATT TGGATTTTAT TATATATAAC TAGCTGCTAT TCAAAATGTA GTCTACCACT 960
 TTTAATTTAT GGTTCACCTG TTTGTGAGAC GAATTCCTGC AATGCATAAG ATATAAAAGC 1020
 AAATATGACT CACTCATTTT TGGGGTGGT ATTCTGATT TCAGAAGAGG ATCATAACTG 1080
 AAACAACATA AGACAATATA ATCATGTGCT TTTAACATAT TTGAGAATAA AAAGGACTAG 1140
 CC

Seq ID NO: 397 Protein sequence
 Protein Accession #: NP_006519

1 11 21 31 41 51
 MDPARPLGLS ILLFLTEAA LGDAAQEPTG NNAEICLLPL DYGPCRALLL RYYYDRYTQS 60
 CRQFLYGGCE GNANFNFTWE ACDDACWRIE KVPKVCRLQV SVDDQCEGST EKYFFNLSSM 120
 TCEKFFSGGC HRNRIENRFP DEATCMGFCA PKKIPFCYS PKDEGLCSAN VTRYVFNPRY 180
 RTCDAFYTYG CGNDNNFVS REDCKRACAK ALKKKKKMPK LRFASIRIKI RKKQF

Seq ID NO: 398 DNA sequence
 Nucleic Acid Accession #: NM_001508.1
 Coding sequence: 1..1361

1 11 21 31 41 51
 ATGGCTTCAC CCAGCCTCCC GGGCAGTGAC TGCTCCCAA TCATTGATCA CAGTCATGTC 60
 CCGAGTTTG AGGTGGCCAC CTGGATCAAA ATCACCCTTA TTCTGGTGA CCTGATCATC 120
 TTCTGTATGG GCCTTCTGGG GAACAGCGTC ACCATTCGGG TCACCCAGGT GCTGCAGAG 180
 AAAGGATACT TGCAGAGGA GGTGACAGAC CACATGGTGA GTTTGGCTTG CTGGACATC 240
 TTGGTGTTC TCATCGGATP GCCCATGGAG TTCTACAGCA TCATCTGGAA TCCCTGACC 300
 ACCTCCAGCT ACACCTGTCT CTGCAAGCTG CACACTTTCC TCTTCGAGGC CTGCAGCTAC 360
 GCTACGCTGC TGCAGCTGCT GACGCTCAGC TTTGAGCGCT ACATCGCCAT CTGTACCCCC 420
 TTCAGGTACA AGGCTGTGTC GGGACCTTGC CAGGTGAAGC TGCTGATTGG CTTCGTCTGG 480
 GTCACTCTCG CCCTGGTGGC ACTGCCCTTG CTGTTTGCCA TGGGTACTGA GTACCCCTCG 540
 GTGAACGTGC CCAGCCACCG GGGTCTCACT TGCAACCGCT CCAGCACCCG CCACCACGAG 600
 CAGCCCGAGA CCTCCAATAT GTCCATCTGT ACCAACCTCT CCAGCCGCTG GACCGTGTTC 660
 CAGTCCAGCA TCTTCGGGCG CTTCGTGGTC TACCTCGTGG TCTGCTCTC CGTAGCCTTC 720
 ATGTGCTGGA ACATGATGCA GGTGCTCATG AAAAGCCAGA AGGGCTCGCT GGCCGGGGGC 780
 ACGCGCCTC CGCAGCTGAG GAAGTCCGAG AGCGAAGAGA GCAGGACCGC CAGGAGGCG 840
 ACCATCATCT TCTGAGGCT GATTGTTGTG ACATTGGCCG TATGCTGGAT GCCCAACGAG 900
 ATTGCGAGGA TCATGCTTGC GGCCAAACCC AAGCACGACT GGACGAGGTC CTACTTCCGG 960
 GCGTACATCA TCTCTCTCCC CTTCCTGGAG ACGTTTTTCT ACCTCAGCTC GGTATCAAC 1020
 CCGCTCCTGT ACACGGTGTG CTCGAGCAG TTTGGGGGGG TGTTCTGTGA GGTGCTGTGC 1080
 TGGCGCTGT CGCTGCAGCA CGCCAAACCC GAGAAGCGCC TGGCGTACA TGCGCACTCC 1140
 ACCACGAGCA GCGCCCGCTT TGTGCAGCGC CCGTTGCTCT TCGCTGCCG CGCCAGTCC 1200
 TCTGCAAGGA GAAGTGAAGA GATTTCTTA AGCACTTTTC AGAGCGAGGC CGAGCCCCAG 1260
 TCTAAGTCCC AGTCATTGAG TCTCGAGTCA CTAGAGCCCA ACTCAGGCGC GAAACGAGCC 1320
 AATTCTGCTG CAGAGAATGG TTTTCAGGAG CATGAAGTTT GA

Seq ID NO: 399 Protein sequence
 Protein Accession #: NP_001499.1

1 11 21 31 41 51
 MASPSLPGSD CSQIIDHSHV PEFEVATWIK ITLILVYLII FVMGLLGNV TIRVTQVLQK 60
 KGYLQKEVTD HMVSLACSDI LVFLIGMPME FYSIIWNPLT TSSYTLSCKL HTFLFEACSY 120
 ATLLHLVTLF FERYAICHFP FRYKAVSGPC QVKLLIGFVW VTSALVALPL LFMAGTEYPL 180
 VNVPSHRGLT CNRSSTRHHE QPETSNNMSIC TNLSSRWTFV QSSIFGAFV YLVVLLSVAF 240
 MCWNMMQVLM KSQKSLLAGG TRPPQLRKSE SEESRTARRQ TIIFLRLIV TLAVCWMPNQ 300
 IRRIMAAAKP KHDWTRSYFR AYMLLPFSE TFFYLSSVIN PLLLYTVSSQ FRRVFVQVLC 360
 CRLSLQHANH EKRLRVHAHS TTDSARFVQR PLLFASRRQS SARRTEKIFL STFQSEAEPPQ 420
 SKQSLSLES LEFNSGAKFA NSAAENGFOE HEV

Seq ID NO: 400 DNA sequence
 Nucleic Acid Accession #: NM_006475.1
 Coding sequence: 28..2538

1 11 21 31 41 51
 AACAGAACTG CAACGGAGAG ACTCAAGATG ATTCCCTTTT TACCATGTT TTCTCTACTA 60
 TTGCTGCTTA TTGTTAACCC TATAAACGCC AACAAATCATT ATGACAAGAT CTGGGCTCAT 120
 AGTCGTATCA GGGGTCGGGA CCAAGGCCCA AATGTCGTGT CCGTTCAACA GATTTTGGGC 180
 ACCAAAAGA AATACTTCAG CACTTGTAAG AACTGGTATA AAAAGTCCAT CTGTGGACAG 240
 AAAACGACTG TTTTATATGA ATGTTGCCCT GGTATATGA GAATGGAAGG AATGAAAGGC 300
 TGCCAGCAG TTTTGCCCAT TGACCATGTT TATGGCACTC TGGGCATCGT GGGAGCCACC 360
 ACAACGACAG GCTATTCTGA CGCCTCAAAA CTGAGGGAGG AGATCGAGGG AAGGGATCC 420
 TTCACTTACT TTGCACCGAG TAATGAGGCT TGGGACAAC TGGATTCTGA TATCCGTAGA 480
 GGTGTGGAGA GCAACGTGAA TGTGGAATTA CTGAATGCTT TACATAGTCA CATGATTAAT 540
 AAGAGAAATG TGACCAAGGA CTTAAAAAAT GGCATGATTA TTCTTCAAT GTATAACAAT 600
 TTGGGGCTTT TCATTAAACA TTATCCTAAT GGGGTGTGCA CTGTTAATTG TGCTCGAATC 660
 ATCCATGGGA ACCAGATTGC AACAAATGGT GTTGTCATG TCATTGACCG TGTGCTTACA 720
 CAAATTGGTA CCTCAATTCA AGACTTCATT GAAGCAGAAG ATGACCTTTC ATCTTTTAGA 780
 GCAAGCTGCCA TCACATCGGA CATATTGGAG GCCCTTGGAA GAGACGGTCA CTTCACTC 840
 TTTGCTCCCA CCAATGAGGC TTTTGAGAAA CTTCCACGAG GTGCTCTAGA AAGGTTCTAG 900
 GGAGACAAAG TGCTTCCGA AGCTCTTATG AAGTACCACA TCTTAAATAC TCTCCAGTGT 960
 TCTGAGTCTA TTATGGGAGG AGCAGTCTTT GAGACGCTGG AAGGAAATAC AATTGAGATA 1020

5 GGATGTGACG GTGACAGTAT AACAGTAAAT GGAATCAAAA TGGTGAACAA AAAGGATATT 1080
 GTGACAAATA ATGGTGTGAT CCATTGTGATT GATCAGGTCC TAATTCCTGA TTCTGCCAAA 1140
 CAAGTTATTG AGCTGGCTGG AAAACAGCAA ACCACCTTCA CGGATCTTGT GGGCCCAATTA 1200
 GGCTTGGCAT CTGCTCTGAG GCCAGATGGA GAATACACTT TGCTGGCACC TGTGAATAAT 1260
 GCATTTTCTG ATGATACTCT CAGCATGGTT CAGCGCCTCC TTAATTAAT TCTGCAGAAT 1320
 CACATATTGA AAGTAAAGT TGGCCTTAAT GAGCTTTACA ACGGGCAAAT ACTGGAACCC 1380
 ATCGGAGGCA AACAGCTCAG AGTCTTCGTA TATCGTACAG CTGTCTGCAT TGAATAATCA 1440
 TGCATGGAGA AAGGGAGTAA GCAAGGGAGA AACGGTGGCA TTCACATATT CCGCGAGATC 1500
 10 ATCAAGCCAG CAGAGAATC CCTCCATGAA AAGTTAAAC AAGATAAGCG CTTTAGCACC 1560
 TTCCTCAGCC TACTTGAAGC TGCAGACTTG AAGAGCTCC TGACACAACC TGGAGACTGG 1620
 ACATTATTGG TGCCAACCAA TGATGCTTTT AAGGGAATGA CTAGTGAAGA AAAAGAAATT 1680
 CTGATACGGG ACAAAATATG TCTTCAAAAC ATCATTCTTT ATCACCTGAC ACCAGGAGTT 1740
 TTCATTGGAA AAGGATTTGA ACCTGGTGT ACTAACATTT TAAAGACCAC ACAAGGAAGC 1800
 15 AAAATCTTTC TGAAGAAGT AAATGATACA CTTCTGGTGA ATGAATTGAA ATCAAAAGAA 1860
 TCTGACATCA TGACAACAAA TGGTGTAAAT CATGTTGTAG ATAAACTCCT CTATCCAGCA 1920
 GACACACCTG TTGGAATGA TCAACTGCTG GAAATACCTA ATAAATTAAT CAAATACATC 1980
 CAAATTAAGT TTGTTCTGGG TAGCACCTTC AAAGAAATCC CCGTGACTGT CTATACAACCT 2040
 AAAATTATTA CCAAGTTGT GGAACCAAAA ATTAAGTGA TTGAAGGCAG TCTTCAGCCT 2100
 20 ATATCAAAA CAGAGGACC CACATAACA AAGTCAAAA TTGAAGGTGA ACCTGAATTC 2160
 AGACTGATTA AAGAGGTGA AACATAACT GAGTGATCC ATGGAGAGCC AATTATTAAA 2220
 AAATACACCA AAATCATTTA TGGAGTGCCT GTGGAATAA CTGAAAAGA GACACGAGAA 2280
 GAACGAATCA TTACAGGTCC TGAAATAAAA TACACTAGGA TTTCTACTGG AGGTGGAGAA 2340
 ACAGAAGAAA CTCTGAAGAA ATTGTTACAA GAAGAGGTCA CCAAGGTGAC CAAATTCATT 2400
 25 GAAGGTGGTGA ATGGTCAATT ATTTGAAGAT GAAGAAATTA AAGACTGCT TCAGGGAGAC 2460
 ACACCCGTGA GGAAGTTGCA AGCCCAACAA AAGTTCAAG GTTCTAGAAG ACGATTAAAG 2520
 GAAGGTGCTT CTCAGTGAAT ATCCAAAAC CAGAAAATA TGTTTATACA ACCCTAAGTC 2580
 AATAACCTGA CCTTAGAAAA TTGTGAGAGC CAAGTTGACT TCAGGAACCTG AAACATCAGC 2640
 ACAAGAAGC AATCATCAAA TAATTTCTGAA CACAAATTTA ATATTTTITT TTCTGAATGA 2700
 30 GAAACATGAG GGAATTTGGT GAGTTAGCCT CCGTGGTAA AGGAATTGAA GAAAATATA 2760
 CACCTTACAC CCTTTTTCAT CTGACATTA AAGTTCTGG CTAACTTTGG AATCCATTAG 2820
 AGAAAAATCC TTGTCACCAG ATTCATTACA ATTCAAATCG AAGAGTTGTG AACTGTTATC 2880
 CCATTGAAAA GACCGAGCCT TGTATGTATG TTATGGATAC ATAAATGCA CGCAAGCCAT 2940
 35 TATCTCTCCA TGGGAAGCTA AGTTATAAAA ATAGGTGCTT GGTGTACAAA ACTTTTTATA 3000
 TCAAAAGGCT TTGCACATT CTATATGAGT GGGTTTACTG GTAAATTATG TTATTTTTTA 3060
 CACTAATTT TGTACTCTCA GAATGTTTGT CATATGCTTC TTGCAATGCA TATTTTTTAA 3120
 TCTCAAAGCT TTCAATAAAA CCATTTTCA GATATAAAGA GAATTACTTC AAATTGAGTA 3180
 ATTCAGAAAA ACTCAAGATT TAAGTTAAAA AGTGGTTTGG ACTTGGGAA

Seq ID NO: 401 Protein sequence
 Protein Accession #: NP_006466.1

45 1 11 21 31 41 51
 MIPFLPMFSL LLLIIVNPIN ANHYDKILA HSRIRGRDQG PNVCALQQIL GTKKKYFSTC 60
 KNWYKKSICG QKTTVLYECC PGYMRMEGMC GCPAVLPIDH VYGTGLGIVA TTTQRYSDAS 120
 KLREEIEGKG SFTYFAPSNE AWDNLDSDIR RGLSENVNVE LLNALHSHMI NKRLMTKDLK 180
 NGMIIPSMYN NLGLFNIHYP NGVVTVNCAI IHHGNQIATN GVVHVIVRVL TQIGTSIQDF 240
 IEAEDDLSSP RAAAITSDIL EALGRDGHFT LFAPTNEAPE KLPRGVLEBF MGDKVASEAL 300
 50 MKYHILNTLG CSESMGGAV FETLEGNTIE IGCDGDSITV NGIKMVNKKD IVTNNGVIHL 360
 IDQVLIPDSA KQVIELAGKQ QTTFTDLVAQ LGLASALRPD GEYTLAPVN NAFSDDTLMS 420
 VORILLKILQ NELLKVKVGL NELYNGQILE TIGGKQLRVF VYRTAVCIEN SMEKGSKQG 480
 RNGAIHTFRE IIPAKKSLH EKLKQDKRFS TFLSLLEAAD LKELLTQPGD WTLFVPTNDA 540
 PKGMTSBEKE ILIRDKNALQ NIILYHLTPG VFIKGFEPG VTNILKTTQG SKIFLKEVND 600
 55 TLLVNEKSK ESDIMTNGV IHVVDKLLYP ADTPVGNQDL LEILNKLIKY IQIKFVRGST 660
 FKEIPVTVYT TKIITKVVEP KIKVIEGSLQ PIKTEGPTL TKVKIEGEPE FRLIKEGETI 720
 TEVIHGEPII KKYTKIDGV PVEITEKETR EERLIITGPEI KYTRISTGGG STEETLKILL 780
 QEEVTKVTKF IEGGDGHLFE DEEIKRLQGG DTPVRKLQAN KKVQGSRRRL REGRSQ

Seq ID NO: 402 DNA sequence
 Nucleic Acid Accession #: NM_002416
 Coding sequence: 40..417

65 1 11 21 31 41 51
 ATCCAATACA GGAGTGACTT GGAACCTCCAT TCTATCACTA TGAAGAAAAG TGGTGTCTT 60
 TTCCTCTTGG GCATCATCTT GCTGGTCTG ATTGGAGTGC AAGGAACCCC AGTAGTGAGA 120
 AAGGGTGGCT GTTCCTGCTC CAGCACCAAC CAAGGGACTA TCCACCTACA ATCCTTGAAA 180
 GACCTTAAAC AATTTGCCCC AAGCCCTTCC TCGGAGAAAA TTGAATCAT TGCTACACTG 240
 70 AAGAATGGAG TTCAAACATG TCTAAACCCA GATTCAAGAG ATGTGAAGGA ACTGATTAAA 300
 AAGTGGGAGA AACAGGTGAG CCAAAAGAAA AAGCAAAAGA ATGGGAAAAA ACATCAAAAA 360
 AAGAAAGTTC TGAAGTTTCC AAAATCTCAA CGTTCTCGTC AAAAGAAGAC TACATAAGAG 420
 ACCACTTCAC CAATAAGTAT TCTGTGTTAA AAATGTTCTA TTTTAATTAT ACCGCTATCA 480
 TTCCAAAGGA GGATGGCATA TAATACAAAG GCTTATTAAT TTGACTAGAA AATTATAAAC 540
 75 ATTAATCTGA AATTGTAACT AAGTTAGAAA AGTTGATTTT AAGAATCCAA ACGTTAAGAA 600
 TTGTTAAAGG CTATGATTGT CTTTGTCTCT CTACCAACCA CCAGTTGAAT TTCATCATGC 660
 TTAAGGCCAT GATTTTAGCA ATACCCATGT CTACACAGAT GTTACCCCAA CCACATCCCA 720
 CTCACAACAG CTCGCTGGAA GAGCAGCCCT AGGCTTCCAC GTACTGCAGC CTCGAGAGAG 780
 TATCTGAGCG ACATGCTCAG AAGTCCTAAG CCGTTTAGCA TGCTGGTGAG CCAAGCAGTT 840
 80 TGAATTGAG CTGGACCTCA CCAAGCTGCT GTGGCCATCA ACCTCTGTAT TTGAATCAGC 900
 CTACAGGCCT CACACAAT GTGCTGAGA GATTATGCT GATTGTTATT GGGTATCACC 960
 ACTGGAGATC ACCAGTGTGT GGCTTTTCTA GCCTCCTTTC TGGCTTTGGA AGCCATGTGA 1020
 TTCCATCTG CCCGCTCAGG CTGACCACTT TATTTCTTTT TGTTCCTCTT TGCTTCATTC 1080
 AAGTCAGCTC TTCTCCATCC TACCACAATG CAGTGCCCTT CTTCTCTCCA GTGCACCTGT 1140
 85 CATATGCTCT GATTTATCTG AGTCAACTCC TTTCTCATCT TGTCCCAAC ACCCCACAGA 1200
 AGTGTCTTCT TCTCCCAATT CATCTCACT CAGTCCAGCT TAGTTCAAGT CCTGCCTCTT 1260
 AAATAAACCT TTTTGGACAC ACAAATTATC TTAATACTCC TGTTCACCT GGTTCAGTAC 1320
 CACATGGGTG AACACTCAAT GGTTAACTAA TTCTGGGTG TTTATCTAT CTCTCCAACC 1380

AGATTGTCTAG CTCCTTGAGG GCAAGAGCCA CAGTATATTT CCCTGTTTCT TCCACAGTGC 1440
 CTAATAATAC TGTGGAACCTA GGTTTTAATA ATTTTAAAT TGATGTTGTT ATGGGCAGGA 1500
 TGGCAACACG ACCATTGTCT CAGAGCAGGT GCTGGCTCTT TCCTGGCTAC TCCATGTTGG 1560
 CTAGCCTCTG GTAACCTCTT ACTTATTATC TTCAGGACAC TCCTACAGG GACCAGGGAT 1620
 GATGCAACAT CCTGTCTTTT TTATGACAGG ATGTTTGCTC AGCTTCTCCA ACAATAAGAA 1680
 GCACGTGTGA AAACACTTGC GGATATTCTG GACTGTTTTT AAAAAATATA CAGTTTACCG 1740
 AAAATCATAT AATCTTACAA TGAAAAGGAC TTTATAGATC AGCCAGTGAC CAACCTTTTC 1800
 CCAACCATAC AAAAATTCCT TTTCCCGAAG GAAAAGGGCT TTCTCAATAA GCCTCAGCTT 1860
 TCTAAGATCT AACAGATAG CCACCGAGAT CCTTATCGAA ACTCATTTTA GGCAAAATAG 1920
 AGTTTTATG TCCGTTTACT TGTTCAGAG TTTGTATTGT GATTATCAAT TACCACACCA 1980
 TCTCCCATGA AGAAAGGGAA CGGTGAAGTA CTAAGCGCTA GAGGAAGCAG CCAAGTCGGT 2040
 TAGTGAAGC ATGATTGGTG CCCAGTTAGC CTCTGCAGGA TGTGGAACCC TCCTTCCAGG 2100
 GGAGGTTCTAG TGAATTGTGT AGGAGAGGTT GTCTGTGGCC AGAATTTAAA CCTATACTCA 2160
 CTTTCCCAAA TTGAATCACT GCTCACACTG CTGATGATTT AGAGTGCTGT CCGGTGGAGA 2220
 TCCCACCGAA ACCTGCTTATC TAATCATGAA ACTCCCTAGT TCCTTCACTG AACCTCCCTG 2280
 AAAAATCTAA GTGTTTCTATA AATTGAGAG TCTGTGACCC ACTTACCTTG CATCTCACAG 2340
 GTAGACAGTA TATAACTAAC AACCAGAGAC TACATATTGT CACTGACACA CACGTATATA 2400
 TCATTATACA TATATATACA TACATGCATA CACTCTCAA GCAATAAAT TTTCACTTCA 2460
 AAACAGTATT GACTTGTATA CCTTGAATTT TGAAATATTT TCTTTGTATA AATAGAATGG 2520
 TATCAATAAA TAGACCATTA ATCAG

Seq ID NO: 403 Protein sequence
 Protein Accession #: NP_002407

1 11 21 31 41 51
 MKKSGVLFLL GIILLVLIGV QGTPVVRKGR CSCISTNQGT IHLQSLKDLK QFAPSPSCEK 60
 IEIIATLKNG VQTCLNPDSA DVKELIKKWE KQVSQKKKQK NGKKHQKKV LKVRKSQRSR 120
 QKKT

Seq ID NO: 404 DNA sequence
 Nucleic Acid Accession #: NM_006670
 Coding sequence: 85..1347

1 11 21 31 41 51
 CCGGCTCGCG CCCTCCGGGC CCAGCCTCCC GAGCCTTCGG AGCGGGGGCC GTCCAGCCCC 60
 AGCTCCGGGG AAAACGCGAGC CGCGATGCCCT GGGGGGTGCT CCCGGGGGCC CGCGCGCGGG 120
 GACGGGGCTC TCGGGCTGGC GCGACTAGCG CTGGTACTCC TGGGCTGGGT CTCCTCGTCT 180
 TCTCCCACTT CCTCGGCATC CTCTTCTCTC TCCTCGGCGC CGTTCCTGGC TTCGCGCGTG 240
 TCCGCCAGC CCCTGCTGCC GGACCACTGC CCGCGCTGTG GCGAGTGCTG CGAGGCAGCG 300
 CGCACAGTCA AGTGGCTTAA CCGCAATCTG ACCGAGGTGC CCACGCACTT GCCCGCTTAC 360
 GTGCGCAACC TCTTCTTAC CGGCAACCAG CTGGCCGTGC TCCTTGCCGG CGCCTTCGCC 420
 CGCCGGCCGC CGCTGGCGGA GCTGGCCGCG CTCAACCTCA GCGGCAGCGC CTGGACGAG 480
 GTGCGCGCGG GCGCCTTCGA GCATCTGCCC AGCCTGGGCC AGCTCGACCT CAGCCACAA 540
 CCACTGGCCG ACCTCTTCTT CTTGCGCTTC TCGGGCAGCA ATGCCAGCGT CTCGGCCCCC 600
 AGTCCCTCTG TGAACCTGAT CCTGAACCAC ATCGTGCCCC CTGAAGATGA GCGGCAGAAC 660
 CGAGGCTTCG AGGGCATGGT GGTGGCGGCC CTGCTGGCGG GCGGTGCACT CGAGGGGCTC 720
 CGCCGCTTGG AGCTGGCCAG CAACCACTTC CTTTACCTGC CGCGGGATGT GCTGGCCCAA 780
 CTGCCCACTC TCAGGCACCT GGACTTAAAT AATAATTCGC TGGTGAGCCT GACCTACGTG 840
 TCCCTCCGCA TCTGACACA TCTAGAAAGC CTCCACCTGG AGGACAAATG CCTCAAGGTC 900
 CTTCAATGCT GCACCCCTGGC TGAGTTGCAA GGTCTACCCC ACATTAGGGT TTTCTGGGAC 960
 AACCAATCCT GGTCTCGCA CTGCCACATG GCAGACATGG TGACCTGGCT CAAGGAAACA 1020
 GAGGTAGTGC AGGGCAAAGA CCGGCTCACC TGTGCATATC CGGAAAAAAT GAGGAATCGG 1080
 GTCCTCTTGG AACTCAACAG TGCTGACCTG GACTGTGACC CGATTCTTCC CCCATCCCTG 1140
 CAAAACCTCT ATGTCTTCTT TTAGCCTTGA TAGGCGCTAT TTTCTCTCTG 1200
 GTTTTGTATT TGAACCGCAA GGGGATAAAA AAGTGGATGC ATAACATCAG AGATGCCTGC 1260
 AGGGATCACA TGGAAAGGTA TCTTACAGA TATGAAATCA ATGCGGACCC CAGATTAACA 1320
 AACCTCAGTT CTAACCTGGA TGCTGAGAA ATATTAGAGG ACAGACCAAG GACAACTCTG 1380
 CATGAGATGT AGACTTAAGC TTTATCCCTA CTAGGCTTGC TCCACTTTCA TCCTCCACTA 1440
 TAGATACAAAC GGACTTTGAC TAAAAGCAGT GAAGGGGATT TGCTTCTCTG TTATGTAAAG 1500
 TTTCTCGGTG TGTCTCTTGA ATGTAAGACG ATGAACAGTT GTGTATAGTG TTTTACCCTC 1560
 TTTCTTTTCT TGGAACTCCT CAACACGTAT GGAGGGATT TTCAGGTTTC AGCATGAACA 1620
 TGGGCTTCTT GCTGTCTGTC TCTCTCTCAG TACAGTTCAA GGTGTAGCAA GTGTACCCAC 1680
 ACAGATAGCA TTCAACAAAA GCTGCCTCAA CTTTTCGAG AAAAATACTT TATTCATAAA 1740
 TATCAGTTT ATTCTCATGT ACCTAAGTTG TGGAGAAAAAT AATTGCATCC TATAAACTGC 1800
 CTGCAGACGT TAGCAGGCTC TTCAAATAAA CTCCATGGTG CACAGGAGCA CCTGCATCCA 1860
 AGAGCATGCT TACATTTTAC TGTCTGCAAT ATTACAAAAA ATAACCTGCA ACTTCATAAC 1920
 TTTCTTGACA AAGTAAATTA CTTTTTGTAT TGCAGTTTAT ATGAAATGT ACTGATTTT 1980
 TTTTAATAAA CTGCATCGAG ATCCAACCGA CTGAATTGTT AAAAAAATAA AAAAAATAAG 2040
 ATTCCTAAAA GAA

Seq ID NO: 405 Protein sequence
 Protein Accession #: NP_006661

1 11 21 31 41 51
 MPGGCSRGP AAGDRLRLAR LALLVLLGWVS SSSPTSSASS FSSSAPFLAS AVSAQPPLPD 60
 QCPALCBSE AARTVKCVNR NLTEVPTDLP AYVRNLFITG NQLAVLPAGA FARRPPLAEL 120
 AALNLSGRL DEVRAQFEH LPSLRQLDLS HNPLADLSPF AFSGSNASVS APSPLVELIL 180
 NHIVPFEDER QNRSFEGMVV AALLAGRALQ GLRRLELASN HFLYLPDRDL AQLPSLRHLD 240
 LSNNSLVSLT YVSPRNLTSL ESHLEDNAL KVLHNGTLAE LQGLPHIRVF LDNNPWVDC 300
 HMDMVTWLK ETEVVQKDR LTCAYPEKMR NRVLLELNSA DLDCDPLLP SLQTSYVFLP 360
 IVLALIGATF LLLVLYLNKRG IKKWMHNIRD ACRDHMEGYH YRYEINADPR LTNLSSNSDV

Seq ID NO: 406 DNA sequence
 Nucleic Acid Accession #: Eos sequence

Coding sequence: 1..927

5 1 11 21 31 41 51
 | | | | |
 ATGCCTGGGG GGTGCTCCCG GGGCCCCGCC GCCGGGGACG GGGCTCTGCG GCTGGCGCGA 60
 CTAGGCTGTGG TACTCTGTGG CTGGGTCTCC TCGTCTTCTC CCACCTCCTC GGCATCCTCC 120
 TTCTCCTCCT CGCGCCCGTT CCTGGCTTCC GCGGTGTCCG CCCAGCCCCC GCTGCCGGAC 180
 CAGTGCCCGG CGCTGTGCGA GTGCTCCGAG GCAGCGCGCA CAGTCAAGTG CGTTAACCGC 240
 AATCTGACCG AGGTGCCCCC GGACCTGCCC GCCTACGTGC GCAACCTCTT CCTTACCGGC 300
 10 AACCAAGCTGG CCAGCAACCA CTTCCTTTAC CTGCCCGGGG ATGTGCTGGC CCAACTGCCC 360
 AGCCTCAGGC ACCTGGACTT AAGTAATAAT TCGCTGGTGA GCCTGACCTA CGTGTCTTTC 420
 CGCAACCTGA CACATCTAGA AAGCCTCCAC CTGGAGGACA ATGCCCTCAA GGTCTTTCAC 480
 AATGGCACCC TGGCTGAGTT GCAAGGTCTA CCCACACATA GGGTTTCTCT GGACAACAAT 540
 CCCTGGGTCT CGACTGGCCA CATGGCAGAC ATGGTGACCT GGCTCAAGGA AACAGAGGTA 600
 15 GTGCAGGGCA AAGACCGGCT CACCTGTGCA TATCCGAAAA AAATGAGGAA TCGGGTCTTC 660
 TTGGAATCA ACAGTGTCTG CTGGACTGT GACCCGATTC TTCCCCATC CTGCAAAACC 720
 TCTTATGTCT TCCTGGGTAT TGTTTTAGCC CTGATAGGCG CTATTTTCTT CTGGTTTTCG 780
 TATTTGAACC GCAAGGGGAT AAAAAAGTGG ATGCATAACA TCAGAGATGC CTGCAGGGAT 840
 CACATGGAAG GGTATCATTA CAGATATGAA ATCAATGCGG ACCCCAGATT AACAAACCTC 900
 20 AGTTCTAACT CGGATGTCTT CGAGTGA

Seq ID NO: 407 Protein sequence
 Protein Accession #: Eos sequence

25 1 11 21 31 41 51
 | | | | |
 MPGGCSRGPA AGDGRRLRLAR LALVLLGWVS SSSPTSSASS FSSSAPFLAS AVSAQPPLPD 60
 QCPALCECSE AARTVKCVNR NLTEVPTDLF AYVRNLFITG NQLASNHFLY LPRDVLQQLP 120
 30 SLRHLDSLNN SLVSLTYVSP RNLTHLESLH LEDNALKVLH NGTLABELQL PHIRVFLDNN 180
 FWVDCDHMD MVTWLKETEV VQKDRILTCA YPEKMRNRVL LELNSADLDC DPILPPSLQT 240
 SYVFLGIIVLA LIGAILLLVL YLNKRGIKKW MNIRDAACRD HMEGYHYRYE INADPRLTNL 300
 SSNSDVL E

Seq ID NO: 408 DNA sequence
 Nucleic Acid Accession #: NM_000095.1
 Coding sequence: 26..2299

40 1 11 21 31 41 51
 | | | | |
 CAGCACCCAG CTCCCCGCCA CCGCCATGGT CCCCAGACCC GCCTGCGTTC TTCTGCTCAC 60
 CCTGGCTGCC CTGGGCGCGT CCGGACAGGG CCAGAGCCCG TTGGGCTCAG ACCTGGGCCC 120
 GCAGATGCTT CGGGAAGTGC AGGAAACCAA CGCGCGCGTG CAGGACGTGC GGGACTGGCT 180
 GCGGCAGCAG GTCAAGGAGA TCACGTTCTT GAAAAACACG GTGATGGAGT GTGACGCGTG 240
 45 CGGGATGCAG CAGTCAGTAC GCACCGCCTC ACCCAGCGTG CGGCCCTGTC TCCACTGCGC 300
 GCCCGGCTTC TGCTTCCCGG CGGTGCGCTG CATCCAGACG GAGAGCGGCG GCCGTGCGG 360
 CCCCTGCCCC CGCGGCTTCA CGGGCAACGG CTGCACTGTC ACCGACGTCA ACGAGTGCAA 420
 CGCCCAACCC TGCTTCCCGG GAGTCCGCTG TATCAACACC AGCCCGGGGT TCCGTGCGGA 480
 GGCTTGCCCG CGGGGTGACA CGCGCCAC CCACAGGGC GTGGGCTG GTTTCGCCAA 540
 50 GGCCAAACAG CAGGTTTGCA CGGACATCAA CGAGTGTGAG ACCGGGCAAC ATAAGTGCCT 600
 CCCCAACTCC GTGTGCATCA ACACCCGGGG CTCTTCCAG TGCGGCGCGT GCCAGCCCG 660
 CTTCTGGGGC GACCAAGCGT CGGGCTGCCA CGCGCGCGCA CAGCGCTTCT GCCCGACGG 720
 CTCGCCAGC GAGTGCACAG AGCATGCAGA CTGCGTCTTA GAGCGCGATG GCTCGCGGTC 780
 GTGCGTGTGT CGGTGTGGCT GGGCCGCGCA CGGGATCCTC TGTGGTGCAG ACACGTGACT 840
 55 AGACGGCTTC CCGGACGAGA AGCTCGCTG CCGGAGCCG CAGTGCCTGA AGGACAACCTG 900
 CGTGACTGTG CCCAACTCAG GGCAGGAGGA TGTGGACCGC GATGGCATCG GAGACGCTG 960
 CGATCCGAGT GCGGAGCGGG ACGGGGTCCC CAATGAAAAG GACAACTGCC CGCTGGTGC 1020
 GAACCCAGAC CAGCGCAACA CCGGACGAGG CAAGTGGGGC GATGCGTGC ACAAATGCCG 1080
 GTCCCAGAAG AACGACGACC AAAAGGACAC AGACCAAGAC GGCCGGGGCG ATGCGTGCAG 1140
 60 CGACGACATC GACCGGACCC GATCCGCAA CCAGGCCGAC AACTGCCCTA GGGTACCCAA 1200
 CTCAGACAG AAGGACAGTG ATGGCGATGG TATAGGGGAT GCCTGTGACA ACTGTCCCAA 1260
 GAAGAGCAAC CCGATCAGG CGGATGTGGA CCACGACTTT GTGGGAGATG CTTGTGACAG 1320
 CGATCAAGAC CAGGATGGAG ACGGACATCA GGAATCTCGG GACAACTGTC CCAAGGTGCC 1380
 TAACAGTGCC CAGGAGGACT CAGACACGTA TGGCCAGGGT GATGCGTGC ACGACGACGA 1440
 65 CGACAATGAC GGAATCCCTG ACAGTCGGGA CAACTGCCGC CTGGTGCCTA ACCCGGCCA 1500
 GGAGGACCGG GACAGGACG CGGTGGCGCA CGTGTGCCAG GACGACTTTG ATGCAGACAA 1560
 GGTGGTAGAC AAGATCGAGC TGTGTCCGGA GAACGCTGAA GTCACGCTCA CCGACTTCAG 1620
 GGCCTTCCAG ACAGTCTGTC TGGACCCGGA GGGTGACGCG CAGATTGACC CCAACTGGGT 1680
 GGTGCTCAAC CAGGGAAGGG AGATCGTGCA GACAATGAAC AGCGACCCAG GCCTGGCTGT 1740
 70 GGGTTACACT GCCTTCAATG GCGTGGACTT CGAGGGCACG TTCCATGTGA ACACGGTCAC 1800
 GATGACGAC TATGCGGGCT TCATCTTTGG CTACCAAGAC AGCTCCAGCT TCTACGTGGT 1860
 CATGTGGAAG CAGATGGAGC AAACGTATTG GCAGGCGAAC CCCTTCCGTG CTGTGGCCGA 1920
 GCCTGGCATC CAACTCAAGG CTGTGAAGTC TTCCACAGGC CCGGGGGAAC AGCTGCGGAA 1980
 CGCTCTGTGC CATACAGGAG ACACAGAGTC CCAGGTGCGG CTGCTGTGGA AGGACCCGCG 2040
 75 AAACGTGGGT TGGAAAGGACA AGAAGTCCTA TCGTTGGTTC CTGCAGCACC GGCCCCAAGT 2100
 GGGCTACATC AGGGTGCAT TCTATGAGGG CCCTGAGCTG GTGGCCGACA GCAACGTGGT 2160
 CTTGGACACA ACCATGCGGG GTGGCCGCTT GGGGGTCTTC TGCTTCTCCC AGGAGAACAT 2220
 CATCTGGGCG AACCTGCGTT ACCGCTGCAA TGACACCATC CCAGAGGACT ATGAGACCCA 2280
 TCAGCTGCGG CAGGCTTAGG GACCAAGGTG AGGACCCGCG GGATGACAGC CACCTCACC 2340
 80 GCGGCTGGAT GGGGGCTCTG CACCCAGCCC AAGGGGTGGC CGTCTGAGG GGGAGTGAG 2400
 AAGGGCTCAG AGAGGACAAA ATAAAGTGTG TGTGCAGGG

Seq ID NO: 409 Protein sequence
 Protein Accession #: NP_000086.1

85 1 11 21 31 41 51
 | | | | |
 MVPDTACVLL LTALALGASG QGQSPLGSDL GPQMLRELQE TNAALQDVDR WLRQQVREIT 60

WO 02/086443

PCT/US02/12476

FLKNTVMECD ACNQMQSVRT GLPSVRPLLH CAPGFCFPGV ACIQTESGGR CGPCPAGFTG 120
 NGSHCTDVNE CNAHPCFPRV RCINTSPGFR CEACFPFGYSG PTHQGVGLAF AKANKQVCTD 180
 INECETGQHN CVPNSVCINT RGSFQCGPCQ PGFVGDQASG CQRGAQRFCP DGSPSECEH 240
 5 ADCVLERDGS RSCVCRVGWA GNGILCGRDT DLDGFFDEKL RCPEPQCRKD NCVTVPNSGQ 300
 EDVDRDGIAD ACDDPADGDDG VPNEKDNCPV VRNPQQRNTD EDKWDGACDN CRSQKNDQK 360
 DTDQDGRGDA CDDIDIDRI RNQADNCPRV PMSDQKDSBG DGIQDADCN PQKSNPDQAD 420
 VDHDVFGDAC DSDQDQDGDG HQDSRDNCPT VPNSAQEDSD HDGQGDACDD DDDNDGVFDS 480
 RDNCLRLVNP GQEDADRDGV GDVCQDDFDA DKVVDKIDVC PENAETVLT D FRAFTVVL D 540
 10 PEGDAQIDPN WVLNQGREGI VQTMNSDPGL AVGYTAFNGV DFEGTFHVNT VTDDDYAGFI 600
 FGQDSSSFY VVMWQMEQT YWQANPFRV AEPGILQKAV KSSTGPGQEL RNALWHTGDT 660
 ESQVRLWKD PRNVGWKK SYRNFLQHRF QVGYIRVRFY EGPELVADSN VVLDTTMRGG 720
 RLGVPFCFSQE NIIWANLRYR CNDTIPEDYE THQLRQA

Seq ID NO: 410 DNA sequence
 Nucleic Acid Accession #: NM_001565.1
 Coding sequence: 67..363

1 11 21 31 41 51
 20 | GAGACATTCC TCAATTGCTT AGACATATTC TGAGCCTACA GCAGAGGAAC CTCCAGTCTC 60
 AGCACCATGA ATCAAACTGC GATTCTGATT TGCTGCCTTA TCTTTCTGAC TCTAAGTGSC 120
 ATTCAGGAG TACCTCTCTC TAGAACCGTA CGCTGTACCT GCATCAGCAT TAGTAATCAA 180
 CCGTGTAAATC CAAGGTCTTT AGAAAACTT GAAATTATTC CTGCAAGCCA ATTTTGTCCA 240
 25 COTGTTGAGA TCATTGCTAC AATGAAAAAG AAGGGTGAGA AGAGATGTCT GAATCCAGAA 300
 TCGAAGGCCA TCAAGAATTT ACTGAAAGCA GTTAGCAAGG AAATGTCTAA AAGATCTCCT 360
 TAAACCCAGA GGGAGGCAAA ATCGATGCAG TGCTTCCAAAG GATGGACCAC ACAGAGGCTG 420
 CCTCTCCCAT CACTTCCCTA CATGGAGTAT ATGTCAAGCC ATAATTGTTC TTAGTTTGCA 480
 GTTACACTAA AAGGTGACCA ATGATGGTCA CCAATCAGC TGCTACTACT CCTGTAGGAA 540
 30 GGTAAATGTT CATCATCTTA AGCTATTGAG TAATAACTCT ACCCTGGCAC TATAATGTAA 600
 GCTCTACTGA GGTGCTATGT TCTTAGTGGA TGTTCGACCT CTGCTTCAA TATTTCCCTC 660
 ACCTTTCCCA TCTTCCAAAG GTACTAAGGA ATCTTTCTGC TTTGGGGTTT ATCAGAAATC 720
 TCAGAAATCTC AAATAACTAA AAGGTATGCA ATCAAACTCT CTTTTTAAAG AATGCTCTTT 780
 ACTTCATGGA CTTCCACTGC CATCCTCCCA AGGGGCCCAA ATTCTTTTCA TGGCTACCTA 840
 35 CATACAATTC CAAACACATA CAGGAAGGTA GAAATATCTG AAAATGTATG TGAAGTATT 900
 CTTATTTAAT GAAAGACTGT ACAAAGTATA AGTCTTAGAT GTATATATT CCTATATTGT 960
 TTTCAAGTGA CATGGAATTA CATGTAATTA AGTACTATGT ATCAATGAGT AACAGGAAAA 1020
 TTTTAAAAAT ACAGATAGAT ATATGCTCTG CATGTTACAT AAGATAAATG TGCTGAATGG 1080
 TTTTCAATA AAAATGAGGT ACTCTCTCG AAATATTAAAG

Seq ID NO: 411 Protein sequence
 Protein Accession #: NP_001556.1

1 11 21 31 41 51
 45 | MNQTALICCC LIPLTLGSIQ GVPLSRTVRC TCISISNQPV NPRSLEKLEI IPASQFCPRV 60
 EIIATMKKKG EKRCNLPESK AIKNLLKAVS KEMSKRSP

Seq ID NO: 412 DNA sequence
 Nucleic Acid Accession #: XM_057014
 Coding sequence: 143..874

1 11 21 31 41 51
 55 | GGGAGGGAGA GAGGCGGCGG GGTGAAAGGC GCATTGATGC AGCCTGCGGC GGCCTCGGAG 60
 CGCGGCGGAG CCAGACGCTG ACCACGTTCC TCTCCTCGGT CTCCTCGGC TCCAGCTCCG 120
 CGCTGCCCCG CAGCCGGGAG CCATGCGACC CCAGGGCCCC GCGGCTCCC CGCAGCGGCT 180
 CGCGGCGCTC CTGCTGCTCC TGCTGCTGCA GCTGCCCCGG CCGTCGAGCG CCTCTGAGAT 240
 CCCCAGGGGG AAGCAAAAGG CGCAGCTCCG GCAGAGGGAG GTTGTGGGACC TGTATAATGG 300
 60 AATGTGCTTA CAAGGGGCGG CAGGAGTGCC TGGTCGAGAC GGGAGCCCTG GGGCCAATGG 360
 CATTCGGGTG ACACCTGGGA TCCAGGTCG GGAATGGATC AAAGGAGAAA AGGGGGAATG 420
 TCTGAGGGAA AGCTTTGAGG AGTCTGGGAC ACCCAACTAC AAGCAGTGTT CATGGAGTTC 480
 ATTGAATTAT GGCATAGATC TTGGGAAAAT TGCGGAGTGT ACATTTACAA AGATGCGTTC 540
 AAATAGTGCT CTAAGAGTTT TGTTCAGTGG CTCACTTCGG CTAAATGCA GAAATGCAATG 600
 CTGTGAGCGT TGGTATTTC CAATCAATGG AGCTGAATGT TCAGGACCTC TTCCCATTTGA 660
 65 AGCTATAATT TATTTGGACC AAGGAAGCCC TGAAATGAAT TCAACAATTA ATATTCAATG 720
 CACTTCTTCT GTGGAAGGAC TTTGTGAAGG AATTGGTGCT GGATTAGTGG ATGTTGCTAT 780
 CTGGGTTGGC ACTTGTTCAG ATTACCCAAA AGGAGATGCT TCTACTGGAT GGAATTCAGT 840
 TTCTCGATC ATTATTGAAG AACTACCAAA ATAAATGCTT TAATTTTCAT TTGCTACCTC 900
 70 TTTTATTATT ATGCTTGGGA ATGGTTCACT TAAATGACAT TTTAAATAAG TTTATGTATA 960
 CATCTGAATG AAAAGCAAAG CTAAATATGT TTACAGACCA AAGTGTGATT TCACACTGTT 1020
 TTTAAATCTA GCATTATTCA TTTTGCTTCA ATCAAAAGTG GTTTCATAT TTTTCTTAGT 1080
 TGGTTAGAAT ACTTCTTCTA TAGTCACATT CTCTCAACCT ATAATTGGA ATATTGTGTT 1140
 GGTCTTTTGT TTTTCTCTT AGTATAGCAT TTTTAAAAAA ATATAAAGC TACCAATCTT 1200
 75 GTACCAATTT GTAAATGTTA AGAATTTTTT TTATATCTGT TAAATAAAAA TTATTCCCAA 1260
 CAACCTTAAA AAAAAA AAAA

Seq ID NO: 413 Protein sequence
 Protein Accession #: XP_057014

1 11 21 31 41 51
 80 | MRPQGPAAFP QRLRGLLLLL LLQLPAPSSA SEIPKQKQKA QLRQREVVDL YNGMCLQGPA 60
 GVPGRDGSFG ANGIPGTPGI PGRDGPKEK GECLRESFEE SWTPNYKQCS WSSLNYGIDL 120
 GKIAECTPTK MRSNSALRLV FSGSLRLKCR NACCQRWYFT FNGAECSSGPL PIEAIYLDQ 180
 85 GSPENMNSTIN IHRSSVEGL CEGIGAGLVD VAIWVGTCSD YPKGDASTGW NSVSRIITE 240
 LPK

WO 02/086443

Seq ID NO: 414 DNA sequence
Nucleic Acid Accession #: XM_084007
Coding sequence: 138..2405

PCT/US02/12476

```

5      1      11      21      31      41      51
      |      |      |      |      |      |
      CTCGTGCCGA ATTCGGCAGC AGACCGCGTG TTCGCGCCTG GTAGAGATTG CTCGAAGACA      60
      CCAGTGGGCC CGTGTGGAA CAAACCTGCG CGCGTGGCCG GGCCGTGGGA CAACGAGGCC      120
      GCGGAGACGA AGGCGCAATG GCGAGGAAGT TATCTGTAAT CTTGATCCTG ACCTTTGGCC      180
10     TCTCTGTAC AAATCCCTT CATGAACATA AAGCAGCTGC TTTCCCCCAG ACCACTGAGA      240
      AAATTAGTCC GAATTGGGAA TCTGGCAITTA ATGTTGACTT GGCAATTTCC ACACGGCAAT      300
      ATCATCTACA ACAGCTTTTC TACCGCTATG GAGAAAAATA TTCTTTGTCA GTTGAAGGGT      360
      TCAGAAAATT ACTTCAAAAT ATAGGCATAG ATAAGATTAA AAGAATCCAT ATACACCATG      420
      ACCACGACCA TCACTCAGAC CACGAGCATC ACTCAGACCA TGAGCGTCAC TCAGACCATG      480
15     AGCATCACTC AGACCAAGAG CATCACTCTG ACCATGATCA TCACTCCCAC CATAATCATG      540
      CTGCTTCTGG TAAAAATAAG CGAAAAGCTC TTTGCCCAGA CCAATGACTC GATAGTTTCA      600
      GTAAAGATCC TAGAAACAGC CAGGGGAAAG GAGCTCACCG ACCAGAACAT GCCAGTGGTA      660
      GAAGGAATGT CAAGGACAGT GTTAGTGCTA GTGAAGTGAC CTCAACTGTG TACAACACTG      720
      TCTCTGAAGG AACTCACTTT CTAGAGACAA TAGAGACTCC AAGACCTGGA AAACCTCTCC      780
20     CCAAGATGTG AAGCAGCTCC ACTCCACCCA GTGTCACATC AAAGAGCCCG GTGAGCCCGC      840
      TGGCTGGTGA GAAACCAAAAT GAATCTGTGA GTGAGCCCGG AAAAGGCTTT ATGATTTCOA      900
      GAAACACAAA TGAATACTCT CAGGAGTGTG TCAATGCATC AAAGCTACTG ACATCTCATG      960
      GCATGGGCAT CAGGATCTCG CTGAATGCAA CAGAGTTCAA CTATCTCTGT CCAGCCATCA      1020
      TCAACCAAAAT TGATGCTAGA TCTTGTCTGA TTCATACAAG TGAAGAAGAG GCTGAAATCC      1080
25     CTCCAAAGAC CTATTCATTA CAAATAGCCT GGGTTGGTGG TTTTATAGCC ATTTCCATCA      1140
      TCAGTTTCTT GTCTCTGCTG GGGGTTATCT TAGTGCCCTC CATGAATCGG GTGTTTTTCA      1200
      AATTTCTCTT GAGTTTCTCT GTGGCACTGG CCGTTGGGAC TTTGAGTGTG GATGCTTTT      1260
      TACACCTTCT TCACATTTCT CATGCAAGTC ACCACCATAG TCATAGCCAT GAAGAACAG      1320
      CAATGGAAAT GAAAGAGGGA CCACTTTTCA GTCATCTGTC TTCTCAAAAC ATAGAAGAAA      1380
30     GTGCCATATT TGATTCACAG TGAAGGGTTC TAACAGCTCT AGGAGGCCCTG TATTTTCAAT      1440
      TTCTTGTGTA ACATGCTCTC ACATTGATCA AACAATTTAA AGATAAGAAG AAAAAGAATC      1500
      AGAAGAAACG TGAATAATGAT GATGATGTGG AGATAAGAA GCAAGTTGTC AAGTATGAAT      1560
      CTCAACTTTC AACAAATGAG GAGAAAGTAG ATACAGATGA TCGAACTGAA GGTATTTTAC      1620
      GAGCAGACTC ACAAGAGCCC TCCCACTTTG ATTCTCAGCA GCCTGCAATC TTGGAAGAAG      1680
35     AAGAGGTGAT GATAGTCTAT GCTCATCCAC AGGAAGTCTA CAATGAATAT GTACCCAGAG      1740
      GGTGCAAGAA TAAATGCCAT TCACATTTCC ACGATACACT CGGCCAGTCA GACGATCTCA      1800
      TTCACACCCA TCATGACTAC CATCATATTC TCCATCATCA CCACCAACCA AACCAACATC      1860
      CTCACAGTCA CAGCAGCTGC TACTCTCGGG AGGAGCTGAA AGATGCCCGC GTGCGCACTT      1920
      TGGCCTGATG GGTGATTAAT GGTGATGGCC TGCACAAATT CAGCGATGGC CTAGCAATTT      1980
40     GTGCTGCTTT TACTGAAGGC TTATCAAGTG GTTTAAGTAC TTCTGTTGCT GTGTTCTGTC      2040
      ATGAGTTGCC TCATGAATTA GGTGACTTTG CTGTTCTACT AAAGGCTGGC ATGACCGTTA      2100
      AGCAGGCTGT CCTTTATAAT GCATTTGTCAG CCATGCTGGC GTATCTTGGA ATGGCAACAG      2160
      GAATTTTCAT TGGTCATTAT TGTGAAAAATG TTTCTATGTG GATATTGCA CTTACTGCTG      2220
      GCTTATTCAT GTATGTTGCT CTGGTTGATA TGGTACCTGA AATGCTGCAC AATGATGCTA      2280
45     GTGACCATGG ATGTAGCCGC TGGGGGTATT TCTTTTTTACA GAATGCTGGG ATGCTTTTGG      2340
      GTTTTGGAAAT TATGTTACTT ATTTCCATAT TGAACATAA AATCGTGTGT CGTATAAAT      2400
      TCTAGTTAAG GTTTAAATGC TAGAGTAGCT TAAAAAGTTG TCATAGTTTC AGTAGGTCAT      2460
      AGGAGATGTA GTTTGATATG GTTACTATGC AGCGTTTAAA GTTAGTGGGT TTTGTGATT      2520
      TGTATTGAA TATTGCTGTC TGTACAAAG TCAGTTAAAG GTACGTTTAA ATATTAAAT      2580
50     TATTCTATCT TGGAGATAAA ATCTGTATGT GCAATTCAAC GGTATTACCA GTTTATTATG      2640
      TAAACAAGAG ATTTGGCATG ACATGTTCTG TATGTTTCAG GGAATAATGT CTTTAATGCT      2700
      TTTTCAAGAA CTAACACAGT TATTCCTATA CTGGATTTTA GGTCCTGTA GAACTGTCTG      2760
      TGTTTAGGAA TAAAGATGTG CATGAAGCCT AAAATACCAA GAAAGCTTAT ACTGAATTTA      2820
      AGCAAGAAAG TAAAGAGGAA AAGAGAGGAA TCTGAGAAAT GGGGAGGCAT AGATTCTTAT      2880
55     AAAAATCACA AAATTTGTG TAAATTAGAG GGGAGAAATT TAGAATTAAG TATAAAAGG      2940
      CAGAATTAGT ATAGAGTACA TTCATTAAAC ATTTTGTGCA GGATTATTTC CCGTAAAAAC      3000
      GTAGTGAGCA CTCTCATATA CTAATTAGTG TACATTTAAC TTTGTATAAT ACAGAAATCT      3060
      AAATATATT AAATGAATTC AGCAATATAC ACTTGACCAA GAAATTGGAA TTTCAAAATG      3120
      TTCGTGCGGG TTAATATACA GATGAGTACA GTGAGTAGTT TATGATCAC CAGACTGGGT      3180
60     TATTGCCAAG TTATATATCA CCAAAAGCTG TATGACTGGA TGTCTGGTT ACCTGGTTTA      3240
      CAAAATTATC AGAGTAGTAA AACTTTGATA TATATGAGGA TATTAACACT ACACTAAGTA      3300
      TCATTTGATT CGATTTCAGAA AGTACTTTGA TATCTCTCAG TGCTTCAGTG CTATCATTTG      3360
      GAGCAATTGT CTTTATATAC GGTACTGTAG CCATACTAGG CCTGCTGTG GCATTCTCTA      3420
65     GATGTTTCTT TTTTACACAA TAAATTCCTT ATATCAGCTT G

```

Seq ID NO: 415 Protein sequence
Protein Accession #: XP_084007

```

70     1      11      21      31      41      51
      |      |      |      |      |      |
      MARKLSVILI LTFALSVTNP LHELKAAAFP QTTEKISFNW ESGINVDLAI STRQYHLQOL      60
      FYRYGENNSL SVEGFRKLLQ NIGIDKIKRI HIHHDHSHS DHEHHSDBER HSDHEHSDH      120
      EHHSDHSHS HHNHAASGKN KRKALCPDHD SDSSGKDFRN SQKGGAHRPE HASGRNRVKD      180
75     SVSASEVTST VYNTVSEGTH FLETIETPRP GKLPFKDVSS STPPSVTSKS RVSRLAGRKT      240
      NESVSEPRKG FMYSRNTNEN PQECFNASKL LSHGMGIQV PLNATEFNVL CPAIINQIDA      300
      RSCLHTSEK KAEIPPKTVS LQIAWVGFI AISIISFLSL LGVILVPLMN RVFFKFLSLF      360
      LVALAVGTLS GDAFLHLLPH LTLIKQFKDK KKKNQKKPEN DDDVEIKXQL SKYESQLSTN      420
      TWKGLTALGG LYFMFLVEHV LTLIKQFKDK KKKNQKKPEN DDDVEIKXQL SKYESQLSTN      480
      EEKVDTDDRT EGYLRADSQE PSHFDSQQPA VLEEEVEMIA HAHPQEVYNE YVPRGCKNVI      540
80     HSHFDHDLGQ SDLIHSHHSH YHHILHSHSH QNHHPHSHSQ RYSREELKDA GVATLAWMVI      600
      MGDGLHNFSD GLAIGAAFTS GLSSGLSTSV AVFCHLEPHE LGDFAVLLKA GMTVQAVLY      660
      NALSAMLAYL GMATGIFIGH YAEVSMWIF ALTAGLFMYV ALVDMVPEML HNDASDHGCS      720
      RWGYFFLQNA GMLLGFGLML LISIFEKIV PRINP

```

Seq ID NO: 416 DNA sequence
Nucleic Acid Accession #: NM_015419.1
Coding sequence: 1..8487

	1	11	21	31	41	51	
5	ATGCCCAAGC	GCGCGCACTG	GGGGGCCCTC	TCCGTGGTGC	TGATCCTGCT	TTGGGGCCAT	60
	CCGCGAGTGG	CGCTGGCCTG	CCCGCATCCT	TGTGCTCTGT	ACGTCCCCAG	CGAGGTCCAC	120
	TGCACGTTCC	GATCCCTGGC	TTCCGTGCCC	GCTGGCATTTG	CTAGACACGT	GGAAAGAAATC	180
	AATTTGGGGT	TTAATAGCAT	ACAGGCCCTG	TCAGAAACCT	CATTTCGAGG	ACTGACCAAG	240
	TTGGAGCTAC	TTATGATTCA	CGGCAATGAG	ATCCCCAGCA	TCCCCGATGG	AGCTTTAAGA	300
10	GACCTCAGCT	CTCTTCAGGT	TTTCAAGTTC	AGCTACAACA	AGCTGAGAGT	GATCACAGGA	360
	CAGACCCCTC	AGGGTCTCTC	TAACTTAATG	AGGCTGCACA	TTGACCAACA	CAAGATCGAG	420
	TTTATCCACC	CTCAAGCTTT	CAACGGCTTA	ACGTCTCTGA	GGCTACTCCA	TTTGGAAGGA	480
	AATCTCCTCC	ACCAGCTGCA	CCCCAGCACC	TTCTCCACGT	TCACATTTTT	GGATTATTTT	540
	AGACTCTCCA	CCATAAGGCA	CCTCTACTTA	GCAGAGAACA	TGGTTAGAAC	TCTTCTCTCC	600
	AGCATGCTTC	GGAACTGCCC	GCTTCTGGAG	AATCTTTACT	TGCAGGGAAA	TCCGTGGACC	660
15	TGCGATTGTG	AGATGAGATG	GTTTTTGGAA	TGGGATGCAA	AATCCAGAGG	AATTCTGAAG	720
	TGTA AAAAGG	ACAAAGCTTA	TGAAGGCGGT	CAGTTGTGTG	CAATGTGCTT	CAGTCCAAAG	780
	AAGTTGTACA	AACATGAGAT	ACACAAGCTG	AAGGACATGA	CTTGTCTGAA	GCCTTCAATA	840
	GAGTCCCCTC	TGAGACAGAA	CAGGAGCAGG	AGTATTGAGG	AGGAGCAAGA	ACAGGAAGAG	900
20	GATGGTGGCA	CCAGCTCATG	CCTGGAGAAA	TTCCAACCTG	CCCAGTGGAG	CATCTCTTTG	960
	AATATGACCG	ACGAGCACGG	GAACATGGTG	AACCTGGTCT	GTGACATCAA	GAACCAATG	1020
	GATGTGTACA	AGATTCACTT	GAACCAACG	GATCCTCCAG	ATATTGACAT	AAATGCAACA	1080
	GTTGCTTGG	ACTTTGAGTG	TCCAATGACC	CGAGAAAAC	ATGAAAAGCT	ATGAAAATTG	1140
	ATAGCATACT	ACAGTGAAGT	TCCCGTGAAG	CTACACAGAG	AGCTCATGCT	CAGCAAAAGC	1200
25	CCAGAGTCA	GCTACCAAGT	CAGGCAGGAT	GCTGATGAGG	AAGCTCTTTA	CTACACAGGT	1260
	GTGAGAGCCC	AGATTCTTGC	AGAACCAGAA	TGGGTCTATC	AGCCATCCAT	AGATATCCAG	1320
	CTGAACCGAC	GTCAAGTATC	GGCCAAGAAG	GTGCTACTTT	CCTACTACAC	CCAGTATTCT	1380
	CAAAACAATAT	CCACCAAGA	TACAAGGCAG	GCTCGGGGCA	GAAGCTGGGT	AATGATTGAG	1440
	CCTAGTGGAG	CTGTGCAAG	AGATCAGACT	GTCCCTGGAAG	GGGGTCCATG	CCAGTTGAGC	1500
30	TGCAACGTGA	AAGCTTCTGA	GAGTCCATCT	ATCTTCTGGG	TGCTTCCAGA	TGGCTCCCAT	1560
	CTGAAGGCGC	CCATGGATGA	CCCAGACAGC	AAGTTCTCCA	TTCTCAGCAG	TGGCTGGCTG	1620
	AGGATCAAGT	CCATGGAGCC	ATCTGACTCA	GGCTTGTACC	AGTGCATTGC	TCAAGTGAGG	1680
	GATGAAAATG	ACCGCATGGT	ATATAGGGTA	CTTGTGCAGT	CTCCCTCCAC	TCAGCCAGCC	1740
	GAGAAAGACA	CAGTGACAA	TGGCAAGAAC	CCAGGGGAGT	CGGTGACATT	GCCTTGCAAT	1800
35	GCTTTAGCAA	TGCCCGAAGC	CCACCTTAGC	TGGATTCTTC	CAACAGAAAG	GATAATTAAT	1860
	GATTTGGGTA	ACACATCACA	TGTATACATG	TTGCCAAATG	GAATCTTTTC	CATCCCAAAG	1920
	GTCCAAGTCA	GTGATAGTGG	TTACTACAGA	TGTGTGGCTG	TCAACCAGCA	AGGGGCAGAC	1980
	CATTTTACGG	TGGGAATCAC	AGTGACCAAG	AAAGGGTCTG	GCTTGCCATC	CAAAAGAGGC	2040
40	AGACGCCAG	GTGCAAGGCG	TCTTTCAGCA	GTCAAGAGAAG	ACATCGTGGG	GGATGAAGGG	2100
	GGCTCGGGCA	TGGGAGATGA	AGAGAACACT	TCAAGGAGAC	TTCTGCATCC	AAAGGACCAA	2160
	GAGGTGTTCC	TCAAAACAAA	GGATGATGCC	ATCAATGGAG	ACAAGAAAGC	CAAGAAAGGG	2220
	AGAAGAAAGC	TGAAGCTCTG	GAAGCATTCG	GAAGAAAGAA	CAGAGACCAA	TGTTGCAGAA	2280
	GGTCGCAGAG	TGTTTGAATC	TAGACGAAGG	ATAAACATGG	CAACCAACA	GATTAATCCG	2340
	GAGCGCTGGG	CTGATATTTT	AGCCAAAGTC	CGTGGGAAAA	ATCTCCCTAA	GGGCACAGAA	2400
45	GTACCCCGGT	TGATTAAAC	CACAAGTCTC	CCATCCTTGA	GCCTAGAAGT	CACACCACCT	2460
	TTTCTGCTG	TTTCTCCCCC	CTCAGCATCT	CCTGTGCAGA	CAGTAACCAAG	TGCTGAAGAA	2520
	TCTCAGCAG	ATGTTGGTGA	GAAGAGCAGG	TTTTGGGTAC	CATTTCCTCA	2580	
	GCCAGCATGG	GGCTAGAACA	CAACCACAAT	GGAGTTATTC	TTGTTGAACC	TGAAGTAACA	2640
	AGCACACCTC	TGGAGGAAGT	TGTTGATGAC	CTTTCGAGA	AGACTGAGGA	GATACTTCC	2700
50	ACTGAAGGAG	ACCTGAAGGG	GACAGCAGCC	CTACACTTA	TATCTGAGCC	TTATGAACCA	2760
	TCTCTACTC	TGCACACATT	AGACACAGTC	TATGAAAAGC	CCACCCATGA	AGAGACGGCA	2820
	ACAGAGGGTT	GGCTCGAGC	AGATGTTGGA	TGCTCACCAG	AGCCACATC	CAGTGAGTAT	2880
	GAGCCTCCAT	TGGATGCTGT	CTCCTTGGCT	GAGTCTGAGC	CCATGCAATA	CTTTGACCCA	2940
	GATTTGGAGA	CTAAGTCACA	ACCAGATGAG	GATAAGATGA	AAGAAGACAC	CTTTGCACAC	3000
55	CTTACTCCAA	CCCCCACCAT	CTGGGTAAAT	GACTCCAGTA	CATCACAGTT	ATTTGAGGAT	3060
	TCTACTATAG	GGGAACAGAG	TGTCCCAGGC	CAATCACATC	TACAAGGACT	GACAGACAAC	3120
	ATCCACCTTG	TGAAAAGTAG	TCTAAGCACT	CAAGACACCT	TACTGATTAA	AAAGGGTATG	3180
	AAAGAGATGT	CTCAGACACT	ACAGGGAGGA	AAATGCTAG	AGGGAGACCC	CACACACTCC	3240
	AGAAGTTCTG	TGAAAAGTGG	CCAGAGAGGC	AAATCCATCA	CTTTGCCCTGA	CTCCACACTG	3300
60	GGTATAATGA	GCAGTATGTC	TCCAGTTAAG	AAGCCTGCGG	AAACCAAGT	TGGTACCCTC	3360
	CTAGACAAG	ACACCACAAC	AGTAACAACA	ACACCAAGGC	AAAAAGTTGC	TCCGTCACTC	3420
	ACCATGAGCA	CTACCCCTTC	TGCAAGGAGA	CCCAACGGGA	GAAGGAGATT	ACGCCCAAC	3480
	AAATTCGCC	ACCGGCACAA	GCAAAACCCA	CCCAACAATT	TTGCCCATC	AGAGACTTTT	3540
	TCTACTCAAC	CAACTCAAGC	ACCTGACATT	AAGATTTCAA	GTCAAGTGGA	GAGTTCTCTG	3600
65	GTTCTCTACG	CTTGGGTGGA	TAACACAGTT	AATACCCCA	AACAGTTGGA	AATGGAGAAG	3660
	AATGCAGAAC	CCACATCCAA	GGGAACACCA	CGGAGAAAAC	ACGGGAAGAG	GCCAAACAAA	3720
	CATCGATATA	CCCCTTCTAC	AGTGAGCTCA	AGAGCGTCCG	GATCCAAAGC	CAGCCCTTCT	3780
	CCAGAAAATA	AACATAGAAA	CATTGTTACT	CCCAGTTAG	AAACTATACT	TTTGCTTAGA	3840
	ACTGTTTCTC	TGAAAAGTGA	GGGCCCTTAT	GATTCCCTAG	ATTACATGAC	AACCAACAGA	3900
70	AAAATATATT	CATCTTACCC	TAAAGTCCAA	GAGACACTTC	CAGTCACATA	TAAACCCACA	3960
	TCAGATGGAA	AAGAAATTAA	GGATGATGTT	GCCACAAATG	TTGACAAACA	TAAAAGTGAC	4020
	ATTTTAGTCA	CTGGTGAATC	AATTACTAAT	GCCATACCAA	CTTCTCGCTC	CTTGGTCTCC	4080
	ACTATGGGAG	AATTTAAGGA	AGAATCCTCT	CCTGTAGGCT	TTCCAGGAAC	TCCAACCTGG	4140
75	AATCCCTCAA	GGAGCGGCCA	GCTTGGGAGG	CTACAGACAG	ACATACCTGT	TACCACTTCT	4200
	GGGGAAAATC	TTACAGACCC	TCCCTTCTT	AAAGAGCTTG	AGGATGTGGA	TTTCACTTCC	4260
	GAGTTTTTGT	CCTCTTTGAC	AGTCTCCACA	CCATTTCACC	AGGAAGAAGC	TGGTTCTTCC	4320
	CAACTCTCT	CAAGCATAAA	AGTGGAGGTG	GCTTCAAGTC	AGGCAGAAAC	CACCACCTTT	4380
	GATCAAGATC	ATCTTGAAG	CACGTGTGGT	ATTCTCCTTT	CTGAAACTAG	ACCACAGAAT	4440
	CACACCCCTA	CTGCTGCCCG	GATGAAGGAG	CCAGCATCCT	CGTCCCCATC	CACAAATCTC	4500
80	ATGTCTTTGG	GACAAACAC	CACCACTAAG	CCAGCACTTC	CCAGTCCAAG	AATATCTCAA	4560
	GCATCTAGAG	ATTCCAAGGA	AAATGTTTTC	TTGAATTATG	TGGGGAATCC	AGAAACAGAA	4620
	GCAACCCAG	TCAACAATGA	AGGAACACAG	CATATGTCAG	GGCCAAATGA	ATTATCAACA	4680
	CCCTCTTCCG	ACCGGGATGC	ATTTAACCTG	TCTACAAGAG	TGGAATTGGA	AAAGCAAGTA	4740
	TTTGGTAGTA	AGAGCTTACG	ACGTGGGCCA	GATAGCCAAC	GCCAGGATGG	AAGAGTTCTAT	4800
	GCTTCTCATC	AACTAACAG	AGTCCCTGCC	AAACCCATCC	TACCAACAGC	AACAGTGAGG	4860
85	CTACCTGAAA	TGTCACACA	AAGCGCTTCC	AGATACTTTC	TAACCTCCCA	GTCACTCTGT	4920
	CACCTGGACCA	ACAAACCGGA	AATAACTACA	TATCCTTCTG	GGGCTTTGCC	AGAGAACAAA	4980
	CAGTTTACAA	CTCCAAGATT	ATCAAGTACA	ACAATTCTCT	TCCCATTTGCA	CATGTCCAAA	5040

	CCCAGCATT	CTAGTAAGTT	TACTGACCGA	AGAACTGACC	AATTCATATGG	TTACTCCAAA	5100
	GTGTTTGGAA	ATAACAACAT	CCCTGAGGCA	AGAAACCCAG	TTGGAAAGCC	TCCCAGTCCA	5160
	AGAATTCTCT	ATTATTCCAA	TGGAGAGACT	CCTTCTTTTA	CCAACAAGAC	TCTTTCTTTT	5220
5	CCACAGTTGG	GAGTCACCCG	GAGACCCAG	ATACCCACTT	CTCCTGCCCC	AGTAATGAGA	5280
	GAGAGAAAAG	TTATTCACAG	TTCTTACAAC	AGGATACATT	CCCATAGCAC	CTTCCATCTG	5340
	GACTTTGGCC	CTCCGGCACC	TCCGTTGTTG	CACACTCCGC	AGACCAAGGG	ATCACCCCTCA	5400
	ACTAATTAC	AGAATATCCC	TATGGTCTCT	TCCACCCAGA	GTTCATCTCT	CTTTATAACA	5460
	TCTTCTGTCC	AGTCCTCAGG	AAGCTTCCAC	CAGAGCAGCT	CAAAGTTCCT	TGCAGGAGGA	5520
10	CCTCTGTCAT	CCAATTTCTG	GTCTCTTGGG	GAAAAGCCCC	AAATCCTCAT	CAAGTCCCCA	5580
	CAGACTGTGT	CCGTACCCGC	TGAGACAGAC	ACTGTGTTCC	CCTGTGAGGC	AACAGGAAAA	5640
	CCAAAGCCTT	TGTTACTTGG	GACAAAGGTT	TCCACAGGAG	CTCTTATGAC	TCCGAATACC	5700
	AGGATACAAC	GGTTTGAGGT	TCTCAAGAAC	GGTACCTTAG	TGATACGGAA	GGTTCAGTA	5760
	CAAGATACAG	CCAGTATAT	GTGCACCGCC	AGCAACCTGC	ACGGCTTGGA	CAGGATGGTG	5820
	GTCTTGCTTT	CGGTACCCGT	GCAGCAACCT	CAAACTCTAG	CCTCCCACTA	CCAGGACGTC	5880
15	ACTGTCTACC	TGGGAGACAC	CATTGCAATG	GAGTGTCTGG	CCAAAGGGAC	CCCAGCCCCC	5940
	CAAAATTTCT	GGATCTTCCC	TGACAGGAGG	GTGTGGCAAA	CTGTGTCCCC	CGTGGAGAGC	6000
	CGCATCACCC	TGCACGAAAA	CCGGACCCCT	TCCATCAAGG	AGGCGTCTCT	CTCAGACAGA	6060
	GGCGTCTATA	AGTCGCTGGC	CAGCAATGCA	GCCGGGGCGG	ACAGCCTTGG	CATCCGCTGT	6120
20	CACGTGGCGG	CAGTGCAGGC	CGTTATCCAC	CAGGAGAAAG	TGGAGAACAT	CTCGCTGCCC	6180
	CCGGGGCTCA	GCATTCACAT	TCACTGCAC	GCCTCCCTGC	CGCCCTGCCC	CAGCGTGGCG	6240
	TGGGTGCTCG	GGGACGGTAC	CCAGATCCGC	CCCTCGCAGT	TCCTCCACGG	GAACCTGTTT	6300
	GTTTTCCCCA	ACGGGACGCT	CTACATCCGC	AACCTCGCGC	CCAAGGACAG	CGGGCGCTAT	6360
	GAGTGCCTGG	CCGCCAACCT	GGTAGGCTCC	GCAGCAGGGA	CGGTGACAGT	GAACGTGCAG	6420
25	CGTGCAGCAG	CCAAACGGCG	CATCACGGGC	ACCTCCCGCG	GGAGGACGGA	CGTCAGGTAC	6480
	GGAGGACACC	TCAAGCTGGA	CTGCAGCGCC	TCCGGGGACC	CCTGGCCCGG	CATCCTCTGG	6540
	AGGCTGCCGT	CCAAAGAGGT	GATCGACGCG	CTCTTCAGTT	TTGATAGCAG	AATCAAGGTG	6600
	TTTGCCAATG	GGACCCCTGT	GGTGAAATCA	GTGACGGACA	AAGATGCCGG	AGATTACCTG	6660
	TGCGTAGCTC	GAATTAAGGT	TGGTGATGAC	TACGTGGTGC	TCAAAGTGGA	TGTGGTGATG	6720
30	AAACCGGCGA	AGATTTGAACA	CAAGGAGGAG	AACGACCCCA	AAGTCTTCTA	CGGGGTGAC	6780
	CTGAAAGTGG	ACTGTGTGGC	CACCGGGCTT	CCCAATCCCG	AGATCTCCTG	GAGCCTCCCA	6840
	GACGGGAGTG	TGGTGAATCT	CTTCATGCG	TGGGATGACA	CGGTGGGAAG	CACCAAGCGC	6900
	TATGTCTGCT	TCAACAATGG	GACACTCTAC	TTTAACGAA	TGGGGATGAG	GGAGGAAGGA	6960
	GACTACACCT	GCTTTGCTGA	AAATCAGGTC	GGGAAGGACG	AGATGAGAGT	CAGAGTCAAG	7020
35	GTGGTGACAG	CGCCCGCCAC	CATCCGGAAC	AAGACTTACT	TGGCGGTCTA	GGTGCCCTAT	7080
	GGAGACGTGG	TCACTGTAGC	CTGTGAGGCC	AAAGGAGAAC	CCATGCCCAA	GGTGACTTGG	7140
	TTGTCCCCAA	GATCAAAAGT	GATCCCCACC	TCCTCTGAGA	AGTATCAGAT	ATACCAAGAT	7200
	GGCACTCTCC	TTATTCAGAA	AGCCACGCGT	TCTGACGCG	GCAACTACAC	CTGCCCTGGT	7260
	AGGAACAGCG	CGGGAGAGGA	TAGGAAGACG	GTGTGGATTG	ACGTCAACGT	CCAGCCACCC	7320
40	AAGATCAACG	GTAAACCCAA	CCCCATCACC	ACCGTGCGGG	AGATAGCAGC	CGGGGCGAGT	7380
	CGGAAACTGA	TGTAGTGCAA	AGCTGAAGGC	ATCCCCACCC	CGAGGGTGTG	ATGGGCTTTT	7440
	CCCGAGGGTG	TTGTTCTGCG	AGCTCCATAC	TATGGAACCC	GGATCACTGT	CCATGGCAAC	7500
	GGTTCCCTGG	ACATCAGGAG	TTTGAGGAAG	AGCGACTCCG	TCCAGCTGGT	ATGCATGGCA	7560
	CGCAACGAGG	GAGGGGAGGC	GAGGTTGATC	GTGCAGCTCA	CTGTCTTGG	GCCCATGGAG	7620
45	AAACCCATCT	TCCACGACCC	GATCAGCGAG	AAGATCAGCG	CCATGGCGGG	CCACACCATC	7680
	AGCCTCAACT	GCTCTGCGCG	GGGGACCCCG	ACACCCAGCC	TGGTGTGGGT	CCTTCCCAAT	7740
	GGCACCGATC	TGCAGAGTGG	ACAGCAGCTG	CAGCGCTTCT	ACCACAAAGC	TGACCGGATG	7800
	CTACACATTA	GCGGTCTCTC	CTCGGTGGAC	GCTGGGGCCT	ACCGCTCGCT	GGCCCGCAAT	7860
	GCCGCTGGCC	ACAAGGAGAG	GCTGGTCTCC	CTGAAGGTGG	GACTGAAAGC	AGAAGCAAA	7920
50	AAGCAGTATC	ATAACCTGGT	CAGCATCATC	AATGGTGAGA	CCCTGAAGCT	CCCCTGCACC	7980
	CCTCCCGGGG	CTGGGCAAGG	ACGTTTCTCC	TGGAACGCTC	CCATATGGCA	GCATCTGGAG	8040
	GGCCCCCAAA	CCCTGGGACG	GGTTTCTCTT	CTGGACAATG	GCACCCCTAC	GGTTGCTGAG	8100
	GGCTCGGTGT	TTGACAGGGG	TACCTATGTA	TGCAGGATGG	AGACGGAGTA	CGGCCCTTCG	8160
	GTCAACAGCA	TCCCGCTGAT	TGTGATCGCC	TATCCTCCCG	GGATCACCAG	CGAGCCACCC	8220
55	CGGTCATCT	ACACCCGGCC	CGGGAACACC	GTGAAACTGA	ACTGCATGGC	TATGGGGATT	8280
	CCCAAAGCTG	ACATCAAGTG	GGAGTTACCG	GATAAGTCGC	ATCTGAAGGC	AGGGGTTTCA	8340
	GCTCGTCTGT	ATTGGAACAG	ATTTCTTCTC	CCCCAGGGAT	CAGTGACCAT	CCAGCATGCC	8400
	ACACAGAGAG	ATGCCGGCTT	CTACAAGTGC	ATGGCAAAAA	ACATTTCTCG	CAGTGACTCC	8460
	AAAACAACTT	ACATCCACGT	CTTCTGAAAT	GTGGATTCCA	GAATGATTGC	TTAGGAAGCT	8520
60	ACAACAAAGC	GGGTTTGTGA	AGGGAAGCCA	GGTTGGGGAA	TAGGAGCTCT	TAAATAATGT	8580
	GTCAAGTATC	ATGTTGGCCT	CTGGTGGGTT	TCAAGTTGAG	GTGTAGCTTG	ATCTACAATT	8640
	GTGGGAAAAA	GGAAAGCAAT	CAGACACGAG	AAGGAGGGCT	CAGCCTTGCT	GAGACACTTT	8700
	CTTTTGTGTT	TACATCATGC	CAGGGGCTTC	ATTCAAGGGT	TCTGTGCTCT	GACTGCAATT	8760
	TTTCTTCTTT	TGCAAAATGCC	ACTCGACTGC	CTTCATAAGC	GTCCATAGGA	TATCTGAGGA	8820
65	ACATTTCATCA	AAAATAAGCC	ATAGACATGA	ACACACCTTC	ACTACCCCAT	TGAAGACGCA	8880
	TCACCTAGTT	AACCTGCTGC	AGTTTTTACA	TGATAGACTT	TGTTCCAGAT	TGACAAGTCA	8940
	TCTTTCAAGT	ATTTCTCTCT	TCACCTTCAA	ACTCCAGCTT	GCCCAATAAG	GATTTAGAAC	9000
	CAGAGTGACT	GATATATATA	TATATATTTT	AATTCAGAGT	TACATACATA	CAGCTACCAT	9060
	TTTATATGAA	AAAAGAAAAA	CATTTCTTCC	TGGAACCTAC	TTTTTATATA	ATGTTTATTA	9120
70	TATATATTTT	TTCTTTTCAA	ATCAGACGAT	GAGACTAGAA	GGAGAAATAC	TTTCTGTCTT	9180
	ATTAATAATT	ATAAATTATT	GGTCTTTACA	AGACTTGGAT	ACATTACAGC	AGACATGGAA	9240
	ATATAATTTT	AAAAAATTTC	TCTCCAACCT	CCTTCAAATT	CAGTCACCAC	TGTTATATTA	9300
	CCTTCTCCAG	GAACCCCTCCA	GTGGGGAAAG	CTGCGATATT	AGATTTCTCT	GTATGCAAA	9360
	TTTTTGTGTA	AAGCTGTGCT	CAGAGGAGGT	GAGAGGAGAG	GAAGGAGAAA	ACTGCATCAT	9420
75	AACTTTACAG	AATTGAATCT	AGAGTCTTCC	CCGAAAAGCC	CAGAAACTTC	TCTGCAGTAT	9480
	CTGGCTTGTC	CATCTGGTCT	AAGGTGGCTG	CTTCTTCCCC	AGCCATGAGT	CAGTTTGTGC	9540
	CCATGAATAA	TACACGACCT	GTTATTTCCA	TGACTGCTTT	ACTGATTTT	TAAGGTCAAT	9600
	ATACTGTACA	TTTGATAATA	AAATAATATT	CTCCCCAAAA	AAAAA		

Seq ID NO: 417 Protein sequence
Protein Accession #: NP_056234.1

	1	11	21	31	41	51	
85	MPKRAHWGAL	SVVLILLWGH	PRVALACPHP	CACYVPSEVH	CTFRSLASVP	AGIARHVERI	60
	NLGFNSIQAL	SETSFAGLTK	LELLMIHNE	IPSIDPGLR	DLSSLQVKE	SYNKLRVITG	120
	QTLGLSLNLM	RLHIDHNKIE	FIHPQAFNGL	TSRLRLHLEG	NLLHQLHPST	FSTFTFLDYF	180
	RLSTIRHLYL	AENMVRTLPA	SMLRNMPLLE	NLYLQGNPWT	CDCMRWFLE	WDAKSRGILK	240

	CKKDKAYEGG	QLCAMCFSPK	KLYKHEIHLK	KDMTCLKPSI	ESPLRQNRSR	SIEEEQEQUE	300
	DGGSQLELEK	FQLPQWSISL	NMTDEHGMV	NLVCDIKKPM	DVYKIHNLQT	DPPDIDINAT	360
	VALDFECFMT	RENYEKLWKL	IAYSEVPVK	LHRELMLSKD	PRVSYQYRQD	ADEEALYITG	420
5	VRAQILAEPE	WVNLQPSIDIQ	LNRRQSTAKK	VLLSYTYQYS	QTISTKDTKQ	ARGRSWVMIE	480
	PSGAVQRDQT	VLEGGPCQLS	CNVKASESPS	IFWVLPDGS	LKAPMDDDPS	KFSILSSGWL	540
	RIKSMEPSDS	GLYQCIAQVR	DEMDRMVYRV	LVQSPSTQPA	EKDTVTIGKN	PGESVTLPCN	600
	ALAIPEAHL	WILPNRRIIN	DLANTSHVYM	LPNGTLSIPK	VQVSDSGYVR	CVAVNQGGAD	660
	HFTVGTITVK	KSGSLPSKRG	RRFGAKALSR	VREDIVEDEG	GSGMGDEENT	SRLLHLPKQD	720
10	EVFLKTKDDA	INGDKKAKKG	RRKLKLWKHS	EKEPETNVAE	GRRVFESRRR	INMANKQINP	780
	ERWADILAKV	RGNLPLKGT	VPPLIKTTSF	PSLSLEVTTP	FPAVSPSPAS	PVQVTSAAE	840
	SSADVLLGE	EEHVLGTISS	ASMGLEHNNH	GVILVEPEVT	STPLEEVVDD	LSEKTEEITS	900
	TEGDLKGTAA	PTLISEPYEP	SPTLHTLDTV	YEKPTHEETA	TEGWSAADVG	SSPEPTSSEY	960
	EPFLDAVSLA	ESEPMQYFDP	DLETKSQDPE	DKMKEDTFAH	LTPPTTIWVN	DSSTSQOLF	1020
	STIGEPGVPG	QSHLQGLTDN	IHLVKSLSL	QDTLLIKKGM	KEMSQTLQGG	NMLEGDPHDS	1080
15	RSESEGGQES	KSITLDPSTL	KIMSMSPVK	KPAETTVGTL	LKDDTTVT	TPRQKVPSS	1140
	TMSTHPSRRV	PNGRHRLRPN	GFRRHKKQTP	PTTFAPSETF	STQPTQAPDI	KISSQVESSL	1200
	VPTAWVDNTV	NTPKQLEMEK	NAEPTSKGTP	RRKHGKRFNK	HRYPSTVSS	RASGSKSPS	1260
	PENKRNIVT	PSSETILLPR	TVSLKTEGYP	DSLDMYTTTR	KIYSSYPKVQ	ETLPVITYKPT	1320
20	SDGKEIKDDV	ATNVDKHKSD	ILVTGESITN	AIPTSRSLVS	TMGEFKEESS	PVGFPPTPTW	1380
	NPSRTAQFGR	LQTDIPVTTT	GENLTDPLL	KELEDVDFTS	EFLSSLTSTV	PFHQEAGSS	1440
	TTLSSIKVEV	PDHLETTVA	ILLSETRPQN	HTPTAARMKE	PASSSPSTIL	PASSSPSTIL	1500
	MSLGQTTTTK	PALPSPRISQ	ASRDSKENVF	LMYVGNPETE	ATPVNNEGTO	HMSGPNELST	1560
	PSSDRDAFNL	STKLELEKQV	FGSRSLPRGP	DSQRQDGRVH	ASHQLTRVPA	KPILPTATVR	1620
25	LEPMSTQAS	RYVFTSQSPR	HWTKNKEITT	YPSGALPENK	QFTTFLRLST	TIPLPLHMSK	1680
	PSIPSKFTDR	RTDQFNYSK	VFGNNNIPEA	RNPVGKPPSP	RIPHYNGLRL	PFPTNKTLSP	1740
	PQLGVTTRRP	IPTSPAPVMR	ERKVIPIGSYN	RIHSHSTFHL	DFGPPAPPLL	HTPQTGSPS	1800
	TNLQNIPIV	STQSSISFIT	SSVQSSGSPH	QSSSKFFAGG	FPASKFWSLG	EKPQILTKSP	1860
30	QTVSVTAETD	TVFPCEATGK	PKPFVTWTKV	STGALMTPTN	RIQRFEVLKN	GTILVIRKQV	1920
	QDRGQYMCCTA	SNLHGLDRMV	VLLSVTVQPP	QILASHYQDV	TVYLGDTIAM	ECLAKGTAPV	1980
	QISWTFPPDR	VWQTVSPVES	RTLHENRTL	SIKEASFSDR	GVYKCVASNA	AGADSLAIRL	2040
	HVAALPPVIH	KTYLAVQVPY	PGLSIHIHCT	AKAAPLPVSR	WVLGDTGTIR	PSQFLHGNLF	2100
	VFPNGTLYIR	NLAPKDSGRY	ECVAANLVGS	ARRTVQLNVQ	RAAANARITG	TSFRRTDVRY	2160
	GGTLKLDCA	SGDPWPRILW	RLPSKRMDA	LFSFDSRIKV	FANGTLVVKS	VTDKDAGDYL	2220
35	CVARNKVGDD	VYVLKVDVVM	KPAKIEHKEE	NDHKVFYGGD	LKVDVCVATG	PNPEISWSLP	2280
	DGSLVNSFMQ	SDDSGGRTKR	YVVFNNGLTY	FNEVGMRREG	DYTCFAENQV	GKDEMVRVVK	2340
	VVTAPATIRN	KTYLAVQVPY	GDVVTVACEA	XGEPMPKVTV	LSPTNKVIPT	SSEKYQIYQD	2400
	GTLILQKAQR	SDSGNYTCLV	RNSAGEDRKT	VWIIHVNQPP	KINGNPNPIT	TVREIAAGGS	2460
	RKLIDCKAEG	IPTPRVLWAF	PEGVVLPAFY	YGNRITVHGN	GSLDIRSLRK	SDSVQLVCM	2520
40	RNEGGEARLI	VQLTVLEPME	KPIFHDPISE	KITAMAGHTI	SLNCSAAGTP	TPSLVWVLPN	2580
	GTDLQSGGQL	QRFYHKADGM	LHISGLSSVD	AGAYRCVARN	AAGHTERLVS	LKVGKPEAN	2640
	KQYHNLVSI	RMETLKLPT	PGAGQGRFS	WTLPLNGHLE	GQPLTGRVSR	LDNGTLTVRE	2700
	ASVFDRTGYV	CRMETEYGPS	VTSIPVIVIA	YPPRITSEPT	PVIYTRPGNT	VKLNCMAMGI	2760
	PKADITWELP	DKSHLKAGVQ	ARLYGNRPLH	PQGSLLTIQHA	TQRDAGFYKC	MAKNILGSDS	2820
45	KTTYIHVFP						

Seq ID NO: 418 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..5001

50	1	11	21	31	41	51	
	ATGCCAGGCA	CAAACTAAC	CCGAACAGGC	GCCCCAGCAG	ACTACAGAGT	GATATTGAAG	60
	ACCTCTCAAG	AGGACGAATT	GGATGTACCT	GACGACATCA	GCGTCCGGGT	TATGTCATCT	120
55	CAGTCTGTGC	TTGTGTCTCTG	GGTGGATCCT	GTTCTGGAAA	AACAGAAAGAA	AGTTGTTGCA	180
	TCAAGACAGT	ACACCGTGGC	CTATCGAGAG	AAGGGGGAAAT	TGGCCAGGTG	GGATTATAAG	240
	CAGATCGCTA	ACAGGCGTGT	GCTGATTGAG	AACCTGATTC	CAGACACTGT	GTATGAATTT	300
	GCAGTCCGTA	TTTCACAGGG	TGAAAGAGAT	GGCAAAATGGA	GTACGTCAGT	CTTCCAAAGA	360
	ACACCAAGAT	CTGCCCTAC	CACAGCTCCT	GAAAACCTGA	ACGTCGTGGC	AGTCAATGGC	420
60	AAACCTACAG	TTGTGCTGTC	ATCTTGGGAT	GCGCTACCAG	AGACTGAGGG	GAAAGTGAAA	480
	GTCTGTCTGC	TGGACACAGG	ACTGTTTTCA	GTTTCTCTCT	TCCAACCATC	TGCCAAATCA	540
	TTTCAGAATA	CATCTTTTCA	TACGCCCCGG	CTCTCAAACC	ATTGGAGAGC	AAGTCCCTCA	600
	CCTATCCTGG	AGACACTACT	TCTGCCCTGG	TGGATGGTCT	GCAGCCTGGG	GAAACGCTATC	660
	TTTTCAAAAT	CCGGGCCACA	AACAGGAGAG	GCCTGGGACC	TCACTCCAAA	GCCTTCATG	720
65	TGCTATGCC	AACAGAATG	CAGCTGTACC	CAGAAGGATT	TCAGTTGTCT	AGCTTACCTG	780
	ATCGATATCC	AAACCAACA	AGTTAATAAA	GATCCACAAC	TGGAAGGGAG	TGTTTTTGGA	840
	CCATGTTTTC	TTTTCTACTT	CCTCACATT	ATGCTGGATA	TTGGCGGCTT	TTCTTCATT	900
	ATGTGCTATG	AAGACCCANN	TGTTTCTTCT	TTGACAGGCA	ATTCTTTAAA	ATCTGTTGCA	960
	GCCAGTAAGG	CGGATGTTCA	CGAGAACACG	GAGGACAATG	GGAAACCCGA	AAAACTTGAG	1020
70	CCTTCTCAC	CTTCTCCAG	AGCTCCAGCT	TCCTCCCAAC	ACCCCTCTGT	GCCTGCTTCT	1080
	CCCCAAGGGA	GAAATGCCAA	GGACCTTCTT	CTTGACTTGA	AGAACAATA	ATTGGCTAAT	1140
	GGTGGGGCGC	CCGAAAACCC	CCAGCTTCGC	GCCRAAGAAG	CAGAGGAGCT	GGATCTTCAG	1200
	TCGACAGAAA	TCACTGGGGA	GGAGGAGCTG	GGTTCGCCGG	AGGACTCGCC	CATGTCACCC	1260
	TCAGACACCC	AAGACCAGAA	ACGGACCCCT	AGGCCGCCAA	GTAGACACGG	CCAATCGGTG	1320
75	GTTGCTCCCG	CGAGGACTGC	AGTGAGGGCC	CGGATGCCAG	CGCTGCCCGG	AAGGGAAGGC	1380
	GTAGATAAGC	CTGGCTTTTC	CCTGGCCAGC	CAGCCCCGCC	CAGGGCGGCC	CCCCTCGGCT	1440
	TCGGCTCTCT	CTGCCACCA	CGCGTCCACC	CAGGGCACCT	CTCATCGTCC	TTCCCTCGCT	1500
	GCCAGCTTGA	ATGACAAACG	CTTGGTGGAC	TCAGACGAG	ATGAGCGCGC	TGTGGGCTCC	1560
	CTCCACCCCA	AGGCGGCTT	CGCCAGCCCC	CGGCCAGCCC	TGTCCCGCCG	CGCCAGTCC	1620
80	CGGTCCAGCG	TTCTCCGCGA	CAGAAGCTCT	GTGCAACCCG	CGCAGAAAGC	AGCCTCGCCG	1680
	GCGCGGAGGA	CCCCCATTC	AGGGGCCGCA	GAGGAAGATT	CCAGTGCTCT	AGCCCCACCC	1740
	TCAAGACTTT	CTCCACCCCA	TGGGGGATCA	TCTCGGCTGC	TGCCACCCCA	GCCACACCTG	1800
	AGCTCTCCAC	TTTCCAAGGG	CGGGAAGGAT	GGTGAGGACG	CCCCAGCCAC	CAACTCCAAT	1860
	GCGCATCAC	GCTCCACCAT	GTCTCTCTCT	ATCTCTCTCT	CTCTCTCTCT	CAGGACGCGC	1920
85	GTCTCTGAGG	GAGCGGAGGC	TTCTGATGGT	GAAAGCCACG	GTAGCGGCGA	TAGGGAAGAC	1980
	GGCGGAAGGC	AGGCGGAGGC	CACGGCCCGC	ACGCTGCGGG	CCGGGCTCTG	CTCTGGACAC	2040
	TTCCATTGTC	TCAGACACAA	ACCCCTTTGCT	GCCAACGGGA	GGTCTCCAAG	CAGGTTCCAG	2100
	ATTGGGCGGG	GACCTCGGCT	GCAGCCCTCC	AGCTCCCAAC	AGTCAGACTGT	GCCCTCCCGA	2160

Seq ID NO: 419 Protein sequence
Protein Accession #: Eos sequence

	1	11	21	31	41	51	
70	MPG TKL TRTG	APADYRVILK	TSQEDEL DVP	DDISVRVMSS	QSVLVSVNDP	VLEKQKKVVA	60
	TRSTVYTRYRE	KGELARNDYK	QIANRRVLIE	NLIPDTVYEF	AVRTSQGERD	GKWSVSFVQR	120
	TPESAPTATP	ENLNVHPVNG	KPTVVAASVD	ALNPETGEKVK	VCLLDLTGLFS	VSSFQPSAKS	180
75	PONTFTFPTP	LSNHLQSPSS	PIELTLLLPV	WMVCSLGNAI	FSKSGPQTGLF	ANDLTPKPSL	240
	SLCQCECSTC	QKD FSC LAYL	IDIQTKVNK	DDQLEGSVFG	PCFLFYFLTF	MLDIGGFSFI	300
	MCYEDPVSSL	TGNSLKSVA	SKADVPQNTQ	DNGKPEKPEP	SSPSRPAPAS	SOHSPVPASP	360
	QGRNKADLLL	DLKNKILANG	GAPRKPQLRA	KKAEELDLQS	TEITTGEBELG	SREDSFMPSS	420
	DTQDQKRTL	PPSRHGHSVV	APGRTA VRAR	MPALPRRREGV	DKPGFSLATL	PRFGAPFAS	480
80	ASPAHHAOST	GTSHRPSPLA	SLNNDNLVDS	DEDERAVGSL	HPKGAQAQPR	PALSPSRQSP	540
	SSVLDRSSV	HPGAKPASP	PLRTPHSGAAE	EDSSASAPPS	SLSPFHGGSS	RLLP TQPHLS	600
	SPLSKGGKDG	EDAPATNSNA	PSLR TMSSSV	SSHLSSRTQV	SEGAEASDGE	SHGQDGRDGE	660
	GRQAEATAQT	LRARPASGHF	HLRLHKPFPA	NGRSPERFSI	GRGPRLPQSP	SPQSTVPSRA	720
	HPRVVPSHDS	HPKLSSSGIGH	DEEGEKPLPA	TVVNDHVPS	SRQPSRGWE	DLARSPQRGA	780
85	SLHRKEPISE	NPKSTGADTH	PQDKYKSLAS	KAQDVQSTDT	ADTEGHSFSP	QPGSTDRHAS	840
	PARPFAARSQ	QHPSVPRRMT	PGRAPEQQFP	PPVATSQHEH	GFQSRDARGS	PQPRLRLSLQ	900
	AGDPRPTSOG	RHSSSDPYT	ASRGMLPTA	LNQODEDAOG	LNQODESTEVE	AQDVRAAPTA	960

ARAKEAAASL PKHQVSESPT GAGAGGDHRS QRGHAAASPAR PSRPGGQPSR ARVPSRAAPG 1020
 KSEPPSKRPL SSKSQSVSA EDEEEDAGF PKGGKEDLLS SSVPKWBSST TPRGGKDADG 1080
 SLAKEEREPAL IALAPRGSL APVKRPLPPP PGSSPRASHV PSRPPPSRAA TVSPVAGTHP 1140
 WPRYTTRAPP GHFTSTPMLS LRQRMHARF RNPLSRQPAR PSYRQYNGR PNVEGKVLPG 1200
 SNGKFNQGR IINGPQGTWKV VLDLDRGLVLN AEGRYLDQSH GNPLRIKLGG DGRITVDLEG 1260
 TPVVSFDGLP LFGQGRHGT LANAQDKPIL SLGGKPLVGL EVIKKTHPP TTTMQPTTTT 1320
 TPLPTTTTPR PTTATTMQPT TTTTLPPTTT PRPTTATRR TTTTRPTTV RTTTRTTT 1380
 TPKPTTPIPT CPPGTLERHD DGNLIMSSN GIPECYAEED EFSGLEIDTA VPTTEAYVIY 1440
 DEDYEFETSR PPTTTEPSTT ATTPRVIPEE GAISFPPEEE FDLAGRKRKF APYVTVLNKD 1500
 PSAPCSLTDALDHFQVDSL EIIIPNDLKKS DLPPQHAPRN ITVVAVEGCH SFVIVDWDKA 1560
 TPGDLVTGYL VYSASYEDFI RNKFSTQASS VTHLPIENLK PNTRYVFKVQ AQNPBGYGF 1620
 SPVSFVFTES DNPLLVVRPP GGELSGSHSL SNMIPATRTA MDGNM

Seq ID NO: 420 DNA sequence
 Nucleic Acid Accession #: NM_022743
 Coding sequence: 128..1237

1 11 21 31 41 51
 GTGGATTTC GAGATACCTC CCCTCCTTCT GCTCAGCTGC CTTGCAGTAA TTAAACTCTT 60
 TCTCTGCTGC AACACCCCTA CTGTTCTCCG TGTATTGGCT TTTCTGGGCA GCAGGAAGGA 120
 AAAAGCTGATG CAGATGCTCTC AGTGCCGCGT CGCCAAATAC TGTAGTGCTA AGTGTGAGAA 180
 AAAAGCTTGG CCAGACACCA AGCGGGAATG CAAATGCCTT AAAAGCTGCA AACCCAGATA 240
 TCTCCAGAG TCCGTTGAC TRCTTGGCAG AGTTGTCTTC AAACCTATGG ATGGAGCACC 300
 TTCAGAAATC GAGAAGCTTT ACTCATTTTA TGATCTGGAG TCAATATTA ACAAACTGAC 360
 TGAAGATAAG AAGAGGGGCC TCAGGCAACT CGTAATGACA TTTCAACATT TCATGAGAGA 420
 AGAAATACAG GATGCCCTCT AGCTGCCACC TGCCCTTGAC CTTTGTGAAG CCTTTGCAAA 480
 AGTGATCTGC AACTCTTTCA CCATCTGTAA TGCGGAGATG CAGGAAGTTG GTGTTGGCCT 540
 ATATCCCAAT ATCTCTTTGC TCAATCACAG CTGTGACCCC AACTGTTGCA TTGTGTTCAA 600
 TGGGCCCCAC CTCTTACTGC GAGCAGTCCG AGACATCGAG GTGGGAGAGG AGCTCACCAT 660
 CTGCTACCTG GATATGCTGA TGACCACTGA GGAGCGCCGG AAGCAGCTGA GGGACCAGTA 720
 TGCTTTGAA TTGACTGTT TCCGTTGCCA AACCAGGAGC AAGGATGCTG ATATGCTAAC 780
 TGGTGATGAG CAAGTATGGA AGGAAGTTCA AGAATCCCTG AAAAAAATTG AAGAACTGAA 840
 GGCACACTGG AAGTGGGAGC AGGTTCTGGC CATGTGCCAG GCGATCATAA GCAGCAATTG 900
 TGAAGCGGCT CCCGATATCA ACATCTACCA GCTGAAGGTG CTCGACTGCG CCATGGATGC 960
 CTGCATCAAC CTACGCCCTG TGGAGGAAGC CTTGTTCTAT GGTACTCGGA CCATGGAGCC 1020
 ATACAGGATT TTTTCCCAG GAAGCCATCC CGTCAGAGGG GTTCAAGTGA TGAAGTTGG 1080
 CAAACTGCGAG TCATACCAAG GCATGTTTCC CCAAGCAATG AAGAATCTGA GACTGGCTTT 1140
 TGATATTATG AGATGACAC ATGGCAGAGA ACACAGCCTG ATTGAAGATT TGATTCTACT 1200
 TTTAGAAGAA TGCGACGCCA ACATCAGAGC ATCCTAAGGG AACGCAGTCA GAGGGAAATA 1260
 CGGCGTGTGT TTTGTTGAA TGCTTATTG AGGTACACA CTCTATGCTT TGTAGCTGT 1320
 GTGAACCTCT CTTATTGAA ATTCTGTTCC GTGTTGTGT AGGTAATAA AGGCAGACAT 1380
 GGTTTGCAAA CCACAAGAA CATTAGTTGT AGAGAAGCAC GATTATAATA AATTCAAAAC 1440
 ATTTGGTTGA GGATGCCAAA AAAAAA AAAAAA

Seq ID NO: 421 Protein sequence
 Protein Accession #: NP_073580

1 11 21 31 41 51
 MRCSQCRVAK YCSAKCKKA WPDHKRECK LKSKCPRYPP DSVRLLRVV FKLMDGAPSE 60
 SEKLYSFYDL ESNINKLTED KKEGLRLQVM TFOHFMREEI QDASQLPPAF DLFEAFKVI 120
 CNSFTICNAE MQEVGVGLYP SISLNHSCD PNCISVFNPG HLLLRVRDI EVGEELTICY 180
 LDMLMTSEER RKQLRDQYCF ECDPCRCQTQ DKDADMLTGD BQVWKEVQES LKKIEELKAH 240
 WKWEQVLAMC QAISSNSER LPDINIYQLK VLDCAAMDACI NLGLLEBALF YGTRTMEPYR 300
 IFPPGSHFVR GVQVMKVGKL QLRQGMFFQA MXNLRLAFDI MRVTHGREHS LIEDLILLLE 360
 ECDANIRAS

Seq ID NO: 422 DNA sequence
 Nucleic Acid Accession #: NM_003014.2
 Coding sequence: 238..648

1 11 21 31 41 51
 GGCGGTTTC GCGCCCGAAG GCTGAGAGCT GGCGCTGCTC GTGCCCTGTG TGCCAGACGG 60
 CGGAGCTCG GCGCGGACC CCGCGGCCCC GCTTTGCTGC CCACTGGAGT TTGGGGGAAG 120
 AAACCTCTCT GCGCCCCAGA AGATTTCTTC CTCGGGGAAG GGACAGCGAA AGATGAGGGT 180
 GGCAGGAAGA GAAGGCGCTT TCTGTCTGCC GGGGTGCGAG CGCGAGAGGG CAGTGCCATG 240
 TTCTCTCCA TCCTAGTGGC GCTGTGCTG TGGCTGCACC TGGCGCTGGG CGTGCAGGCG 300
 GCGCCCTGCG AGGCGGTGCG CATCCCTATG TGCCGCGACA TGCCCTGGA CATCACGCG 360
 ATGCCCAACC ACCTGCACCA CAGCACGCG GAGAACGCCA TCCTGGCCAT CGAGCAGTAC 420
 GAGGAGCTGG TGGAGGTGAA CTGCAGCGCC GTGCTGCGCT TCTTCTCTG TGCCATGTAC 480
 GCGCCCATTT GCACCTTGGG GTTCCTGCAC GACCCTATCA AGCCGTGCAA GTCGGTGTGC 540
 CAACGCGCGC GCGACGACTG CGAGCCCTTC ATGAAGATGT ACAACACAG CTGGCCGGA 600
 AGCCTGGCCT GCGACGAGCT GCCTGTCTAT GACCGTGGCG TGTGCATTTC GCCTGAAGCC 660
 ATCGTCACGG ACCTCCCGGA GGATGTTAAG TGGATAGACA TCACACCAGA CATGATGGTA 720
 CAGGAAGAGC CTCTTGATGT TGACTGTAAA CGCCTAAGCC CCGATCGGTG CAAGTGTAAA 780
 AAGGTGAAGC AACTTTGGC AACGTATCTC AGCAAAAACT ACAGCTATGT TATTATGCC 840
 AAAATAAAG CTGTGCAGAG GAGTGGCTGC AATGAGGTCA CAACGGTGGT GGATGTAAA 900
 GAGATCTTCA AGTCTCATC ACCCATCCCT CGAACTCAAG TCCCCTCAT TACAAATTCT 960
 TCTTGCCAGT GTCCACACAT CCTGCCCAT CAAGATGTTT TCATCATGTG TTACGAGTGG 1020
 CGTTCAAGGA TGATGCTTCT TGAATAATGC TTAGTTGAAA AATGGAGAGA TCAGCTTAGT 1080
 AAAAGATCCA TACAGCTGGA AGAGAGGCTG CAGGAACAGC GGAGAACAGT TCAGGACAGA 1140
 AAGAAACAG CCGGCGCAC CAGTCGTAGT AATCCCCCA AACCAAGGG AAAGCCTCCT 1200
 GCTCCCAAC CAGCCAGTCC CAAGAAGAAC ATTAAAACTA GGAGTGCCCA GAAGAGAACA 1260
 AACCCGAAAA GAGTGTGAGC TAACTAGTTT CCAAGCGGA GACTTCCGAC TTCTTACAG 1320
 GATGAGGCTG GGCATTGCCCT GGCACAGCCT ATGTAAGGCC ATGTGCCCTT TGCCCTAAC 1380

	ACTCACTGCA	GTGCTCTTCA	TAGACACATC	TTGCAGCATT	TTTCTTAAGG	CTATGCTTCA	1440
	GTTTTTCTTT	GTAAGCCATC	ACAAGCCATA	GTGGTAGGTT	TGCCCTTTGG	TACAGAAGGT	1500
	GAGTTAAAGC	TGGTGGAAAA	GGCTTATTGC	ATTGCATTCA	GAGTAACCTG	TGTGCATACT	1560
5	CTAGAAGAGT	AGGGAATAAT	ATGCTTGTTA	CAATTGCGACC	TAATATGTGC	ATTGTAAAAAT	1620
	AAATGCCATA	TTTCAACAA	AACACGTAAT	TTTTTTACAG	TATGTTTTAT	TACCTTTTGA	1680
	TATCTGTGTT	TGCAATGTTA	GTGATGTTTT	AAAAATGTAT	GAAAAATATA	TGTTTTTAAG	1740
	AAGGAACAGT	AGTGAATGA	ATGTTAAAAAG	ATCTTTATGT	GTTTATGGTC	TGCAGAAGGA	1800
	TTTTTGTGAT	GAAAGGGGAT	TTTTTGAAAA	ATTAGAGAAG	TAGCATATGG	AAAAATTATA	1860
10	TGTGTTTTTT	TACCAATGAC	TTGAGTTTCT	GTTTTTAGCT	AGAAACTTAA	AAACAAAAAT	1920
	AAATAATAAG	AAAAATAAAT	AAAAAGGAGA	GGCAGACAAT	GTCTGGATTC	CTGTTTTTTG	1980
	GTTACCTGAT	TTCCATGATC	ATGATGCTTC	TTGTCAACAC	CCTCTTAAGC	AGCACCAGAA	2040
	ACAGTGAGTT	TGTCTGTACC	ATTAGGAGTT	AGGTACTAAT	TAGTTGGCTA	ATGCTCAAGT	2100
	ATTTTATACC	CACAAGAGAG	GTATGTCACT	CATCTTACTT	CCCAGGACAT	CCACCCTGAG	2160
	AAATAATTGA	CAAGCTTAAA	AATGGCCTTC	ATGTGAGTGC	CAAATTTTGT	TTTTCTTCAT	2220
15	TTAAATATTT	TCTTTGCTTA	AATACATGTG	AGAGGAGTTA	AAATATAAATG	TACAGAGAGG	2280
	AAAGTTGAGT	CCCACCTCTG	AAATGAGAAT	TACTTGACAG	TTGGGATACT	TTAATCAGAA	2340
	AAAAAGAACT	TATTTGCAGC	ATTTTATCAA	CAAATTTTAT	AATTTGTGAC	AATTGGAGGC	2400
	ATTTATTTTA	AAAAACAATT	TTATTGGCCT	TTTGCTAACA	CAGTAAGCAT	GTATTTTATA	2460
20	AGGCATTCAA	TAACTGACAG	ACGCCCAAGG	GAAAAATAAT	CCTATCTAAT	CCTACTCTCC	2520
	ACTACACAGA	GGTAATCACT	ATTAGTATTT	TGGCATATTA	TTCTCCAGGT	GTTTGCTTAT	2580
	GCACATTATA	AATCATTTGA	ACAAATAAAA	CTAGGAACCT	GTATACATGT	GTTTCATAAT	2640
	CTGCTCTCTT	TGCTTGGCCC	TTTATTGAGA	TAAGTTTTCC	TGTCAAGAAA	GCAGAAACCA	2700
	TCTCATTTCT	AACAGCTGTG	TTATATTCCA	TAGTATGCAT	TACTCAACAA	ACTGTTGTGC	2760
25	TATTGGATAC	TTAGGTGGTT	TCTTCACTGA	CAATACTGAA	TAAACATCTC	ACCGGAATTC	

Seq ID NO: 423 Protein sequence
Protein Accession #: NP_003005.1

30	1	11	21	31	41	51	
	MFLSILVALC	LWLHLALGVR	GAPCEAVRIP	MCRHMPWNIT	RMPNHLHST	QENAILAIEQ	60
	YEELVDVNC	AVLRFFPCAM	YAPICTLEPL	HDPIKPKSV	QQRARDCEP	LMKMYNHSWP	120
	ESLACDELFP	YDRGVCSIFE	AIVTDLPEDV	KWIDITPDM	VQERPLDVDC	KRLSPDRCKC	180
35	KKVKPTLATY	LSKNYSYVIH	AKIKAVQRS	CNEVTTVVDV	KEIFKSSSPI	PRTQVPLITN	240
	SSQCCHILP	HQDVLIMCYE	WRSRMMLLEN	CLVEKWRDQL	SKRSIQWEER	LQEQRRVTQD	300
	KKKTAGRTSR	SNPPKPKGKP	PAPKPASPCK	NIKTRSAQKR	TNPKRV		

Seq ID NO: 424 DNA sequence
Nucleic Acid Accession #: BC010423
Coding sequence: 248..1780

40	1	11	21	31	41	51	
	CACAGCGTGG	GAAGCAGCTC	TGGGGGAGCT	CGGAGCTCCC	GATCACGGCT	TCTTGGGGGT	60
45	AGCTACGGCT	GGGTGTGTAG	AACGGGGCCG	GGGCTGGGGC	TGGGTCCCTT	AGTGGAGACC	120
	CAAGTGCAG	AGGCAAGAAC	TCTGCAGCTT	CCTGCCTTCT	GGGTCAAGTT	CTTATTCAAG	180
	TCTGCAGCG	GCTCCAGGG	AGATCTCGGT	GGAACCTCAG	AAACGCTGGG	CAGTCTGCCT	240
	TTCAACCATG	CCCCTGTCCC	TGGGAGCCGA	GATGTGGGGG	CCTGAGGCCT	GGCTGTGCT	300
50	GCTGCTACTG	CTGGCATCAT	TTACAGGCCG	GTGCCCCGGG	GGTGAGCTGG	AGACCTCAGA	360
	CGTGGTAAC	GTGGTGTGG	GCCAGGACGC	AAAACCTGCC	TGCTTCTACC	GAGGGGACTC	420
	CGGCGAGCAA	GTGGGGCAAG	TGGCTGTGGC	TGCGGTGGAC	GCGGGCGAAG	GCGCCGAGGA	480
	ACTAGCGCTA	CTGCACTCCA	AATACGGGCT	TCATGTGAGC	CCGGCTTACG	AGGGCCGCGT	540
	GGAGCAGCCG	CCGCCCCAC	GCAACCCCTT	GGACGGCTCA	GTGCTCCTGC	GCAACGCACT	600
55	GCAGGCGGAT	GAGGGCGAGT	ACGAGTGCCG	GGTCAGCACC	TTCCCCCGCG	GCAGCTTCCA	660
	GGCGCGGCTG	CGGCTCCGAG	TGCTGGTGCC	TCCCCCTGCC	TCACCTGAATC	CTGGTCCAGC	720
	ACTAGAAGAG	GGCAGGCGCC	TGACCTTGCC	AGCCTCTGCG	ACAGCTGAGT	GCAGCCGAGC	780
	CCCCAGCGTG	ACCTGGGACA	CGGAGGTCAA	AGGCACAACG	TCCAGCCGTT	CCTTCAAGCA	840
	CTCCCCCTCT	GCTGCGCTCA	CCTCAGAGTT	CCACTTGGTG	CCTAGCCGCA	GCATGAATGG	900
60	GCAGCCACTG	ACTTGTGTGG	TGTCCCATCC	TGGCCTGCTC	CAGGACCAAA	GGATCACCCA	960
	CATCTCCAC	GTGTCTCTCC	TGTCTGAGGC	CTCTGTGAGG	GGCCTTGAAG	ACCAAAATCT	1020
	GTGGCACAT	GGCAGAGAAC	GAGCTATGCT	CAAGTGCCGT	AGTGAAGGGC	AGCCCCCTCC	1080
	CTCATACAAC	TGGACACGGC	TGGATGGGCC	TCTGCCCAGT	GGGGTACGAG	TGGATGGGGA	1140
	CACCTTGGGC	TTTCCCCCAC	TGACCACTGA	GCACAGCGGC	ATCTACGTCT	GCCATGTCTG	1200
65	CAATGAGTTC	TCCTCAAGGG	ATTCTCAGGT	CACGTGTGAT	GTTCTTGACC	CCCAGGAAGA	1260
	CTCTGGGAAG	CAGGTGGAGC	TAGTGTGAGC	CTCGGTGGTG	GTGGTGGGTG	TGATCGCCGC	1320
	ACTCTTGTTC	TGCTTCTTGG	TGGTGGTGCT	GGTGCTCATG	TCCGATATCC	ATCGGGGCAA	1380
	GGCCAGCAG	ATGACCCAGA	AATATGAGGA	GGAGCTGACC	CTGACCGAGG	AGAACTCCAT	1440
	CCGGAGGCTG	CATTCCCATC	ACACGGACCC	CAGGAGCCAG	CCGGAGGAGA	GTGTAGGGCT	1500
70	GAGAGCCGAG	GGCCACCCTG	ATAGTCTCAA	GGACAACAGT	AGCTGCTCTG	TGATGAGTGA	1560
	AGAGCCGAG	GGCCGCGAGT	ACTCCAGGCT	GACCACGGTG	AGGGAGATAG	AAACACAGAC	1620
	TGAACCTGCT	TCTCCAGGCT	CTGGGCGGGC	CGAGGAGGAG	GAAGATCAGG	ATGAAGGCAT	1680
	CAACACAGGC	ATGAACCAT	TTGTTTCAAG	GAATGGGACC	CTACGGGCCA	AGCCACCGGG	1740
	CAATGGCATC	TACATCAATG	GGCGGGGACA	CCTGGTCTGA	CCCAGGCCTG	CCTCCCTTCC	1800
75	CTAGGCTCTG	CTCCTTCTGT	TGACATGGGA	GATTTTAGCT	CATCTTGGGG	GCCTCCTTAA	1860
	ACACCCCAT	TTCTTGGGGA	AGATGCTCCC	CATCCCACTG	ACTGCTTGAC	CTTTACTCTC	1920
	AACCTTCTGT	TTCTTGGGGA	GGGCTCCACC	AATTGAGTCT	CTCCCACTAT	GCATGCAGGT	1980
	CACCTGTGTG	GTGCATGTGT	GCCTGTGTGA	GTGTGAGTCT	ACTGTGTGTG	TGTGGAGGGG	2040
	TGACTGTCCG	TGGAGGGGTG	ACTGTGTCCG	TGGTGTGTAT	TATGCTGTCA	TATCAGAGTG	2100
	AAGTGAACCT	TGGTGTATGT	GCCACGGGAT	TTGAGTGGTT	GCGTGGGCAA	CACGTGTGAG	2160
80	GTTTGGCGTG	TGTGTCTATG	GGCTGTGTGT	GACCTCTGCC	TGAAAAAGCA	GGTATTTTCT	2220
	CAGACCCGAG	AGCAGTATTA	ATGATGCAGA	GGTTGGAGGA	GAGAGGTGGA	GACTGTGGCT	2280
	CAGACCCAGG	TGTGCGGGCA	TAGCTGGAGC	TGGAATCTGC	CTCCGCTGTG	AGGGAACCTG	2340
	TCTCCTACCA	CTTGGAGGCC	ATGGGGGCAA	GTGTGAAGCA	GCCAGTCCCT	GGGTGAGCCA	2400
	GAGGCTTGAA	CTGTTACAGA	AGCCCTCTGC	CCTCTGGTGG	CCTCTGGGCC	TGCTGCATGT	2460
85	ACATATTTTC	TGTAATATATA	CATGCGCGCG	GAGCTTCTTG	CAGGAATACT	GCTCCGAATC	2520
	ACTTTTAATT	TTTTTCTTTT	TTTTTCTTGT	CCCTTTCAT	TAGTGTGATT	TTTTTATTAT	2580
	TTTTTATTTT	ATTTTATTTT	AGAGTTTGAG	TCCAGCCTGG	ACGATATAGC	CAGACCTGT	2640

CTGTAAAAAA ACCAAAAACC AAAAAAAAAA AAAAAAAAAA

Seq ID NO: 425 Protein sequence
Protein Accession #: AAH10423

5

1	11	21	31	41	51	
MPLSLGAEMW	GPEAWLLLLL	LLASFTGRCP	AGELETSADV	TVVLGQDAKL	PCFYRGDSGE	60
QVGQVAWARV	DAGEGAQELA	LLHSKYGLHV	SPAYEGRVEQ	PPPPRNPLDG	SVLLRNAVQA	120
DEGEYECRV	TFPAGSFQAR	LRLRVLVPL	PSLNPGPALE	EGQGLTLAAS	CTAEGSPAPS	180
VTWDTVEKGT	TSSRSFKHSR	SAAVTSEFHL	VPSRSMNGQP	LTCVVSHPL	LQDQRITHIL	240
HVSFLAEASV	RGLEDQNLWH	IGREGAMKLC	LSEGGPPPSY	NWTRLDGFLP	SGVRVDGDTL	300
GFPPLTTEHS	GIYVCHVNE	FSSRDSQVTV	DVLDPQEDSG	KQVDLVASV	VVGVIAALL	360
FCLLVVVVVL	MSRYHRRKAQ	QMTQKYEEEL	TLTRENSIRR	LHSHHTDPRS	QPEESVGLRA	420
EGHPDLSKDN	SSCSVMSSEP	EGRSYSTLTT	VREIETQTEL	LSPSGRAE	EEDQDEGIKQ	480
AMNHPVQENG	TLRAKPTGNG	IYINGRGHLV				

Seq ID NO: 426 DNA sequence
Nucleic Acid Accession #: NM_003474.2
Coding sequence: 37..3036

20

1	11	21	31	41	51	
CACTAACGCT	CTTCTAGTC	CCCGGGCCAA	CTCGACAGT	TTGCTCATT	ATTGCAACGG	60
TCAAGGCTGG	CTTGTGCCAG	AACGGCGCGC	GCGCGACGCA	CGCACACACA	CGGGGGGAAA	120
CTTTTAA	AATGAAAGGC	TAGAAGAGCT	CAGCGCGCGC	CGGGCGCTG	CGCGAGGCT	180
CGGAGCTGA	CTCGCGAGG	CAGGAAATCC	CTCCGGTGC	GACGCGCGC	CCCGCTCGGC	240
GCCCCGCTGG	GATGCTGAG	CGCTCGCCGC	CGGGCCCGAG	AGCTGCTGCA	CTGAAGGCCG	300
GCGACGATGG	CAGCGCGCCC	GCTGCGCGTG	TCCCCCGCCC	CGCCCTCTCT	GCTCGCCCTG	360
GCCCGTGTCT	TGCTCGCGCC	CTCGGAGGCC	CGAGGGGTGA	GCTTATGGAA	CGAAGGAAGA	420
GCTGATGAAG	TTGTGATGC	CTCTGTTCGG	AGTGGGGACC	TCTGGATCCC	AGTGAAGAGC	480
TTGCACTCCA	AGAATCATCC	AGAAGTGCTG	AATATTGAC	TACAACGGGA	AAGCAAGAA	540
CTGATCATAA	ATCTGGAAG	AAATGAAGGT	CTCATTGCCA	GCAGTTTCAC	GGAAACCCAC	600
TATCTGCAAG	ACGGTACTGA	TGTCTCCCTC	GCTCGAAATT	ACACGGTAAT	TCTGGGTAC	660
TGTTACTACC	ATGACATGT	ACGGGATAT	TCTGATTCAG	CAGTCAGTCT	CAGCAGCTGT	720
TCTGTCTCA	GGGACTTAT	TGTGTTTGA	AATGAAAGCT	ATGTCTTAGA	ACCAATGAA	780
AGTGCAACCA	ACAGATACAA	ACTCTTCCA	GCGAAGAAGC	TGAAAGCGT	CCGGGATCA	840
TGTGGATCAC	ATCACAACAC	ACCAAACCTC	GCTGCAAGA	ATGTGTTTCC	ACCACCTCT	900
CAGACATGGG	CAAGAAGGCA	TAAAAGAGAG	ACCCTCAAGG	CAACTAAGTA	TGTGGAGCTG	960
GTGATCGTGG	CAGACAACCG	AGAGTTTCAG	AGGCAAGGAA	AAGATCTGGA	AAAAGTTAAG	1020
CAGCGATTAA	TAGAGATTGC	TAATCACGTT	GACAAGTTT	ACAGACCATT	GAACATTGG	1080
ATCGTGTGG	TAGCGTGGG	AGTGTGGAAT	GACATGGACA	AATGCTCTGT	AAGTCAGGAC	1140
CCATTCCACA	GCCTCCATGA	ATTTCTGGAC	TGGAGGAAGA	TGAAGCTTCT	ACCTCGCAA	1200
TCCCATGACA	ATGCGCAGCT	TGTCAGTGGG	GTTTATTTCC	AAGGACCAC	CATCGGCATG	1260
GCCCCAACTA	TGAGCATGTG	CACGGCAGAC	CAGTCTGGGG	GAATTGTCT	GGACCATTC	1320
GACAATCCCC	TTGGTGTGAG	CGTGACCTG	GCACATGAGC	TGGGCCACAA	TTTCGGGATG	1380
AATCATGACA	CATGAGACG	GGGCTGTAGC	TGTCAAATGG	CGGTGAGAA	AGGAGGCTGC	1440
ATCATGAACG	CTTCCACCGG	GTACCCATT	CCCATGGTGT	TCAGCAGTTG	CAGCAGGAAG	1500
GACTTGAGGA	CCAGCCTGGA	GAAAGGAATG	GGGGTGTGCC	TGTTTAACTT	GCCGGAAGTC	1560
AGGGAGTCTT	TGGGGGGCCA	GAAGTGTGGG	AACAGATTGG	TGGAAGAAGG	AGAGGAGTGT	1620
GACTGTGGGG	AGCCAGAGGA	ATGTATGAAT	CGCTGTGCA	ATGCCACCAC	CTGTACCTTG	1680
AAGCCGAGCG	CTGTGTGCGC	ACATGGGCTG	TGCTGTGAAG	ACTGCCAGCT	GAAGCCTGCA	1740
GGAAACAGGT	GCAGGACTC	CAGCAACTCC	TGTGACCTCC	CAGAGTTCTG	CACAGGGGCC	1800
AGCCCTCACT	GCCCAGCCAA	CGTGTACTTG	CACGATGGGC	ACTCATGTCA	GGATGTGGAC	1860
GGCTACTGCT	ACAATGGCAT	CTGCCAGACT	CACGAGCAGC	AGTGTGTCT	ACTCTGGGGA	1920
CCAGGTGCTA	AACCTGGCCC	TTGGATCTGC	TTTGAGAGAG	TCAATTCTGC	AGGTGATCCT	1980
TATGGCAACT	GTGGCAAGAT	CTCGAAGAGT	TCCTTTGCCA	AATGCGAGAT	GAGAGATGCT	2040
AAATGTGAA	AAATCCAGTG	TCAAGGAGGT	GCCAGCGGCG	CAGTCATTGG	TACCAATGCC	2100
GTTTCCATAG	AAACAACAT	CCCCCTGCAG	CAAGGAGGCC	GGATTCTGTG	CCGGGGGACC	2160
CACGTGTACT	TGGGCGATGA	CATGCCGGAC	CCAGGGCTTG	TGCTTGCAGG	CACAAAGTGT	2220
GCAGATGGAA	AAATCTGCCT	GAATCGTCAA	TGTCAAAATA	TTAGTGTCTT	TGGGGTTCAC	2280
GAGTGTGCAA	TGCAGTGCCA	CGGCAGAGGG	GTGTGCAACA	ACAGGAAGAA	CTGCCACTGC	2340
GAGGCCCAT	GGCAGCTTCC	CTTCTGTGAC	AAGTTTGGCT	TTGGAGGAAG	CACAGACAGC	2400
GGCCCCATCC	GGCAAGCAGA	TAACCAAGGT	TTAACCATAG	GAATCTGGT	GACCATCTTG	2460
TGTCTTCTTG	CTGCCGGATT	TGTGGTTTAT	CTCAAAAGGA	AGACCTTGAT	ACGACTGCTG	2520
TTTCAAAATA	AGAAGACCAC	CATTGAAAAA	CTAAGGTGTG	TGCGCCCTTC	CCGGCCACCC	2580
CGTGGCTTCC	AACCTGTCA	GGCTCACCTC	GGCCACCTTG	GAAAAGGCCT	GATGAGGAAG	2640
CCGCCAGATT	CCTACCCAGT	GAAGGACAAT	CCCAGGAGAT	TGCTGCAGTG	TCAGAAATGT	2700
GACATCAGCA	GACCCCTCAA	CGGCCTGAAT	GTCCCTCAGC	CCAGTCAAC	TCAGCAGATG	2760
CTTCTCTCCC	TCCACCGGGC	CCCACGTGCA	CCTAGCGTCC	CTGCCAGACC	CCTGCCAGCC	2820
AAGCCTGCAC	TTAGGCAAGG	CCAGGGGACC	TGTAAGCCAA	ACCCCTCTCA	GAAGCCTCTG	2880
CCTGCAGATC	CTCTGGCCAG	AACAACCTCG	CTCACTCATG	CCTTGGCCAG	GACCCAGGAA	2940
CAATGGGAGA	CTGGGCTCG	CTCGGCACCC	CTCAGACCTG	CTCCACAATA	TCCACACCAA	3000
GTGCCCAGAT	CCACCCACAC	CGCCTATATT	AAGTGAGAAG	CCGACACCTT	TTTCAACAG	3060
75	TGAAGACAGA	AGTTTGCAT	ATCTTTCAGC	TCCAGTTGGA	GTTTTTGTGA	3120
GGATTTTTTT	TAATGTTTAA	AACATCATTA	CTATAAGAAC	TTTGAGCTAC	TGCCGTCACT	3180
GCTGTGCTGT	GCTATGTGTC	TCTGTCTACT	TGCACAGGTA	CTTGTAAATT	ATTAATTTAT	3240
GCAGAAATGT	GATTAGTGTG	CAGTGCCTG	TAGTAGGCAT	TTTTACCATT	ACTGAGTTTT	3300
CCATGGCAGG	AAGGCTTGT	GTGCTTTTAG	TATTTTAGTG	AACCTTGAAT	ATCCTGCTTG	3360
80	ATGGGATTCT	GGACAGATG	TGTTTGCTTT	CTGATCAAGG	CCTTATTTGA	3420
CCAACCTACCC	CCAGCTGTGC	TTATGGTACC	AGATGCAGCT	CAAGAGATCC	CAAGTAGAAT	3480
CTCAGTTGAT	TTTCTGATT	CCCCATCTCA	GGCCAGAGCC	AAGGGGCTTC	AGGTCCAGGC	3540
TGTGTTGGG	GATTCAAGAG	CCCTGTGCCC	CCTTGACAAC	TGGCAGGCG	GCTCCAGGG	3600
ACACCTGGGA	GAAATCTGGC	TTCTGGCCAG	GAAAGCTTGG	TGGAACCTG	GGTTGCAGAC	3660
85	AGGAATCTTA	AGGTGTAGCC	ACACAGGAT	AGAGACTGGA	ACACTAGACA	3720
TGACCTGAG	CTGACAGCC	GTGAGCATGT	TGGAAGGGG	TCTGTAGTGT	CACTCAAGGC	3780
GGTGCTTGAT	AGAAATGCCA	AGCACTTCTT	TTTCTGCTG	TCCTTCTAG	AGCACTGCCA	3840

	CCAGTAGGTT	ATTAGGTTG	GGAAGGTGG	TGTTTCTGTA	AGAAACCTAC	TGCCCAGGCA	3900
	CTGCAAAACCG	CCACCTCCCT	ATACTGCTTG	GAGCTGAGCA	AATCACCACA	AACTGTAATA	3960
	CAATGATCCT	GTATTCAGAC	AGATGAGGAC	TTTCCATGGG	ACCACAACCTA	TTTTAGATG	4020
5	TGAACCAITA	ACCAGATCTA	GTCAATCAAG	TCTGTTTACT	GCAAGGTTCA	ACTTATTAAC	4080
	AATTAGGCAG	ACTCTTTATG	CTTGCAAAAA	CTACAACCAA	TGGAATGTGA	TGTTTCATGGG	4140
	TATAGTTTAT	GTCTGCTATC	ATTATTGCTA	GATATTGGAC	AAAGAACCTT	CTCTATGGGG	4200
	CATCCTCTTT	TTCCAACCTG	GCTGCAGGAA	TCTTTAAAG	ATGCTTTTAA	CAGAGTCTGA	4260
	ACCTATTCT	TAAACACTTG	CAACCTACCT	GTGAGCATC	ACAGAATGTG	ATAAGGAAAT	4320
10	CAACTTGCTT	ATCAACTTCC	TAAATATTAT	GAGATGTGGC	TTGGGCAGCA	TCCCCTTGAA	4380
	CTCTTCACTC	TTCAAATGCC	TGACTAGGGA	GCCATGTTTC	ACAAGGTCTT	TAAAGTGACT	4440
	AATGGCATGA	GAAATACAAA	AATACTCAGA	TAAGGTAAAA	TGCCATGATG	CCTCTGTCTT	4500
	CTGGACTGGT	TTTCACATTA	GAAGACAATT	GACAACAGTT	ACATAATTCA	CTCTGAGTGT	4560
	TTTATGAGAA	AGCCTTCTTT	TGGGGTCAAC	AGTTTTCCTA	TGCTTTGAAA	CAGAAAAATA	4620
	TGTACCAAGA	ATCTTGTTT	GCCTTCCAGA	AAACAAAACCT	GCATTTCACT	TTCCCGGTGT	4680
15	TCCCCACTGT	ATCTAGGCAA	CATAGTATTC	ATGACTATGG	ATAAACTAAA	CACGTGACAC	4740
	AAACACACAC	AAAAGGGAAC	CCAGCTCTAA	TACATTCCAA	CTCGTATAGC	ATGCATCTGT	4800
	TTATTCTATA	GTTATTAAGT	TCTTTAAAT	GTAAGCCAT	GCTGGAAAAT	AATACTGCTG	4860
	AGATACATAC	AGAATTACTG	TAAGTGATTA	CACTTGGTAA	TTGTACTAAA	GCCAAACATA	4920
20	TATATACTAT	TAAAAAGGTT	TACAGAAATT	TATGGTGAT	TACGTGGGCA	TTGTCTTTTT	4980
	AGATGCCCAA	ATCCTTAGAT	CTGGCATGTT	AGCCCTTCCT	CCAATTATAA	GAGGATATGA	5040
	ACCAAAAAAA	AAAAAAA	AA				

Seq ID NO: 427 Protein sequence

Protein Accession #: NP_003465

25	1	11	21	31	41	51	
	MAARPLVPSP	ARALLLALAG	ALLAPCEARG	VSLWNEGRAD	EVVSASVRSR	DLWIPVKSFD	60
30	SKNHPEVLNI	RLQRESKELI	INLERNEGLI	ASSFTETHYL	QDGTVDVSLAR	NYTVILGHYCY	120
	YHGHVRGYS	SAVSLSTCSG	LRGLLIVFENE	SVVLEPMKSA	TNRYKLFPAK	KLKSVRSGCG	180
	SHHNTFNLA	KNVFPFPPSQ	WARRHKRETL	KATKYVELVI	VADNREFORQ	GKDLKVKQR	240
	LIBIANHVDK	FYRPLNIRIV	LVGVEVWMDM	DKCSVSQDPF	TSLHEFLDWR	KMKLLPRKSH	300
	DNAQLVSGVY	FQGTITIGMAP	IMSCTADQS	GGIVMDHSDN	PLGAAVTLAH	ELGHNFGMNH	360
35	DTLDRGCSQ	MAVEKGGCIM	NASTGYFFPM	VFSSCSRKDL	ETSLEKMGV	CLFNLPEVRE	420
	FGGGQKCGNR	FVEEGEEDCD	GEPEECMNR	CNATTTCLKP	DAVCAHLGCC	EDQCLKPAGT	480
	ACRDSNSDC	LPEFTGASP	HCPANVYLHD	GHSCQDVVDY	CYNGICQTHE	QQCVTLWPGS	540
	AKPAPGICFE	RVNSAGDPYG	NCGKVSXSS	AKCEMRDACC	GKIQCGGAS	RPVIGTNAVS	600
	IEINIPLOQ	GRILCRGTHV	YLGDMDPDG	LVLAGTKCAD	GKICLNROCC	NISVFGVHEC	660
40	AMQCHGRGVC	NMRKNCHCEA	HWAPPCDKF	FGGGSTDSGP	IRQADNQLGT	IGILVTILCL	720
	LAAGFVVYLK	RKTLIRLLFT	NKRTTIEKLR	CVRPSRPPRG	FQPCQALHGH	LGKGLMRKPF	780
	DSYPPKDNPR	LLQCGQNDI	SRPLNGLNVP	PQSTQRLVLP	PLHRAPRAPS	VPARPLPAKP	840
	ALRQAGGTCK	PNPPQKPLPA	DPLARTRLT	HALARTPGQW	ETGLRLAPLR	PAPQYPHQVP	900
	RSHTYAIK						

Seq ID NO: 428 DNA sequence

Nucleic Acid Accession #: NM_003714

Coding sequence: 135..1043

50	1	11	21	31	41	51	
	GAGGAGGAGG	GAAAAGGCGA	GCAAAAAGGA	AGAGTGGGAG	GAGGAGGGGA	AGCGGCGAAG	60
	GAGGAAGAGG	AGGAGGAGGA	AGAGGGGAGC	ACAAAGGATC	CAGGTCTCCC	GACGGGAGGT	120
	TAATACCAAG	AACCATGTGT	GCCGAGCGGC	TGGGCCAGTT	CATGACCTGT	GCTTTGGTGT	180
55	TGGCCACCTT	TGACCCGCGC	CGGGGACCG	ACGCCACCAA	CCCACCCGAG	GGTCCCCAAG	240
	ACAGGAGCTC	CCAGCAGAAA	GGCCGCTGT	CCCTGCAGAA	TACAGCGGAG	ATCCAGCACT	300
	GTTTGGTCAA	CGCTGGCGAT	GTGGGGTGTG	GCCTGTTTGA	ATGTTTCGAG	AACAACTCTT	360
	GTGAGATTGG	GGGCTTACAT	GGGATTTGCA	TGACTTTTCT	GCACAACGCT	GGAAAAATTTG	420
	ATGCCCAGGG	CAAGTCATT	ATCAAGAGCG	CCTTGAATG	TAAGGCCAC	GCTCTGCGGC	480
60	ACAGGTTCCG	CTGCATAAGC	CGGAAGTGCC	CGGCCATCAG	GGAAATGGTG	TCCCAGTTGC	540
	AGCGGGAATG	CTACCTCAAG	CACGACCTGT	GGCGGCTG	CCAGGAGAAC	ACCCGGGTGA	600
	TAGTGAGAT	GATCCATTTC	AAGGACTTGC	TGCTGCACGA	ACCTACGTG	GACCTCGTGA	660
	ACTTGTCTGT	GACCTGTGGG	GAGGAGGTGA	AGGAGGCCAT	CACCCACAGC	GTGCAGGTTT	720
	AGTGTGAGCA	GAACTGGGGA	AGCCTGTGCT	CCATCTTGAG	CTTCTGCACC	TCCGGCATCC	780
65	AGAAGCCTCC	CACGGCGCCC	CCCGAGCGCC	AGCCCCAGGT	GGACAGAAC	AAGCTCTCCA	840
	GGGCCCCACCA	CGGGGAAGCA	GGACATCACC	TCCAGAGCC	CAGCAGTAGG	GAGACTGGCC	900
	GAGGTGCCAA	GGGTGAGCGA	GGTAGCAAGA	GCCACCCAAA	CGCCCATGCC	CGAGGCAGAG	960
	TGGGGGCGCT	TGGGGCTCAG	GGACCTTCCG	GAAGCAGCGA	GTGGGAAGAC	GAACAGTCTG	1020
	AGTATTCTGA	TATCCGAGG	TGAAATGAAA	GGCCTGGCCA	CGAAATCTTT	CCTCCACGCC	1080
70	GTCCATTTC	TTATCTATGG	ACATTCCAAA	ACATTTACCA	TTAGAGAGGG	GGGATGTAC	1140
	ACGCAGGATT	CTGTGGGAC	TGTGGACTTC	ATCGAGGTGT	GTGTTCCGCG	AACGGACAGG	1200
	TGAGATGGAG	ACCCCTGGGG	CCGTGGGGTC	TCAGGGGTGC	CTGGTGAATT	CTGCACTTAC	1260
	ACGTACTCAA	GGGAGCGCGC	CCGCGTTATC	CTCGTACCTT	TGTCTTCTTT	CCATCTGTGG	1320
	AGTCAGTGGG	TGTCGGCGC	TCTGTTGTGG	GGGAGGTGAA	CCAGGGAGGG	GCAGGGCAAG	1380
75	GCAGGGCCCC	CAGAGCTGGG	CCACACAGTG	GGTGCTGGGC	CTCGCCCGCA	AGCTTCTGGT	1440
	GCAGCAGCCT	CTGGTGCTGT	CTCCGCGGAA	GTGAGGCGG	CTGATTTCCA	GGACAGGAGT	1500
	GAATGTAAAA	ATAAATATCG	CTTAGAATGC	AGGAGAGGG	TGGAGAGGAG	GCAGGGGCGG	1560
	AGGGGGTGCT	TGGTGCCAAA	CTGAAATTC	GTTTCTTGTG	TGGGGCCTTG	CGGTTCCAGAG	1620
	CTCTTGGCGA	GGGTGGAGGG	AGGAGTGTCA	TTTCTATGTG	TAATTTCTGA	GCCATTGTAC	1680
80	TGTCGTGGCT	GGGGGGGACA	CTGTCCAAGG	GAGTGGCCCC	TATGAGTTTA	TATTTAAACC	1740
	ACTGCTTCAA	ATCTCGATTT	CACTTTTTTT	ATTTATCCAG	TTATATCTAC	ATATCTGTCA	1800
	CTTAAATAAA	TGGCTTTCAA	ACAAAGCAAC	TGGGTCAATTA	AAACCAGCTC	AAAGGGGGTT	1860
	TAAAAAATAA	AAAAACAGCC	CATCCTTTGA	GGCTGATTTT	TCTTTTTTTT	AAGTTCTATT	1920
	TTAAAGCTA	TCAAACAGCG	ACATAGCCAT	ACATCTGACT	GCCTGACATG	GACTCTGGCC	1980
	CACTTGGGGG	AAACCTTATA	CCCAGAGGAA	AATACACACC	TGGGGAGTAC	ATTTGACAAA	2040
85	TTTCCCTTAG	GATTTCTGTA	TCTCACCTTG	ACCCTCAGCC	AAGATTGGTA	AAGCTGCGTC	2100
	CTGGCGATT	CAGGAGACCC	AGCTGGAAC	CTGGCTTCTC	CATGTGAGGG	GATGGGAAAG	2160
	GAAAGAGAG	AATGAAGACT	ACTTAGTAAT	TCCCATCAGG	AAATGCTGAC	CTTTTACATA	2220

WO 02/086443

PCT/US02/12476

AAATCAAGGA GACTGCTGAA AATCTCTAAG GGACAGGATT TTCCAGATCC TAATTGGAAA 2280
TTTAGCAATA AGGAGAGGAG TCCAAGGGGA CAAATAAAGG CAGAGAGAGA GAGAGAGAGA 2340
GGGAGAGGAA GAAAGAGAG AGAGAAAAGA GCCTCGTGCC

5 Seq ID NO: 429 Protein sequence
Protein Accession #: NP_003705

1 11 21 31 41 51
10 MCAERLQGM TLALVLATFD PARGTDATNP PEGPQDRSSQ QKGRLSLQNT AEIQHCLVNA 60
GDVGGCVFEC FENNNSCEIRG LHGICMTFLH NAGKFDAGQK SFIKDALKCK AHALRHRFGC 120
ISRKCPAIRE MVSQLQRECY LKHDLCAAAQ ENTRVIVEMI HFKDLLLHEP YVDLVNLLLT 180
CGEEVKEAIT HSVQVQCEQN WGSILCSILSF CTSAIQKPPT APPERQPVVD RTKLSRAHHG 240
EAGHHLPEPS SRETGRGAKG ERGSKSHPNH HARGRVGGLG AQQPSGSSEW EDEQSEYSDI 300
15 RR

Seq ID NO: 430 DNA sequence
Nucleic Acid Accession #: NM_005940
Coding sequence: 23..1489

20 1 11 21 31 41 51
AAGCCACGCA GCGCCGCGGC GGATGGCTCC GGCCGCGCTGG CTCCGACGCG CGGCCGCGCG 60
CGCCCTCCTG CCGCCGATGC TGCTGCTGCT GCTCCAGCGG CCGCCGCTGC TGGCCGCGGC 120
25 TCTGCGCGCG GAGCTCCACC ACCTCCATGC CGAGAGGAGG GGGCCACAGC CCTGGCATGC 180
AGCCCTGCGC AGTAGCCCGG CACCTGCCCC TGCCACGCGG GAAGCCCCCG GGCCCTGCCAG 240
CAGCCTCAGG CCTCCCGCT GTGGCGTGCC CGACCCATCT GATGGGCTGA GTGCCGCGCA 300
CGACAGAGA AGGTTCGTGC TTCTGGCGG CGCTGGGAG AAGACGGACC TCACCTACAG 360
GATCCTTCGG TTCCCATGGC AGTTGGTGCA GGAGCAGGTG CGGCAGACGA TGGCAGAGGC 420
30 CCTAAAGGTA TGGAGCGATG TGACGCCACT CACCTTTACT GAGGTGCAAG AGGGCCGTGC 480
TGACATCATG ATCCAAAGTC CCAGGTACTG GCATGGGGAC GACCTGCGCT TTGATGGGCG 540
TGGGGGCATC CTGGCCCATG CCTTCTTCCC CAAGACTCAC CGAGAAGGGG ATGTCCACTT 600
CGACTATGAT GAGACCTGGA CTATCGGGGA TGACCAAGGC ACAGACCTGC TGCAGGTGGC 660
35 AGCCCATGAA TTTGGCCACG TGCTGGGGCT GCAGCACACA ACAGCAGCCA AGGCCCTGAT 720
GTCCGCGCTC TACACCTTTC GCTACCCACT GAGTCTCAGC CCAGATGACT GCAGGGGCGT 780
TCAACACCTA ATGGCCGAGC CTGGGCCACG TGTCACTCC AGGACCCGAG CCCTGGGCCC 840
CCAGGCTGGG ATAGACACCA ATGAGATTGC ACGCTGGAG CCAGACGCCC CGCCAGATGC 900
CTGTAGGGCC TCCTTTGAGC CGGTCTCCAC CATCCGAGGC GAGCTCTTTT TCTTCAAAGC 960
40 GGGCTTTGTG TGGCGCCTCC GTGGGGGCCA GCTGCAGCCC GGCTACCCAG CATTTGGCCTC 1020
TGCACCTGTC CAGGACATGC CCAGCCCTGT GGAAGCTGCC TCGAGGATG CCCAGGGCCA 1080
CATTTGGTTC ATCCAAAGTC CTGAGTACTG GGTGTACGAC GGTGAAAAGC CAGTCTCTGG 1140
CCCCGACCCC CTCACCGAGC TGGGCTGGT GAGGTTCGCG GTCCATGCTG CCTTGGTCTG 1200
GGGTCCGAG AAGAACAGA TCTACTTCTT CCGAGGCAGG GACTACTGGC GTTTCACACC 1260
45 CAGCACCCGG CGTGTAGACA GTCCCGTGCC CGCAGGGGCC ACTGACTGGA GAGGGGTGCC 1320
CTCTGAGATC GAGCTGCTCT TCCAGGATGC TGTGGCTAT GCCTACTTCC TGCGCGGCGG 1380
CCTCTACTGG AAGTTTGACC CTGTGAAGGT GAAGGCTCTG GAAGGCTCTC CCGTCTCTGT 1440
GGGTCTGAG TTCTTTGGCT GTGCCGAGCC TGCCAAACTT TTCTCTGAC CATGGCTTGG 1500
ATGCCCTCAG GGGTGTCTGAC CCTGTCCAGG CCAAGAAAT CAGGCTAGAG ACCCATGGCC 1560
50 ATCTTTGTGG CTGTGGGCAC CAGGCATGGG ACTGAGCCCA TGCTCTCTGC AGGGGATGG 1620
GGTGGGGTAC AACCACCATG ACAACTGCCG GGAGGGGCCA GCAGGTCTGT GTCCACTGCC 1680
AGCGACTGTC TCAGACTGGG CAGGGAGGCT TTGGCATGAC TTAAGAGGAA GGGCAGTCTT 1740
GGGACCCGCT ATGCAGTCTC TGGCAAACCT GGTGCCCCGT TCTCATCCCT GTCCCTCAGG 1800
GTAGACCATC GGCAGGACTG GGGGAACTGG AGTGTCTTTC CTGTATCCCT GTTGTGAGGT 1860
55 TCCTTCCAGG GGTGCGCACT GAAGCAAGGG TGCTGGGGCC CCATGGCCCT CAGCCCTGGC 1920
TGAGCAACTG GGTGTAGGG CAGGGCCACT TCCTGAGGTC AGGTCTTGGT AGGTGCTGTC 1980
ATCTGTCTGC CTCTGTGCTG ACAATCTTGG AAATCTGTTC TCCAGAAATC AGGCCAAAAA 2040
GTTACAGTCT AAATGGGGAG GGGTATTTCT CATGCAAGAG ACCCCAGGCC CTGGAGGCTG 2100
CAACATACCT CAATCTGTGC CCAGGCCGGA TCCTCTCTGA GCCCTTTTCG CAGCACTGCT 2160
60 ATCTTCCAAA GCCATTGTAA ATGTGTGTAC AGTGTGTATA AACCTTCTTC TTCTTTTTTT 2220
TTTTTAAACT GAGGATTGTC ATTAACACAA GTTGTTTTCT

Seq ID NO: 431 Protein sequence
Protein Accession #: NP_005931

65 1 11 21 31 41 51
MAPAAWLRS AARALLPPML LLLLQPPPLL ARALPPDVHH LHAERRGPQP WHAALPSSPA 60
PAPATQEAPR PASSLRPPRC GVPDPDGLS ARNRQKRFVL SGGRWEKTDL TYRILRFPWQ 120
70 LVQEQVRQTM AEALKVWSDV TPLTFTEVHE GRADIMIDFA RYWHGDDLFP DPGGILAHA 180
FFPKTHREGD VHFYDETWT IGDDQGTDL QVAAHEFGHV LGLQHTTAAK ALMSAFYTFR 240
YPLSLSPDDC RGVOHLYGQP WPTVTSRTPA LGPQAGIDTN EIAPLEPDAP PDACBASFDA 300
VSTIRGELFF FKAGFVWRLR GGQLQPGYPA LASRHWQGLP SPVDAAPEDA QGHIWFFQGA 360
QVWVYDGEKP VLGPAPLTEL GLVRFPPVHAA LVWGPEKNKI YFFRGRDYWR FHPSTRRVD 420
75 FVPRRATDWR GVPSEIDAAF QDADGYAYFL RGRLYWKFDP VKVKALEGFP RLVGPDFFGC 480
AEPANTFL

Seq ID NO: 432 DNA sequence
Nucleic Acid Accession #: NM_024022
Coding sequence: 202..1563

80 1 11 21 31 41 51
ACCGGCACCC GGACGGCTCG GGTACTTTTC TTCTTAATTA GGTATGCCCC GTGTGAGCCA 60
GGAAAGGGCT GTGTTTATGG GAAGCCAGTA ACATCTGTGC TACTATCTCT TTCCTGGTGG 120
85 CCATCTACAT TTTTGGGACT CGGGAATTAT GAGGTAGAGG TGGAGGCGGA GCGGATGTC 180
AGAGTCCCTG AAATAGTCAC CATGGGGGAA AATGATCCGC CTGCTGTGTA AGCCCTCTTC 240
TCATTCCGAT CGCTTTTGG CCTTGATGAT TTGAAAATAA GTCTGTGTGC ACCAGATGCA 300

GATGCTGTTG CTGCACAGAT CCTGTCACTG CTGCCATTGA AGTTTTTTTC AATCATCGTC 360
 ATTGGGATCA TTGCATTGAT ATTAGCACTG GCCATTGGTC TGGGCATCCA CTTCGACTGC 420
 TCAGGGAAGT ACAGATGTCT CTATCCTTTT AAGTGTATCG AGCTGATAGC TCGATGTGAC 480
 GGAGTCTCGG ATTGCAAGA CGGGGAGGAC GAGTACCGCT GTGTCCGGGT GGGTGGTCAG 540
 5 AATGCCGTGC TCCAGGTGTT CACAGCTGCT TCGTGAAGA CCATGTGCTC CGATGACTGG 600
 AAGGGTCACT ACGCAATGTG TGCCTGTGCC CACTGGGTTT TCCCAAGCTA TGTGAGTTCA 660
 GATAACCTCA GAGTGAGCTC GCTGGAGGGG CAGTTCCGGG AGGAGTTTGT GTCCATCGAT 720
 CACCTCTTGC CAGATGACAA GGTGACTGCA TTACACCACT CAGTATATGT GAGGGAGGGA 780
 TGTGCCCTCG GCCACGTGGT TACCTTGACG TGCACAGCCT GTGGTCATAG AAGGGGCTAC 840
 10 AGCTCACGCA TCGTGGGTGG AAACATGTCC TTGCTCTCGC AGTGGCCCTG GCAGGCCAGC 900
 CTTCACTTCC AGGGCTACCA CCTGTGCGGG GGCTCTGTCA TCAGGCCCTT GTGGATCATC 960
 ACTGTGTCAC ACTGTGTTTA TGACTTGTAC CTCCCCAAGT CATGGACCAC CCAGGTGGGT 1020
 CTAGTTTCCC TGTGGACAA TCCAGCCCCA TCCCACCTGG TGGAGAAGAT TGTCTACCAC 1080
 AGCAAGTACA AGCCAAAGAG GCTGGGCAAT GACATCGCCC TTATGAAGCT GGCCGGGCCA 1140
 15 CTCACGTTCA ATGAATGAT CCAGCCTGTG TGCCTGCCCA ACTCTGAAGA GAACTTCCCC 1200
 GATGGAAAG TGTGCTGGAC GTGAGGATGG GGGGCCACAG AGGATGGAGG TGACGCCCTC 1260
 CCTGTCTTGA ACCACGGGGC CGTCCCTTTT ATTTCCAACA AGATCTGCAA CCACAGGGAC 1320
 GTGTACGGTG GACATCTCTC CCCTCCATG CTCTGCGCGG GCTACCTGAC GGTGTGGCGT 1380
 GACAGCTGCC AGGGGGACAG CGGGGGGCCC CTGGTGTGTC AAGAGAGGAG GCTGTGGAAG 1440
 20 TTAGTGGGAG CGACCAGCTT TGGCATCGGC TGCSCAGAGG TGAACAAGCC TGGGGTGTAC 1500
 ACCCGTGTCA CCTCCTTCTT GGACTGGATC CACGAGCAGA TGGAGAGAGA CCTAAAAACC 1560
 TGAAGAGGAA GGGGACAGAT AGCCACCTGA GTTCTGTAGG TGATGAAGAC AGCCCGATCC 1620
 TCCCCTGGAC TCCGTGTAGT GAACCTGCAC ACGAGCAGAC ACCCTTGGAG CTCTGAGTTC 1680
 CGGCACCACT AGCAGGCCCG AAGAGGGCAC CCTTCCATCT GATTCCAGCA CAACCTTCAA 1740
 25 GCTGCTTTT GTTTTTTGT TTTTGTAGGT GGAGTCTCGC TCTGTTGCCC AGGCTGGAGT 1800
 GCAGTGGCGA AATCCCTGCT CACTGCAGCC TCCGCTTCCC TGGTTCAGC GATTCTCTTG 1860
 CCTCAGCTTC CCCAGTAGCT GGGACCAAGG GTGCCCGCCA CCACACCCAA CTAATTTTGT 1920
 TATTTTATG AGAGACAGGG TTGACCATG TTGGCCAGGC TGCTCTCAA CCCTGACCT 1980
 CAAATGATGT GCCTGCTTCA GCCTCCACA GTGCTGGGAT TACAGGCATG GGCCACCACG 2040
 30 CCTAGCCTCA CGCTCCTTTC TGATCTTAC TAAGAACAAA AGAAGCAGCA ACTTGCAAG 2100
 GCGGCTTTC CCACCTGGTC ATCTGGTTT CTCTCCAGGG GTCTTGCAA ATTCTGACG 2160
 AGATAAGCAG TTATGTGACC TCACGTGCAA AGCCACCAAC AGCCACTCAG AAAAGACGCA 2220
 CAGGCCGAGA AGTGCAGAAC TCAGTCACT GCACGTTTT ATCTTAGGG ACCAGAACCA 2280
 AACCACCCCT TTCTACTTCC AAGACTTATT TTCACATGTG GGGAGGTTAA TCTAGGAATG 2340
 35 ACTCGTTTAA GGCCTATTTT CATGATTTCT TTGTAGCAT TGGTGTGTA CGTATTATTG 2400
 TCCTTTGATT CCAATAATA TGTTCCTTC CCTCAAAAA AAAAAA AAAA 2460
 AAAAA

Seq ID NO: 433 Protein sequence
 Protein Accession #: NP_076927

1 11 21 31 41 51
 45 MGENDPPAIV APFSFRSLFG LDDLKISPVA PDADAVAAQI LSLLPLKFFP IIVIGIILI 60
 LALAIGLGIH FDCSGKYRCR SSFKCIELIA RCDGVSDCKD GEDEYRCVRV GGQNAVQLQVP 120
 TAASWKTMCS DDWKHYANV ACAQLGFPSY VSSDNLRVSS LEGQFREEFV SIDHLLPDDK 180
 VTALHHSYVY REGCASHGVV TLQCTACGHR RGYSSRIVGG NMSLLSQWVP QASLQFQGYH 240
 LCGGSVITPL WIITAAHCYV DLYLPKSWTI QVGLVSLLDN PAPSHLVEKI VYHSKYKPKR 300
 50 LGNDIALMKL AGPLTFNEMI QPVCLPNSEE NFPPDKVQWT SGWGATEDGG DASPVLNHAH 360
 VPLISNKIN HRDVGGLIIS PSLCAGYLT GGVDSQGDG GGPLVCQERR LWKLVGATSF 420
 GIGCAEVNKP GUYTRVTSFL DWIHEQMERD LKT

Seq ID NO: 434 DNA sequence
 Nucleic Acid Accession #: NM_000493.2
 Coding sequence: 97..2139

1 11 21 31 41 51
 60 CACCTTCTGC ACTGCTCATC TGGGCAGAGG AAGCTTCAGA AAGCTGCCAA GGCACCATCT 60
 CCAGGAATCT CCAGCAGGCA GAATCCATCT GAGAATATGC TGCCACAAT ACCCTTTTGT 120
 CTGCTAGTAT CCTTGAACCT GGTTCATGGA GTGTTTTACG CTGAACGATA CCAATGCCCC 180
 ACAGGCATAA AAGGCCCACT ACCCAACACC AAGACACAGT TCTTCATTCC CTACACCATA 240
 AAGAGTAAAG GTATAGCAGT AAGAGGAGAG CAAGGTACTC CTGGTCCACC AGGCCCTGCT 300
 65 GGACCTCAGG GGCACCCAGG TCCTTCTGGA CCACAGGAA AACCAGGCTA CGGAAGTCTT 360
 GGACTCCAAG GAGAGCCAGG GTTGCCAGGA CCACCGGAC CATCAGCTGT AGGGAACCA 420
 GGTGTGCCAG GACTCCAGG AAAACAGGA GAGAGAGGAC CATATGGACC AAAAGGAGAT 480
 GTTGGACCAG CTGGCCTACC AGGACCCCGG GGCACCCAG GACCACTGG AATCCCTGGA 540
 CCGGCTGGAA TTTCTGTGCC AGGAAAACCT GGACACAGG GACCCACAGG AGCCCCAGGA 600
 70 CCCAGGGGCT TTCCTGGAGA AAAGGGTGCA CCAGGAGTCC CTGGTATGAA TGGACAGAAA 660
 GGGGAAATGG GATATGGTGC TCCTGGTCTG CCAGGTGAGA GGGGTCTTCC AGGCCCTCAG 720
 GGTCCACAGG GACCATCTGG CCTCTCTGGA GTGGGAAAAA GAGGTGAAAA TGGGGTTCCA 780
 GGACAGCCAG GCATCAAAGG TGATAGAGGT TTTCCGGGAG AAATGGGACC AATTGGCCCA 840
 CCAGGTCCCC AAGGCCCTCC TGGGGAACGA GGGCCAGAAG GCATTGGAAA GCCAGGAGCT 900
 75 GCTGGAGCCC CAGGCCAGCC AGGGATTCCA GGAAACAAAG GTCTCCCTGG GGCTCCAGGA 960
 ATAGCTGGGC CCCAGGGGCC TCCTGGCTTT GGGAAACCAAG GCTTGGCAGG CCTGAAGGGA 1020
 GAAAGAGGAC CTGCTGGCCT TCCTGGGGGT CCAGGTGCCA AAGGGGAACA AGGGCCAGCA 1080
 GGTCTTCTCG GGAAGCCAGG TCTGACTGGA CCCCCTGGGA ATATGGGACC CCAAGGACCA 1140
 AAAGGCATCC CGGGTAGCCA TGGTCTCCCA GGCCCTAAG GTGAGACAGG GCCAGCTGGG 1200
 CCTGCAGGAT ACCCTGGGGC TAAGGGTGAA AGGGGTTCCT CTGGGTGAGA TGGAAAAACA 1260
 80 GGGTACCCAG GAAACACAGG TCTCGATGGT CCTAAGGGTA ACCCAGGTT ACCAGGTCCA 1320
 AAGGTGATC CTGAGTTGG AGGACCTCCT GGTCTCCAG GCCCTGTGGG CCCAGCAGGA 1380
 GCAAGGGGAA TGCOCGGA CAATGGAGAG GCTGGCCCAA GAGGTGCCCC TGGAAATCCA 1440
 GGTACTAGAG GCCCTATTGG GCCACAGGC ATTCCAGGAT TCCCTGGGTC TAAAGGGGAT 1500
 CAGGAAAGTC CCGTCTCTCC TGGCCAGCT GGCATAGCAA CTAAGGGGCT CAATGGACCC 1560
 85 ACCGGGCCAC AGGTCCAAGA GGCACCTCTG GAGAGCCTGG TCTTCCAGGG 1620
 CCCCCTGGGC CTCAGGCCCC ACCAGGTCAA GCAGTCATGC CTGAGGGTTT TATAAGGCA 1680
 GGCCAAAGGC CCAATCTTTC TGGGACCCCT CTGTATTAGT CCAACCAAGG GGTAAACAGGA 1740

ATGCTGTGT CTGCTTTTAC TGTATTCTC TCCAAAGCTT ACCCAGCAAT AGGAAGTCCC 1800
 ATACCATTTG ATAAAATTTT GTATAACAGG CAACAGCATT ATGACCCCAAG GACTGGAATC 1860
 TTTACTTGTG AGATACCAGG AATATACTAT TTTTCATACC ACGTGCATGT GAAAGGGACT 1920
 CATGTTTGGG TAGGCTGTGA TAAGAATGGC ACCCTGTGTA TGTACACCTA TGATGAATAC 1980
 ACCAAAGGCT ACCTGGATCA GGCTTCAGGG AGTGCCATCA TCGATCTCAC AGAAAATGAC 2040
 CAGGTGTGGC TCCAGCTTCC CAATGCCGAG TCAAATGGCC TATACTCCTC TGAGTATGTC 2100
 CACTCCTCTT TCTCAGGATT CCTAGTGGCT CCAATGTGAG TACACCCACC AGAGCTAATC 2160
 TAAATCTTGT GCTAGAAAAA GCATTCTCTA ACTCTACCCC ACCCTACAAA ATGCATATGG 2220
 AGGTAGGCTG AAAAGAATGT AATTTTATT TTCTGAAATA CAGATTGAG CTATCAGACC 2280
 AACAAACCTT CCCCCTGAAA AGTGAGCAGC AACGTAAAAA CGTATGTGAA GCCTCTCTTG 2340
 AATTTCTAGT TAGCAATCTT AAGGCTCTTT AAGGTTTCTT CCAATATTAA AAAATATCAC 2400
 CAAAGAGTCT CTGCTATGTT AAAAACAAAC AACAAAAAAC AAAGCAACAA AAAAAAAAT 2460
 TAAAAAATAT TGAAGTTTCT GAGCTCTAAG TTATGTGAAA TTGATTGGA GAACTCGGC 2520
 ATTTCTTTT TAAAAAGCC TGTCTTAAC TATGAATATG AGAAGTCTTA GGAACATCC 2580
 AGGAGGTATC ATATAACTTT GTAGAAGTAA AATACTTGAA TATTCAAATT TAAAGACAC 2640
 TGTATCCCTT AAAATATTTC TGATGGTGCA CTACTCTGAG GCCTGTATGG CCCCTTTCAT 2700
 CAATATCTAT TCAATATATC AGGTGCATAT ATACTTGTTA AAGCTCTTAT ATAAAAAGC 2760
 CCCAAATATC TGAAGTTTCT CTGAAATGCA AGGTGCTTTC ATCAATGAAC CTTTCAAAA 2820
 CTTTCTATG ATTGCAGAGA AGCTTTTAT ATACCCAGCA TAACTTGGA ACAGGTATCT 2880
 GACCTATTCT TATTTAGTTA ACACAAGTGT GATTAAATTG ATTTCTTTAA TTCCTTATTG 2940
 AATCTTATGT GATATTGATT TCTGGATTGA CAGAACATTA GCACATGTAC CTGTGCTCTC 3000
 CCATTCAGT GAAGTATATA TTTACACTGA GGGTTTCAA ATTCTAGTAG AAGTGGAGAT 3060
 ATATTATTTA TTTATGACT TACTGTATT TTTATATTGC TGTTTAAAC TTTTAAGCTG 3120
 TGCCTCACTT ATTAAAGCAC AAAATGTTT ACCTACTCCT TATTACGAC ACAATAAAAT 3180
 AACATCAATA GATTTTATAG CTGAATTAAT TTGAAAGCAG CAATTGCTG TTCTCAACCA 3240
 TTCTTCAAG GCTTTTCATT CGACACAATA AAATAACATC AATAG

Seq ID NO: 435 Protein sequence
 Protein Accession #: NP_000484.2

1 11 21 31 41 51
 MLPIPIPLLL VSLNLVHGVF YAERYQMPTG IKGFLPNTKT QFFIPYTIKS KGIIVRGEQG 60
 TPQPPPGAPG RHHPGSGPP GKPGYGSPLG QGEPGLPGPP GPSAVGKPGV PGLPGKPER 120
 GPYGPVKDVG PAGLPGRPRG PGPPGIPGPA GISVPGKPGQ QGPTGAPGR GPPGKGPAG 180
 VPGMNGQKGE MGYGAPGRPG ERGLPGPQGP TGPSGPPGVG XRGENGVPQ PGIKGDRGFP 240
 GEMGPIPPG PQPPFGERGP EGIGKPGPAG APQPGPIPGT KGLPGAPGIA GPPGPPGFGK 300
 PGLPGLKGER GPAGLPGGPG AKGEQGPAGL PKPGLTGPP GNMGPQGPKG IPGSHGLPFG 360
 KGETGPAGPA GYPGAXGERG SPGSDGKPGY PKPGLDGPK GNPGLGPKG DPGVGGPPGL 420
 PGPVGPAGAK GMPGHNGEAG PRGAPGIPGT RSPGPPGIP GPPGSKGDPG SPGPPGPGI 480
 ATKGLNGPTG PPGPPGPRGH SGEPGLPGPP GPPGPPQAV MPEGPIKAG RPSLSGTPLV 540
 SANQVGTGMP VSAFTVILSK AYPAGTPIP FDKILYNRQ HYDPRGTGIFT CQIPGIYFYS 600
 YHVHVKGTHV WVGLYKNGTF VMYTYDEYTK GYLDQASGSA IIDLTENDQV WLQLFNAESN 660
 GLYSSEVHVS SFSGLVLAAPM

Seq ID NO: 436 DNA sequence
 Nucleic Acid Accession #: XM_062811
 Coding sequence: 1..888

1 11 21 31 41 51
 ATGTGGGGCG CTCGCCGCTC GTCCGCTCTCC TCATCCTGGA ACGCCGCTTC GCTCCTGCAG 60
 CTGCTGCTGG CTGCGCTGCT GCGCGCGGGG GCGAGGGCCA GCGGCGAGTA CTGCCACGGC 120
 TGGCTGGACG CGCAGGGGCT CTGGCGCATC GGCTTCCAGT GTCCCGAGCG CTTCCAGCGC 180
 GGCGACGCCA CCATCTGCTG CGGCAGCTGC GCGTTGCGCT ACTGCTGCTC CAGCGCCGAG 240
 GCGCGCCTGG ACCAGGGCGG CTGCGACAAT GACCGCCAGC AGGCGGCTGG CGAGCCTGGC 300
 CGGCGGACCA AAGACGGCCC CGACGGCTCG GCAGTGCCCA TCTACGTGCC GTTCCTCATT 360
 GTTGGCTCGG TGTTTCTGCG CTTTATCATC TTGGGGTCCC TGTGTGCAGC CTGTTGCTGC 420
 AGATGTCTCC GGCTTAAGCA GGATCCCCAG CAGAGCCGAG CCCCAGGGGG TAACCGCTTG 480
 ATGGAGACCA TCCCAGTAT CCCCAGTGCC AGCACTTCCC GGGGGTCTGT CTCACGCCAG 540
 TCCAGCACAG CTGCCAGTTC CAGCTCCAGC GCCAATCTAG GGGCCCGGGC GCCCCCAACA 600
 AGGTACACAGA CCAACTGTTG CTTGCCGGAA GGGACCATGA ACAACGTGTA TGTCAACATG 660
 CCCACGAATT TCTCTGTGCT GAACTGTGAG CAGGCCACCC AGATTGTGCC ACATCAAGGG 720
 CAGTATCTGC ATCCCCCATA CGTGGGGTAC ACGGTGCAGC ACGACTCTGT GCCCATGACA 780
 GCTGTGCCAC CTTTCATGGA CGGCCTGCAG CTTGGCTACA GGCAGATTCA GTCCCCCTTC 840
 CCTCACACCA ACAGTGAACA GAAGATGTAC CCAGCGGTGA CTGTATAA

Seq ID NO: 437 Protein sequence
 Protein Accession #: XP_062811

1 11 21 31 41 51
 MWGARRSSVS SSWNAASLLQ LLLAALLAAG ARASGEYCHG WLDAQGVWRI GFQCPERFDG 60
 GDATICCGSC ALRYCCSSAE ARLDQGGCDN DRQQGAGEPG RADKDGPDGS AVPIYVPFLI 120
 VGSVFPVPII LGSLVAACCC RCLRPKQDFQ QSRAPGGNRL METIPMIPSA STSRGSSSRQ 180
 SSTAASSSSS ANSGARAPPT RSQTNCCLEP GTMNNVVNM PTNFSVLNCO QATQIVPHQG 240
 QYLHPPYVGY TVQHDSVPMT AVPPFMDGLQ PGYRQIQSPF PHTNSEQKMY PAVTV

Seq ID NO: 438 DNA sequence
 Nucleic Acid Accession #: NM_004004.1
 Coding sequence: 1..681

1 11 21 31 41 51
 ATGGATTGGG GCACGCTGCA GACGATCCTG GGGGGTGTGA ACAAACTCTC CACCAGCATT 60
 GGAAAGATCT GGCTCACCGT CCTCTTCATT TTTGCGATTA TGATCCTCGT TGTGGCTGCA 120
 AAGGAGGTGT GGGGAGATGA GCAGGCCGAC TTTGTCTGCA ACACCTGCA GCCAGGCTGC 180

AAGAACGTGT GCTACGATCA CTACTTCCCC ATCTCCACA TCCGGCTATG GGCCTGCGAG 240
 CTGATCTTCG TGTCCAGCCC AGCGCTCCTA GTGGCCATGC ACGTGGCCTA CCGGAGACAT 300
 GAGAAGAAGA GGAAGTTTCA CAAGGGGGAG ATAAAGAGTG AATTAAAGGA CATCGAGGAG 360
 ATCAAAACCC AGAAGGTCOG CATCGAAGGC TCCCTGTGGT GGACCTACAC AAGCAGCATC 420
 TTCTTCCGGG TCATCTTCGA AGCCGCCCTC ATGTACGCTT TCTATGTCA GTACGACGGC 480
 TTCTCCATGC AGCGGCTGGT GAAGTGCAAC GCCTGGCCTT GTCCCAACAC TGTGGACTGC 540
 TTTGTGTCCC GGGCCACGGA GAAGACTGTC TTCACAGTGT TCATGATTGC AGTGTCTGGA 600
 ATTTGCATCC TGCTGAATGT CACTGAATTG TGTATTTCG TAATTAGATA TTGTTCTGGG 660
 AAGTCAAAAA AGCCAGTTTA A

Seq ID NO: 439 Protein sequence
 Protein Accession #: NP_003995.1

1 11 21 31 41 51
 MDWGLTQTL GGVNKHSTSI GKILVTLVFI PRIMILVVAA KEVWGDEQAD FVCNTLQPGC 60
 KNVCYDHYFP ISHIRLWALQ LIFVSSPALL VAMHVAYRRH EKRRKFIKGE IKSEPKDIEE 120
 IKTKVRIEG SLWWTYTSIS FFRVPEAAP MYVFVYMDG FSMQRLVKCN ANPCPNTVDC 180
 FVSRPTEKTV FTVFMIASVG ICILLNVTEL CYLLIRYCSG KSKKPV

Seq ID NO: 440 DNA sequence
 Nucleic Acid Accession #: XM_061091.1
 Coding sequence: 1..2481

1 11 21 31 41 51
 ATGCCAAATA CTTACAGAAC AACCAGGATT GAAATTTGGC TTCTCCAAGA GCCGCCCGGG 60
 CACCGAGCGC TGGTGCCTCG TCTCCTCCG GTGAGTCCCA GCCCGGAGTT GGCTCTGGCG 120
 CCGGGTACC CGCCAGTGCC GGCTGCCGAT GACCCGATTCA CGCTCCCGAT GATTGGAGGT 180
 CAGATGCATG GTGAGAAGGT AGATCTCTGG AGCCTTGGTG TTCTTTGCTA TGAATTTTAA 240
 GTTGGGAAGC CTCCTTTTGA GGCAAACGAA GTCCATGTAA GCAAGAAAC CATCGGGAAG 300
 ATTTACAGTG CCAGCAAAAT GATGTGGTGC TCGGCTGCAG TGGACATCAT GTTCTGTGTA 360
 GATGGGTCTA ACAGCGTCGG GAAAGGGAGC TTTGAAAGGT CCAAGCACTT TGCCATCACA 420
 GTCTGTGACG GTCTGGACAT CAGCCCCGAG AGGGTCAGAG TGGGAGCATT CCAGTTCACT 480
 TCCACTCTCT ATCTGGAAAT CCCCTTGGAT TCATTTTCAA CCAACACGGA AGTGAAGGCA 540
 AGAATCAAGA GGATGGTTTT CAAAGGAGGG CGCACGGAGA CGGAACCTGC TCTGAAATAC 600
 CTCTGCACA GAGGGTTGCC TGGAGGCAGA AATGCTTCTG TGCCCCAGAT CCTCATCATC 660
 GTCACTGATG GGAAGTCCCA GGGGATGTG GCACCTGCCAT CCAAGCAGCT GAAGGAAGG 720
 GGTGTCACTG TGTCTGCTGT GGGGTCAGG TTTCCAGAGT GGGAGGAGCT GCATGCACTG 780
 GCCAGCGGCG CTAGAGGGCA GCACGTGCTG TTGGCTGAGC AGGTGGAGGA TGCCACCAAC 840
 GGCCTCTTCA GCACCTCAG CAGCTCGGCC ATCTGTCCA GCGCCACGCC AGCTGGGAGC 900
 CCGAGCTTG TCTTCATGGA GCGGTTAATG GGCATCTCTC TGATAGGCC CTGTGACTCG 960
 CAGCCCTGCC AGAATGGAGG CACATGTGTT CCAGAAGGAC TGGACGGCTA CCAGTGCTCT 1020
 TGCCCGCTGG CCTTTGGAGG GGAGGCTAAC TGTGCCCTGA AGCTGAGCCT GGAATGCAGG 1080
 GTGACCTCTC TCTCTCTGCT GGACAGCTCT GCGGGCACCA CTCTGGACGG CTTCCTCGCG 1140
 GCCAAAGTCT TGTGAAGCG GTTGTGCGG GCGGTGCTGA GCGAGGACTC TCGGGCCCGA 1200
 GTGGGTGTGG CCACATACAG CAGGGAGCTG CTGGTGGCGG TGCTGTGGG GGAGTACCAG 1260
 GATGTGCTG ACCTGGTCTG GAGCTCGAT GGCATTCCCT TCCGTGGTGG CCCCACCCTG 1320
 ACGGGCAGTG CCTTGCAGCA GCGGCGAGAG CGTGGCTTCG GGAGCGCCAC CAGGACAGGC 1380
 CAGGACCGGC CACGTAGAGT GGTGGTTTGT CTCACTGAGT CACACTCCGA GGATGAGGT 1440
 GCGGGCCCGA CCGCTCACGC AAGGGCGCGA GAGCTGTCTC TGCTGGGTGT AGGCAGTGAG 1500
 GCGGTGCGGG CAGAGCTGGA GGAGATCACA GGCAGCCCAA AGCATGTGAT GGTCTACTCG 1560
 GATCCTCAGG ATCTGTCAA CCAAATCCCT GAGCTGCAGG GGAAGCTGTG CAGCCGCGAG 1620
 CGGCCAGGGT GCGCGACACA AGCCCTGGAC CTGCTCTTCA TGTGGGACAC CTCTGCCTCA 1680
 GTAGGGCCCG AGAATTTTGC TCAGATGCAG AGCTTTGTGA GAAGCTGTGC CCTCCAGTTT 1740
 GAGGTGAACC CTGACGTGAC ACAGTTCGGC CTGGTGGTGT ATGGCAGCCA GGTGCAGACT 1800
 GCCTTCGGGC TGGACACCAA ACCCACCGG GCTGCGATGC TGCGGGCCAT TAGCCAGGCC 1860
 CCTTACCTAG GTGGGGTGGG CTCAGCCGGC ACCGCCCTGC TGACATCTA TGACAAAGTG 1920
 ATGACCGTCC AGAGGGGTGC CCGGCTTGGT GTCCCCAAAG CTGTGGTGGT GCTCACAGGC 1980
 GGGAGAGGCG CAGAGGATGC AGCCGTTCTT GCCCAGAAGC TGAGGAACAA TGGCATCTCT 2040
 GTCTTGTGCG TGGGCGTGGG GCCTGTCTTA AGTGAGGGTC TGCGGAGGCT TGCAAGTCCC 2100
 CGGATTTCCC TGATCCACGT GGCAGCTTAC GCCGACCTGC GGTACCAACA GGACGTGCTC 2160
 ATTGAGTGAG TGTGTGAGA AGCCAAGCAG CCACTCAACC TCTGCAAAAC CAGCCCGTGC 2220
 ATGAATGAGG CAGAGTGCCT CCTGCAGAA GGGAGCTACC GCTGCAAGTG TCGGATGGC 2280
 TGGGAGGCGC CCCACTGCGA GAACCGTGAG TGGAGCTCTT GCTCTGTATG TGTGAGCCAG 2340
 GGATGGATTC TTGAGACGCC CCTGAGGCAC ATGGCTCCCG TGCAGGAGGG CAGCAGCCGT 2400
 ACCCTGCCCA GCAACTACAG AGAAGGCCCTG GGCACGTAAA TGGTGCCTAC CTTCTGGAAT 2460
 GTCTGTGCCC CAGGTCTCTA G

Seq ID NO: 441 Protein sequence
 Protein Accession #: XP_061091.1

1 11 21 31 41 51
 MPNTSGTTRI EIWLLEPPG HRLVAALLP VSPSPALALA PGYPPVPAAD DRFTLPMIGG 60
 QMHGEKVDLW SLGVLCEYFL VGKPPPEANE VHVSKETIGK ISAASKMMC SAAVDIMFLL 120
 DGSNSVKGGS FERSKHFAIT VCDGLDISFE RVRVGAQFQS STPHLEFPD SFSTQQEVKA 180
 RIKRMVFKGG RTETELALYK LHRGLPGGR NASVPQILII VTDGKSGQDV ALPSKQLKER 240
 GVTVPFVGVFR FPRWEELHAL ASEPRGQHVLA EQVEDATN GLFSTLSSSA ICSSATPAGS 300
 PELVFMERLM GISLIGPCDS QPCQNGGTCV PEGLDGYQCL CPLAFGGEAN CALKLSLECR 360
 VDLEFLDLSS AGTTLDGFLR AKVFVKRFVR AVLSEDSRAR VGVATYSREL LVAVFVGEYQ 420
 DVPLDVSLD GIPFRGGPTL TGSALRQAAE RGFSAATRTG QDRPRRVVL LTESHSEDEV 480
 AGPARHARAL ELLLLGVGSE AVRAELEBIT GSPKHMVYS DPQDLFNQIF ELQGLKCSRQ 540
 RFGCRTQALD LVFMLDTSAS VGPFNAQMQ SFVRSALQF EVNPDVTQV LVVYGSQVQT 600
 APLDTPKPTR AAMLRALISA PYLGGVGSAG TALLHIYDKV MTVQRGARPG VPKAVVVLTG 660
 GRGAEDAAVP AQLRLNNGIS VLVVGVGPVL SEGRLRLAGP RDSLIHVAAY ADLRYHQDVL 720

IEWLCEGEAKQ PVNLCRPSPC MNEGSCVLQN GSYRCKCRDG WEGPHCENRE WSSCSVCVSG 780
GWILETPLRH MAPVQEGSSR TTPSNYREGL GTEMVPTFWN VCAPGP

Seq ID NO: 442 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..2424

```

1      11      21      31      41      51
|      |      |      |      |      |
10  ATGCCCCCTT TCCTGTTGCT GGAGGCCGTC TGTGTTTTCC TGTTTTCCAG AGTGCCCCCA 60
    TCTCTCCCTC TCCAGGAAGT CCATGTAAGC AAAGAAACCA TCGGGAAGAT TTCAGCTGCC 120
    AGCAAAATGA TGTGGTGCTC GGCTGCAGTG GACATCATGT TTCTGTGTAGA TGGGTCTAAC 180
    AGCGTCGGGA AAGGGAGCTT TGAAGAGTCC AAGCACTTTG CCATCACAGT CTGTGACGGT 240
    CTGGACATCA GCCCCGAGAG GGTTCAGAGT GGAGCATTCC AGTTTCAGTTC CACTCCTCAT 300
15  CTGGAATTCC CCTTGGATTG ATTTTCAACC CAACAGGAAG TGAAGGCAAG AATCAAGAGG 360
    ATGGTTTTTA AAGGAGGGCG CACGGAGACG GAACTTGCTC TGAATACCT TCTGCACAGA 420
    GGGTTGCTGT GAGGCAGAAA TGCTTCTGTG CCCCAGATCC TCATCATCGT CACTGATGGG 480
    AAGTCCACAG GGGATGTGGC ACTGCCATCC AAGCAGCTGA AGGAAAGGGG TGTACTGTGT 540
    TTTGCTGTGG GGGTCAGGTT TCCAGGTTGG GAGGAGCTGC ATGCACTGGC CAGCGAGCCT 600
20  AGAGGCGCAG ACGTGTCTGT GGCTGAGCAG GTGGAGGATG CCACCAACGG CCTCTTCAGC 660
    ACCTCAGCAG GTCTGCGCAT CTGCTCCAGC GCCACGCCAG ACTGCAGGGT CGAGGCTCAC 720
    CCCTGTGAGC ACAGGACGCT GGAGATGCTC CGGAGTTTCG CTGGCAATGC CCCATGCTGG 780
    AGAGGATCGC GGGCGACCTT TGCGGTGCTG GCTGCACACT GTCCCTTCTA CAGCTGGAAG 840
    AAGTGTTCCT TAACCCACCC TGCCACCTGC TACAGGACCA CCTGCCAGG CCCCTGTGAC 900
25  TCGCAGCCCT GCCAGAAATG AGGCACATGT GTTCCAGAAG GACTGGACGG CTACCAAGTGC 960
    CTCTGCCCCG TGGCCTTTGG AGGGGAGGCT AACTGTGCCC TGAAGCTGAG CCTGGAATGC 1020
    AGGGTCGACC TCCTCTTCTT GCTGGACAGC TCTGCCGGCA CCATCTGGA CGGCTTCCTG 1080
    GGGGCCAAAG TCTTCGTGAA GCGGTTTGTG CCGGCCGTGC TGAGCGAGGA CTCTCGGGCC 1140
    CGAGTGGGTG TGGCCAGATA CAGCAGGGAG CTGCTGGTGG CGGTGCTGTG GGGGGAGTAC 1200
30  CAGGATGTGC CTGACCTGTT CTGGAGCCTC GATGGCATTG CCTTCCGTGG TGGCCCCACC 1260
    CTGACGGGCA GTCCCTTGCG GCAGGCGGCA GAGCGTGGCT TCGGGAGCGC CACCAGGACA 1320
    GGCCAGGACC GGCCACGTAG AGTGGTGGTT TTGCTCACTG AGTCACACTC CGAGGATGAG 1380
    GTTTCGGGGC CAGCGCTGCA CGCAAGGGCG CGAGAGCTGC TCCTGTCTGG TGTAGGCAGT 1440
    GAGGCGGTGC TGGCAGAGCT GGAGGAGATC ACAGGCAGCC CAAAGCATGT GATGGTCTAC 1500
35  TCGGATCCTC AGGATCTGTT CAACCAAAATC CCTGAGCTGC AGGGGAAGCT GTGCAGCCGG 1560
    CAGCGGCCAG GGTGCGGAGC ACAAGCCCTG GACCTCGTCT TCATGTTGGA CACCTCTGCC 1620
    TCAGTAGGGC CCGAGAAATT TGCTCAGATG CAGAGCTTTG TGAGAAGCTG TGCCTCCAG 1680
    TTTGAGGTGA ACCCTGACGT GACACAGGTC GGCCTGGTGG TGTATGCGAG CCAGGTGCAG 1740
    ACTGCCTTCG GGTGGACAC CAAACCCACC CGGCTGCGA TGCTGCGGGC CATTAGCCAG 1800
40  GCCCCCTACC TAGGTGGGGT GGGCTCAGCC GGCACCGCCC TGCTGCACAT CTATGACAAA 1860
    GTGATGACCG TCCAGAGGGG TGCCCGGCGT GGTGTCCCCA AAGCTGTGGT GGTGTCCACA 1920
    GCGCGGAGAG GCGCAGAGGA TGCAGCCGTT CTGCCCCAGA AGCTGAGGAA CAATGGCATC 1980
    TCTGTCTTGG TCGTGGGCGT GGGGCCCTGT CTAAGTGAGG GTCTGCGGAG GCTTGCAGGT 2040
    CCCCGGGATT CCTTGATCCA CGTGGCAGCT TACGCCGACC TGCGGTACCA CCAGGACGTG 2100
45  CTCATTGAGT GGCTGTGTGG AGAAGCCAAG CAGCCAGTCA ACCTCTGCAA ACCCAGCCCG 2160
    TGCATGAATG AGGGCAGTGC CGTCTGCAG AATGGGAGCT ACCGCTGCAA GTGTGCGGAT 2220
    GGCTGGGAGG GCCCCCCTG CGAGAACCCT GAGTGGAGCT CTGTCTCTGT ATGTGTGAGC 2280
    CAGGGATGGA TTCTTGAGAC GCCCCTGAGG CACATGGCTC CCGTGCAGGA GGGCAGCAGC 2340
    CGTACCCCTC CCAGCAACTA CAGAGAAGGC CTGGGCACTG AAATGGTGCC TACCTCTCG 2400
50  AATGTCTGTG CCCCAGGTCC TTAG

```

Seq ID NO: 443 Protein sequence
Protein Accession #: Eos sequence

```

1      11      21      31      41      51
|      |      |      |      |      |
55  MPFFLLLEAV CVFLFSRVFP SLPLQEVHVS KETIGKISAA SKMMWCSAAV DIMFLDGSN 60
    SVKGGSFERS KHPAITVCDG LDISPERVRV GAFQFSSTPH LEFFLDSFST QQEVKARIKR 120
    MVFKGGRTET ELALKYLHRH GLPGGRNASV PQILIIIVTDG KSQGDVALPS KQLKERGVTV 180
60  FAVGVRFPRW EELHALASEP RGQHVLLAEQ VEDATNGLFS TLSSSAICSS ATPDCRVEAH 240
    PCEHRTLEMV REFAGNAPCW RGSRRTLAVL AAHCFFYSWK RVFLTHPATC YRTTCPGPCD 300
    SQPCQNGGTC VEBGLDGYQC LCPLAFGGEA NCALKLSLEC RVDLLFLDLS SAGTTLDGFL 360
    RAKVFVKRFV RAVLSEDSRA RVGVATYSRE LLVAVPVGEY QDVPDLVWSL DGIPFRGGPT 420
    LTGSALRQAA ERGFGSATRT QDRPRRVVV LLTESHSEDE VAGPARHARA RELLLGVGS 480
65  EAVRAELEBI TGSPKHMVYV SDPQDLFNQI PELQGHLCSS RRPGRCTQAL DLVFMLDTS 540
    SVGPENFAQM QSFVRSCALQ FEVNPVDVTQV GLVVYGSQVQ TAFGLDTKPT RAAMLRAISQ 600
    APYLGGVGSA GTALLHIYDK VMTVQRGARP GVFKAVVVLV GGRGAEDAAY PAQKLRRNGI 660
    SVLVVGVGVP LSEGLRLLAG PRDSLHVAA YADLRYHQDV LIEWLCEGAK QPVNLCRPS 720
    CMNEGSCVLQ NGSYRCKCRD WEGPHCENR EWSSCSVCVS QGWILETPLR HMAPVQEGSS 780
70  RTPPSNYREG LGTEMVPTFW NVCAPGP

```

Seq ID NO: 444 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 89..2356

```

1      11      21      31      41      51
|      |      |      |      |      |
75  GCCCCCTGGC CCGAGCCGCG CCCGGGCTCTG TGAGTAGAGC CGCCCGGGCA CCGAGCGCTG 60
    GTCGCGCTCT TCCTTCGCTT ATATCAACAT GCCCCCTTTC CTGTGCTGGG AAGCCGCTCTG 120
    TGTTTTCCCTG TTTTCCAGAG TGCCCCCATC TCTCCCTCTC CAGGAAGTCC ATGTAAGCAA 180
80  AGAAACCATC GGAAGATTTT CAGCTGCCAG CAAAATGATG TGGTGCTCGG CTGCACTGGA 240
    CATCATGTTT CTGTTAGATG GGTCTAACAG CGTCGGGAAA GGGAGCTTTG AAAGGTCCAA 300
    GCACTTGCTC ATCAGAGTCT GTGACGGTCT GGACATCAGC CCGAGAGGGG TCAGAGTGGG 360
    AGCATTCAGT TTCAGTTCCT CTCCTCATCT GGAATTCCTT TTGATTTCAT TTTCACCCCA 420
85  ACAGGAAGTG AAGGCAGAGA TCAAGAGGAT GGTTTTCAAA GGAGGGCGCA CGGAGACGGA 480
    ACTTGCTCTG AAATACCTTC TGCACAGAGG GTTGCCTGGA GGCAGAAATG CTCTGTGCCC 540
    CCAGATCCTC ATCATCGTCA CTGATGGGAA GTCCAGGGG GATGTGGCAC TGCCATCCAA 600

```

	GCAGCTGAAG	GAAAGGGGTG	TCACTGTGTT	TGCTGTGGGG	GTCAGGTTTC	CCAGGTGGGA	660
	GGAGCTGCAT	GCACTGGCCA	GCAGAGCTAG	AGGGCAGCAC	GTGCTGTGGG	CTGAGCAGGT	720
	GGAGGATGCC	ACCAACGGCC	TCTTCAGCAC	CCTCAGCAGC	TGCGCCATCT	GCTCCAGCGC	780
5	CACGCCAGAC	TGACGGGTG	AGGCTCACCC	CTGTGAGCAC	AGGACCGTGG	AGATGGTCCG	840
	GGAGTTCGCT	GGCAATGCCC	CATGCTGGAG	AGGATCGCGG	CGGACCCCTG	CGGTGCTGGC	900
	TGCACACTGT	CCCTTCTACA	GCTGGAAGAG	AGTGTTCCTA	ACCCACCCCTG	CCACCTGCTA	960
	CAGGACCACC	TGCCCAGGCC	CCTGTGACTC	GCAGCCCTGC	CAGAATGGAG	GCACATGTGT	1020
	TCAGAAAGGA	CTGGACGGCT	ACCAAGTGCT	CTGCCCGCTG	GCCTTTGGAG	GGGAGGCTAA	1080
10	CTGTGCCCTG	AAGCTTGACC	TGGAATGCAG	GGTCGACCTC	CTCTTCCTGC	TGGACAGCTC	1140
	TGCGGGCACC	ACTCTGGACG	GCTTCCTGCG	GGCCAAAGTC	TTCGTGAAGC	GGTTTGTGCG	1200
	GGCGGTGCTG	AGCGAGGACT	CTCGGGCCCG	AGTGGGTGTG	GCCACATACA	GCAGGGAGCT	1260
	GCTGTGTGGC	GTGCTGTGGG	GGGAGTACCA	GGATGTGCCT	GACCTGGTCT	GGAGCCTCGA	1320
	TGGCATTCCT	TTCGCTGGTG	GCCCCACCCT	GACGGGCAGT	GCCTTGGCGC	AGGCGGCAGA	1380
	GGGTGGCTTC	GGGAGCGCCA	CCAGGACAGG	CCAGGACCGG	CCACGTAGAG	TGTTGGTTTT	1440
15	GCTCACTGAG	TCACACTCCG	AGGATGAGGT	TGCGGGCCCA	GCGCGTCACG	CAAGGGCGCG	1500
	AGAGCTGCTC	CTGCTGGGTG	TAGGCAGTGA	GGCCGTGCGG	GCAGAGCTGG	AGGAGATCAC	1560
	AGGCAGCCCA	AAGCATGTGA	TGCTCTACTC	GGATCCTCAG	GATCTGTTC	ACCAATATCC	1620
	TGAGCTGCGA	GGGAAGCTGT	GCAGCCGGCA	GCGGCCAGGG	TGCCGGACAC	AAGCCCTGGA	1680
20	CCTCGTCTTC	AGTGTGGTGA	CCCTCTGCCT	AGTAGGGCCC	GAGAATTTTG	CTCAGATGCA	1740
	GAGCTTTGTG	AGAAGCTGTG	CCCTCCAGTT	TGAGGTGAAC	CCTGACGTGA	CACAGGTCCG	1800
	CCTGTGTGGT	TATGCGAGGC	AGGTGCAGAC	TGCTTCGGG	CTGGACACCA	AACCCACCCG	1860
	GGCTGCGATG	CTGCGGGCCA	TTAGCCAGGC	CCCTTACCTA	GGTGGGTGGG	GCTCAGCCCG	1920
	CACCCGCCCTG	CTGCACATCT	ATGACAAAGT	GATGACCGTC	CAGAGGGGTG	CCCAGCCTGG	1980
25	TGTCCCAAAA	GCTGTGGTGG	TGCTCACAGG	CGGAGAGGCG	GCAGAGGATG	CAGCCGTTTC	2040
	TGCCCAAGAG	CTGAGGAACA	ATGGCATCTC	TGCTTGTGGT	GTGGCGGTGG	GGCCTGTCTT	2100
	AAGTAGGGGT	TGCGGAGGCT	TTGCAGGTCC	CCGGGATTC	CTGATCCACG	TGGCAGCTTA	2160
	CGCCGACCTG	CGGTACCAAC	AGGACGTGCT	CATTGAGTGG	CTGTGTGGAG	AAGCCAAAGC	2220
	GCCAGTCAAC	CTCTGCAAA	CCAGCCCGTG	CATGAATGAG	GCCAGCTGCG	TCCTGCAGAA	2280
30	TGGGAGCTAC	CGCTGCAAGT	GTGCGGATGG	CTGGGAGGGC	CCCCACTGCG	AGAACCGATT	2340
	CTTGAGACGC	CCCTGAGGCA	CATGGCTCCC	GTGCGAGGAG	GCAGCAGCCG	TACCCCTCCC	2400
	AGCAACTACA	GAGAAGGCCT	GGGCACTGAA	ATGGTGCCCTA	CCTTCTGGAA	TGCTGTGCCC	2460
	CCAGTCCCTT	AGAATGTCTG	CTTCCCGCCG	TGGCCAGGAC	CACATATTCT	ACTGAGGGAG	2520
	GAGGATGTCC	CAACTGCAGC	CATGCTGCTT	AGAGACAAGA	AAGCAGCTGA	TGTCACCCAC	2580
35	AAACGATGTT	GTGAAAAAGT	TTTGATGTGT	AAGTAAATAC	CCACTTTCTG	TACCTGTCTG	2640
	GCCTTGTGTA	GGCTATGTCA	TCTGCCACCT	TTCCCTTGAG	GATAAACAGG	GGGTCTCTGA	2700
	GACTTAAATT	TAGCGGCCTG	ACGTTCTCTT	GCACACAATC	AATGCTCGCC	AGAATGTTGT	2760
	TGACACAGTA	ATGCCACGCA	GAGGCCTTTA	CTAGAGCATC	CTTTGGACGG		

Seq ID NO: 445 Protein sequence
Protein Accession #: Eos sequence

	1	11	21	31	41	51	
45	MPPFLLEAV	CVFLFSRVPP	SLPLQEVHVS	KETIGKISAA	SKMMWCSAAV	DIMPLLDGSN	60
	SVGKGSFERS	KHFAITVCDG	LDISPERVRV	GAFQSSSTPH	LEFPLDSFST	QQEVKARIKR	120
	MVFKGGRTE	ELAKYLLHR	GLPGGRNASV	PQILIIIVTDG	KSQGDVALPS	KQLKERGVTV	180
	FAVGVRFPFW	EELHALASEP	RGQHVLAEQ	VEDATNGLFS	TLSSSAICSS	ATPDCRVEAH	240
	PCEHRTLEMV	REFAGNABCV	RGRSRTLAVL	AAHCPFYSWK	RVFLTHPATC	YRTTCPPGCD	300
50	SQPCQNGGTC	VPEGLDGYQC	LCPLAFGGEA	NCALKLSLEC	RVDLLFLDLS	SAGTTLDGFL	360
	RAKVVFVKFV	RAVLSEDSRA	RVGVATYSRE	LLVAVPVGEY	QDVDPDLVWSL	DGIPFRGGPT	420
	LTGSALRQAA	ERGFSGATRT	GQDRPRRVVV	LLTESHSEDE	VAGPARHARA	RELLLLGVGS	480
	EAVRAELEIE	TGSPKHMVY	SDPQDLFNQI	PELQGLKCSR	QRPCRTQAL	DLVFMIDTSA	540
	SVGPENFAQM	QSFRTSCALQ	FEVNPDTVQV	GLVVYGSQVQ	TAFLGLDKPT	RAAMLRASIQ	600
55	APYLGGVGS	GTALLHIYDK	VMTVQRGARP	GVPKAVVVLV	GGRGAEADA	PAQKLNNNGI	660
	SVLVVGVGPV	LSEGLRLRAG	PRDSLIHVAA	YADLRYHQDV	LIEWLCGEAK	QPVNLCCKPS	720
	CNNEGSCVLQ	NGSYRCKRAD	GWEGPHCENR	FLRRP			

Seq ID NO: 446 DNA sequence
Nucleic Acid Accession #: NM_031942.1
Coding sequence: 145..1260

	1	11	21	31	41	51	
65	CCCGAGCCCC	GCCCTCCGG	GCCCGGGTCG	GCGCGCCAG	CCTGCCAGCC	GCGCTGCTGC	60
	TGCTCTCCTC	GCTGTGGGAC	CGCTGACCGC	GCGGCTGCTC	CGCTCTCCCC	GCTCCAAGCG	120
	CCGATCTGGG	CACCCGCCAC	CAGCATGGAC	GCTCGCCGCG	TGCCCGCAGAA	AGATCTCAGA	180
	GTAAAGAAGA	ACTTAAAGAA	ATTGAGATAT	GTGAAGTTGA	TTTCCATGGA	AACCTCGTCA	240
	TCCTCTGATG	ACAGTTGTGA	CAGCTTTGCT	TCTGATAATT	TTGCAAAAC	GAGGCTGCAG	300
70	TCAGTTCGGG	AAGGCTGTAG	GACCCGCGAG	CAGTGCAGGC	ACTCTGGACC	TCTCAGGGTG	360
	GCGATGAAGT	TTCCAGCGCG	GAGTACCAGG	GGAGCAACCA	ACAAAAAAGC	AGAGTCCCCG	420
	CAGCCCTCAG	AGAATTCTGT	GACTGATTCC	AACTCCGATT	CAGAAGATGA	AAGTGGAAATG	480
	AATTTTGTGG	AGAAAAGGGC	TTTAAATATA	AAGCAAAACA	AAGCAATGCT	TGCAAAACTC	540
	ATGTCTGAAT	TAGAAAGCTT	CCCTGGCTCG	TTCCGTGGAA	GACATCCCCC	CCCAGGCTCC	600
75	GACTCACAAT	CAAGGAGACC	GCGAAGGCGT	ACATTCCCGG	GTGTTGCTTC	CAGGAGAAAC	660
	CCTGAACGGA	GAGCTCGTCC	TCTTACCAGG	TCAAGGTCCC	GGATCCTCGG	GTCCCTTGAC	720
	GCTCTACCCA	TGGAGGAGGA	GGAGGAAGAG	GATAAGTACA	TGTTGGTGAG	AAAGAGGAAG	780
	ACCGTGGATG	GCTACATGAA	TGAAGATGAC	CTGCCCAGAA	GCCGTGCTC	CAGATCATCC	840
	GTGACCCCTC	CGCATATAAT	TCGCCAGTGG	GAAGAAATTA	CAGAGGAGGA	GTGGAGAAAC	900
80	GTCTGCAGCA	ATTCTCAGAA	GAAGATATAT	AACCGTTTAC	TGGGCTCTAC	TTGTTCATCA	960
	TGCCGTGAGA	AGACTATTGA	TACCAAAACA	AACCTGCAGAA	ACCCAGACTG	CTGGGGCGTT	1020
	CGAGGCGCAG	TCTGTGGCCC	CTGCCCTTCA	AACCGTTATG	GTGAAGAGGT	CAGGGATGCT	1080
	CTGCTGGATC	CGAACTGGCA	TTGCCCGCCT	TGTCGAGGAA	TCTGCAACTG	CAGTTTCTGC	1140
	CGGCAGCGAG	ATGGACGGTG	TGCGACTGGG	GTCCCTGTGT	ATTAGCCAA	ATATCATGGC	1200
85	TTTGGGAATG	TGCTATGCTA	CTTGAAAAGC	CTGAACACAG	AATTTGAAAT	GCAAGCATAA	1260
	TATCTGAAAG	ATTTGCTGCC	CTGCTTCTAC	TTCTCAAATC	TTTCTGTGAA	AAGTTTCCAA	1320
	TTTTTCACT	GAAACCTGAG	TTAAAATCT	TGATGATCAG	CCTGTTTCAT	AAGAACTCC	1380
	AATCAAGTTA	ATCTTAGCAG	ACATGTGTTT	CTGGAGCATC	ACAGAAGGTA	TATTGCTAGT	1440

TACACTTTGC CCTCTGCAG TTTCTTCTCT GCTCCCAACC CCCATCTCAT AGCATCCCCC 1500
 TCTATTTTCCA ATGCTCTCTT CCAACCGCTT AGTTTCTGAA TTTCTTTTAA ATTACAGTTT 1560
 TATGAAAGCA TATTTTATTT ACTTGGTGTG GAAATAGCCC TCATAAAACC TAAGCACTTG 1620
 5 GAAACACAAAT AATAGTATTA ACTAAGTAGA TCTATTGAAT TTCAGAGAAG AGCCTTCTAA 1680
 CTGTGTTTACA CAAAACCGAG TATGATTAG CACTCATACT AGTTGAAATT TTTAATAGAA 1740
 TCAAGGCACA AAAGTCTTAA AACCATGTGG AAAAATTAGG TAATTATTGC AGATTGATGT 1800
 CTCTCAATCC CATGTATTGC GCTTATGTTA CAAGTTGTGT TCACAGTTGA GACTTAATTT 1860
 CTCCTAATTT CTTCGCCCCG AAGGGAAGT GGTGCGTCCA GCTTACACGA TCATAATTCA 1920
 10 AAGGTTGGTG GGCAATGTAA TACTTAATTA AAATAATGAT GGAAGAGCTA TCTGGAGATT 1980
 ATGAGTAAGC TGATTGTAAT TTTAGTATA AAACCTTAGT ATAATTGTAG TTTGCAAGT 2040
 TTATTTTCACT TCACATGTAA GGTATTGCAA ATAAATTCCT GGACAATTTT GTATGGAAAC 2100
 TTGATATTAA AAACGTAGTCT GTGGTTCTTT GCAGTTTCTT GTAAATTTAT AAACCAGGCA 2160
 CAAGGTTCAA GTTTAGATTT TAAGCACTTT TATAACAATG ATAAGTGCTT TTTGGAGAT 2220
 15 GTAACCTTTA GCAGTTTGTG AACCTGACAT CTCTGCCAGT CTAGTTTCTG GGCAGGTTTC 2280
 CTGTGTCACT ATTCCTCCCTC CTCTTTGCAT TAATCAAGGT ATTTGGTAGA GGTGGAACTC 2340
 AAGTGTTTGT ATGTCCAATT TACTTGCTA TGTAACCAT TGCTGTGCCA TTCAATGTTT 2400
 GATGCATAAT TGGACCTTGA ATCGATAAGT GTAAATACAG CTTTGTATCT GTAATGCTTT 2460
 TATACAAAAG TTTATTTTAA TAATAAATG TTTGTTCTAA AAAAAAAAAA

Seq ID NO: 447 Protein sequence
 Protein Accession #: NP_114148.1

1 11 21 31 41 51
 25 MDARRVPQKD LRVKIKNLKFP RYVKLISMET SSSSDSDSCDS FASDNFANTR LQSVREGCRT 60
 RSQCRHSGPL RVAMKFPARS TRGATNKKAE SRQPSSENSVT DSNDSSEDES GMPLEKRAL 120
 NIKQNKAMLA KLMSLESEFP GSFRGRHPLP GSDSQSRRFR RRTFPGVASR RNPERRARPL 180
 TRSRSRILGS LDALPMEESE EEDKYMIVRK RKTVDGYMME DDLPRSRRSR SSVTLPHIR 240
 30 PVSEITBEEL ENVCNSNREK IYNRSLGSTC HQCRQKRTIDT KTNCRNPDCC GVRGQPCGP 300
 LRNRYGEEVR DALLDPNWHC PPCRGICNCS PCRQDRGRCA TGVLVYLAKY HGFQNVHAYL 360
 KSLKQEFEMQ A

Seq ID NO: 448 DNA sequence
 Nucleic Acid Accession #: NM_019894
 Coding sequence: 1..1314

1 11 21 31 41 51
 40 ATGTTACAGG ATCCTGACAG TGATCAACCT CTGAACAGCC TCGATGTCAA ACCCTGCGC 60
 AAACCCCGTA TCCCATGGA GACCTTCAGA AAGGTGGGGA TCCCATCAT CATAGCACTA 120
 CTGAGCTCTG CGAGTATCAT CATGTGGTT GTCCCTCATCA AGGTGATTCG GGATAAATAC 180
 TACTTCTCTC GCGGGCAGCC TCTCCACTTC ATCCCGAGGA AGCAGCTGTG TGACGGAGAG 240
 CTGGACTGCT CCTTGGGGGA GACGAGGAG CACTGTGTCA AGAGCTTCCC CGAAGGGCCT 300
 45 GCAGTGGCAG TCCGCTCTC CAAGGACCGA TCCCACTGCG AGGTGCTGGA CTGGGCCACA 360
 GGGAACTGGT TCTCTGCTG TTTGACAAAC TTCACAGAAG CTCTCGCTGA GACAGCCTGT 420
 AGGCAGATGG GCTACAGCAG CAAACCCACT TTCAGAGCTG TGGAGATTGG CCCAGACCGA 480
 GATCTGGATG TTGTTGAAAT CACAGAAAAC AGCCAGGAGC TTCGCATGCG GAACTCAAGT 540
 GGGCCCTGTC TCTCAGGCTC CACTGGTCTCC CTGCACTGTC TTGCTGTGG GAAGAGCCTG 600
 50 AAGACCCCCC GTGTGGTGGG TGGGGAGGAG GCCTCTGTGG ATTCTTGGCC TTGGCAGGTC 660
 AGCATCCAGT ACGACAAACA GCACGTCTGT GGAGGGAGCA TCCTGGACCC CCACTGGGTC 720
 CTCACGGCAG CCCACTGTCT CAGGAAACAT ACGATGTGT TCAACTGGAA GGTGCGGGCA 780
 GGCTCAGACA AACTGGGCGA CTTCCTCATCC CTGGCTGTGG CCAAGATCAT CATCATTTAA 840
 55 TTCAACCCCA TGTACCCCAA AGACAATGAC ATCGCCCTCA TGAAGCTGCA GTTCCCACTC 900
 ACTTTCTCAG GCACAGTCAG GCCCATCTGT CTGCCCTTCT TTGATGAGGA GCTCACTCCA 960
 GCCACCCAC TCTGGATCAT TGGATGGGGC TTTACGAAGC AGAATGGAGG GAAGATGTCT 1020
 GACATACTGC TGCAGGCTC AGTCCAGGTC ATTGACAGCA CACGGTGCAA TGACAGCGAT 1080
 GCGTACCAGG GGGAAAGTCA CGAGAAGATG ATGTGTGACG GCATCCCGGA AGGGGGTGTG 1140
 GACACCTGCC AGGTGACAG TGGTGGGCCC CTGATGTACC AATCTGACCA GTGGCATGTG 1200
 60 GTGGGCTCG TTAGCTGGGG CTATGGCTGC GGGGGCCCGA GCACCCAGG AGTATACACC 1260
 AAGGTCTCAG CCTATCTCAA CTGGATCTAC AATGTCTGGA AGGCTGAGCT GTAA

Seq ID NO: 449 Protein sequence
 Protein Accession #: NP_063947.1

1 11 21 31 41 51
 65 MLQDPDSQDP LNSLDVKPLR KPRIPMETFR KVGIPIIIAL LSLASIIIVV VLIKVILDKY 60
 YFLCQGPLHF IPRKQLCDGE LDCPLGEDEE HCVKSPFEPG AVAVRLSKDR STLQVLDSAT 120
 70 GNWFSACFDN FTEALAEATC RQMGYSKPT FRAVEIGPDQ DLDVVEITEN SQELMRNNS 180
 GPCLSGSLVS LHCLACGKSL KTPRVVGEE ASVDSWFWQV SIQYDKQHV GGSILDPHWV 240
 LTAACHFRKH TDVFNWVKRA GSKLGSFPPS LAVAKIIIE FNPMPKIND IALMKLQFPL 300
 TFSGTVRPIC LPFFDEELTP ATPLWIIGWG FTKQNGGKMS DILLQASQV IDSTRCNADD 360
 AYQGEVTEKM MCAGIPEGGV DTCQDSGGP LMYQSDQWHV VGIVSWGYGC GGPSTPGVYT 420

Seq ID NO: 450 DNA sequence
 Nucleic Acid Accession #: XM_051860.2
 Coding sequence: 52..3042

1 11 21 31 41 51
 80 GCTCACCAGG GAAAAATATG CAATCGTCCC ATTGATATAC AGGCCACTAC AATGGATGGA 60
 GTTAACTCTA GCACCGAGGT TGTCTACAAA AAGGCCAGG ATTATAGGTT TGCTTGCTAC 120
 85 GACCGGGGCA GAGCCTGGCG GAGCTACCGT GTACGGTTCC TCTGTGGGAA GCCTGTGAGG 180
 CCAACAACTA CAGTACCAT TGACACCAAT GTGAACAGCA CCATTCTGAA CTTGGAGGAT 240
 AATGTACAGT CATGGAACCC TGGAGATACC CTGGTCATTG CCAGTACTGA TTACTCCATG 300
 TACCAGGCAG AAGAGTTCCA GGTGCTTCCC TGCAGATCCT GCGCCCCCAA CCAGGTCAA 360

	GTGGCAGGGA AACCAATGTA CCTGCACATC GGGGAGGAGA TAGACGGCGT GGACATGCGG 420
	GCGGAGGTTG GGCTTCTGAG CCGGAACATC ATAGTGATGG GGGAGATGGA GGACAAATGC 480
	TACCCCTACA GAAACCATAT CTGCAATTTT TTTGACTTTC ATACCTTTGG GGGCCACATC 540
5	AAGTTTGTCT TGGGATTTAA GGCAGCACAC TTTGAGGGCA CGGAGCTGAA GCATATGGGA 600
	CAGCAGCTGG TGGGTGAGTA CCGGATTGAC TTCCACCTGG CCGGTGATGT AGACGAAAGG 660
	GGAGGTTATG ACCCACCAC ATACATCAGG GACCTCTCCA TCCATCATAC ATTCTCTCGC 720
	TGCGTCAAG TCCATGGCTC CAATGGCTTG TTGATCAAGG ACCTTGTGGG CTATAACTCT 780
	TTGGSCCACT GCTTCTTCAC GGAAGATGGG CCGGAGGAAC GCAACACTTT TGACCACTGT 840
10	CTTGGCTCTC TTGTCAAGTC TGGAAACCTC CTCCCTCGG ACCGTGACAG CAAGATGTGC 900
	AAGATGATCA CAGGAGATC CTACCCAGGG TACATCCCA AGCCGAGGCA AGACTGCAAT 960
	GCTGTGTCCA CTTTCTGGAT GGCCAATCCC AACAAACACC TCATCAACTG TGCCGCTGCA 1020
	GGATCTGAGG AAATGGATT TTGTTTATT TTTCAACAG TACCAACGGG CCCCCTCGTG 1080
	GGAAATGTAT CCCCAGTTA TTCAGAGCAC ATTCCACTGG GAAAATTCTA TAACAACCGA 1140
15	GCACATTCCA ACTACGGGCG TGGCATGATC ATAGACAAAG GAGTCAAAAC CACGAGGGCC 1200
	TCGTCCAAAG ACAAGCGGCC GTTCTCTCTA ATCATCTCTG CCAGATACAG CCCCACCCAG 1260
	GACGCCGACC ACCCACCAC CCGGAGCGCG GCCATCATCA GACACTTCAT TGCCTACAAG 1320
	AACCCAGGACC ACGGGGCGCT GCTGCGCGGC GGGGATGTGT GGCTGGACAG CTGCCGGTTT 1380
	GCTGACAATG GCATTGGCCT GACCCTGGCC AGTGGTGGAA CCTTCCCGTA TGACGACGGC 1440
20	TTCAAGCAAG AGATAAAGAA CAGCTTGTTC GTTGGCGAGA GTGGCAACGT GGGGACGGAA 1500
	ATGATGGACA ATAGGATCTG GGGCCCTGGC GGCTTGGACC ATAGCGGAAG GACCCTCCCT 1560
	ATAGGCCAGA ACTTTCATAT TAGAGGAATT CAGTTATATG ATGGCCCATC CAACATCCAA 1620
	AACTGCACTT TCCGAAAGTT TGTGGCCCTG GAGGGCCGGC ACACAGCGGC CCTGGCCTTC 1680
	CGCCTGAATA ATGCTGGCA GAGCTGCCCT CATAACAAG TGACCGGCAT TGCTTTGAG 1740
25	GAGCTTCCGA TTACTTCCAG AGTGTCTTTC GGAGAGCCTG GGCCCTGGTT CAACCACTG 1800
	GACATGGATG GGGATAAGAC ATCTGTGTTT CATGACGTG ACAGCTCCGT GTCCGAGTAC 1860
	CCTGGCTCCT ACCTCAGGAA GAATGACAAC TGGCTGGTCC GGCACCCAGA CTGCATCAAT 1920
	GTTCGCCACT GGAGAGGGGC CATTTGCAGT GGGTGTATG CACAGATGTA CATTCAGGCC 1980
	TACAAGACCA GTAACTGCG AATGAAGATC ATCAAGAATG ACTTCCCGAG CCACCTCTT 2040
30	TACCTGGAGG GGGCGCTCAC CAGGAGCACC CATTACCCAG AATACCAACC GGTGTGACC 2100
	CTGCACAAGG GCTACACCAT CCACTGGGAC CAGACGGGCC CCGCCGAATC CGCATCTGG 2160
	CTCATCAACT TCAACAAGCC GCACTGGATC CGAGTGGGCG TCTGCTACCC GCGAGGCACC 2220
	ACATTTCTCA TCTCTCGGA TGTTCACAA CGCCTGCTGA AGCAAAACGTC CAAGACGGGC 2280
	GTCTTCTGTA GAGCTTTCGA GATGGACAAA GTGGAGCAGA GCTACCCCTG CAGGAGCCAC 2340
35	TACTACTGGG ACGAGGACTC AGGGCTGTTG TTCCTGAAGC TGAAGGCTCA GAACGAGAGA 2400
	GAGAAGTTTG CTCTTCTGCT CATGAAAGGC TGTGAGAGGA TAAAGATTAA AGCTCTGATT 2460
	CCAAAGAACG CAGGGCTCAG TGACTGCACA GCCACAGCTT ACCCCAGATT CACCGAGAGG 2520
	GCTGTGCTAG ACGTGGCCAT GCCCAAGAAG CTCTTTGGTT CTCAGCTGAA AACAAAGGAC 2580
	CATTTCTTGG AGGTGAAGAT GAGAGTTTCC AAGCAGCACT TCTTCCACTT CTGGAACGAC 2640
40	TTGCTTACA TTGAAGTGA TGGGAAGAAG TACCCAGTT CCGAGGATGG CATCCAGGTG 2700
	GTGGTGATTG ACGGGAACCA AGGGCGCGTG GTGAGCCACA CGAGCTTCAG GAATCCATT 2760
	CTGAAGGCA TACCATGACA GCTTTTCAAC TATGTGGCGA CCATCCCTGA CAATTCCATA 2820
	GTGCTTATGG CATCAAGGG AAGATACGTC TCCAGAGGCC CATGGACAG AGTGCTGGAA 2880
	AAGCTTGGGG CAGACAGGGG TCTCAAGTTG AAAGAGCAAA TGGCATTCTG TGGCTTCAA 2940
45	GGCAGCTTCC GGGCCATCTG GGTGACACTG GACACTGAGG ATCACAAGC CAAAATCTTC 3000
	CAAGTTGTGC CCATCCCTGT GGTGAAGAAG AAGAAGTTGT GAGGACAGCT GCCGCCCGGT 3060
	GCCACCTCGT GGTAGACTAT GACGGTGAAT CTTGGCAGCA GACCAAGTGG GGATGGCTTG 3120
	TTCCCCCAGC CCCTGCCAGC AGCTGCTGCG GAAGGCCGCTG TTTGAGCCCT GATGGGCCAA 3180
	GGGAAGGCTA TCAGAGAGCC TGGTGTGCCC ACCTGCCCTT ACTCAAGTGT CTACCTGGAG 3240
50	CCCTGGGGC GGTGCTGGCC AATGCTGGAA ACATTCACCT TCCTGCGACC TCTTGGGTGC 3300
	TTCTCTCCTA TCTGTGCTCT TTCAGTGGGG GTTTGGGGAC CATATCAGGA GACCTGGGTT 3360
	GTGTGACAG CAAGATCCA CTTTGGCAGG AGCCCTGACC CAGCTAGGAG GTAGTCTGGA 3420
	GGGCTGGTCA TTCACAGATC CCCATGGTCT TCAGCAGACA AGTGAGGGTG GTAAATGTAG 3480
	GAGAAAGAGC TTTGGCCTTA AGGAAATCTT TACTCTGTGA AGCAAGAGCC AACCTCACAG 3540
55	GATTAGGAGC TGGGGTAGAA CTGGCTATCC TTGGGGAAGA GGCAAGCCCT GCCTCTGGCC 3600
	GTGTCCACCT TTCAGGAGC TTTGAGTGGC AGGTTTGGAC TTGAGCTAGA TGACTCTCAA 3660
	AGGCCCTTTT AGTTCTGAGA TTCCAGAAAT CTGCTGCATT TCACATGGTA CCTGGAACCC 3720
	AACAGTTTAT GGATATCCAC TGATATCCAT GATGCTGGGT GCCCCAGCGC ACACGGGATG 3780
	GAGAGGTGAG AACTATCAGG TAGCTTGAGG GGTCTGAGT CCAGTAGGGC AGGCAGTCAG 3840
60	GTCCATGTGC ACTGCAATGC CAGGTGGAGA AATCAGAGG AGGTAAATG GAGGCCAGTG 3900
	CCATTTCAGA GGGGAGGCTC AGGAAGGCTT CTGCTTACA GGAATGAAGG CTGGGGGCAT 3960
	TTTGTCTGGG GGAGATGAGG CAGCCTCTGG AATGGCTCAG GGATTCAGCC CTCCCTGGCG 4020
	CTGCTGCTG AAGCTGTGTA CTACGGGGTC GCCCTTTGCT CACGCTCTCT TGCCCACTC 4080
	ATGATGGAGA AGTGTGGTCA GAGGGGAGCA ATGGGCTTTG CTGCTTATGA GCACAGAGGA 4140
	ATTCACTCCC CAGGCAGCCC TGCTCTGAC TCCAAGAGGG TGAAGTCCAC AGAAGTGAGC 4200
65	TCTGCTCTTA GGGCTCTATT TGCTCTTCT CAGGGAACCT GAGCACAGGG GGCTCCAGC 4260
	AGACCCTAGA TGTGCTGTA CTCCCTCGGC CTGGGATTTT AGAGCTGGAA ATATAGAAAA 4320
	TATCTAGCCC AAAGCCTTCA TTTTAAACAGA TGGGGAAAGT GAGCCCCCAA GATGGGAAAG 4380
	AACCAACAG CTAAAGGAGG GCTTGGGGAG CCCCACCCTA GCCCTTGCTG CCACACCA 4440
70	TTGCTCAAC AACCGGCCCC AGAGTGCCCA GGCACTCTG AGGTAGCTTC TGGAAATGGG 4500
	GACAAGTCCC CTCGAAGGAA AGGAAATGAC TAGAGTAGAA TGACAGCTAG CAGATCTCTT 4560
	CCCTCCTGCT CCCAGCGCAC ACAAACCCGC CCTCCCTTG GTGTGGCGG TCCCTGTGGC 4620
	CTTCACTTTG TTCACTACTT GTGAGCCAG CCTGGGTGCA CAGTAGCTGC AACTCCCCAT 4680
	TGGTGCTACC TGGCTCTCCT GTCTCTGCA CTCTACAGGT GAGGCCAGC AGAGGGAGTA 4740
75	GGGCTGCGCA TGTCTCTGTT GAGCCAATTT GGCTGATCTT GGGTGTCTGA ACAGCTATTG 4800
	GGTCCACCCC AGTCCCTTTT AGCTGCTGCT TAATGCCCTG CTCTCTCCCT GGCCACCTT 4860
	ATAGAGAGCC CAAAGAGCTC CTGTAAGAGG GAGAACTCTA TCTGTGTTT ATAATCTTGC 4920
	ACGAGGACCC AGAGCTTCCC TGGGTCTTGT GATGAACTAC ATTTATCCCC TTTCTGCCC 4980
	CAACCAAAA CTCTCTCCTT CAAAGAGGGC CTGCTGGCT CCCCACCC CACTGCACCC 5040
80	ATGAGACTCG GTCCAAGAGT CCATTCCCA GGTGGGAGCC AACTGTGAGG GAGGTCTTTC 5100
	CCACCAAAA CTCTTCAAGT GCTGGAGGT GACCATAGGG CTCTGCTTTT AAAGATATGG 5160
	CTGCTTCAA GGGCAGATC ACAGGAAGGA CTTCTTCCAG GGAGATTAGT GGTGATGGAG 5220
	AGGAGAGTTA AAATGACCTC ATGTCTTCTT TGTCCACGGT TTTGTTGAGT TTTCACTCTT 5280
	CTAATGCAAG GGTCTCACAC TGTGAACCA TTAGGATGTG ATCACTTCA GGTGGCCAGG 5340
85	AATGTTGAAT GTCTTTGGCT CAGTTCAATT AAAAAAGATA TCTATTGAA AGTCTCAGA 5400
	GTGTACATA GTTTTACAG TACAGGATCT GTACATAAAA GTTTCTTTC TAAACCATC 5460
	ACCAAGAGCC AATATCTAGG CATTTTCTTG GTAGCACAAA TTTCTTATT GCTTAGAAA 5520
	TTGTCTCTCT TGTATTCTT GTTTGTAAGA CTTAAGTGAG TTAGGTCTTT AAGGAAGCA 5580

WO 02/086443

PCT/US02/12476

ACGCTCCTCT GAAATGCTTG TCTTTTTTCT GTTGCCGAAA TAGCTGGTCC TTTTTCGGGA 5640
 GTTAGATGTA TAGAGTGTGT GTATGTAAAC ATTTCTTGTA GGCATCACC A TGAACAAAGA 5700
 TATATTTTCT ATTTATTAT TATATGTGCA CTTCAAGAAG TCACTGTGAG AGAAATAAAG 5760
 AATTGTCTTA AATGTCAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAA

Seq ID NO: 451 Protein sequence
 Protein Accession #: XP_051860.2

1 11 21 31 41 51
 MDGVNLSTEV VYKKQDYRF ACYDRGRACR SYRVRFCLGK PVRPKLTVTI DTNVNSTILN 60
 LEDNVQSWKP GDTLVIASDT YSMYQAEFQ VLFPCRSAPN QVKVAGKPMY LHIGEEIDGV 120
 DMRAEVGLLS RNIIIVMGEME DKCYPYRNHI CNFFDFDTFG GHIFKALGFK AAHLEGTELK 180
 HMQQLVVGQY PIHFHLAGDV DERGGYDEPT YIRDLSEIHT PSRCVTVHGS NGLLIKDVVG 240
 YNSLGHCFPT EDGPBERNTF DHCLGLLVKS GTLLPSDRDS KMCKMITGDS YPGYIPKPRQ 300
 DCNAVSTFWM ANPNNNLINC AAAGSEETGF WFIFHHVPTG PSVGMYSPTY SEHIPGLKPY 360
 NNRAHSNYRA GMIIIDNQVKT TEASAKDKRP FLSIIISARYS PHQDADPLK REPAIIRHPI 420
 AYKNQDHGAW LRGGDVWLDS CRFADNGIGL TLAGSGTFFY DDGSKQBEKN SLFVGESGNV 480
 GTEMNDNRW GPGLLDHSGR TLPIGQNFPI RGIQLYDGP I NIQNTFRKF VALEGRHTSA 540
 LAFLRLNNAW SCPHNNVTIS AFEDVPITSR VFFGEGPWF NQLDMDGDKT SVFHDVDSV 600
 SEYFGSYLTK NDNWLVRHPD CINVPDWRGA ICSGCYAQMY IQAYKTSNLR MKIINKDFPS 660
 HPLYLEGALT RSTHLDQYQF VVTLQKGYTI HWDQTAPAEI AIWLINFNKG DWIRVGLCYP 720
 RGTTFSLSD VHNRLKQTS KTGQVVRITLQ MDKVEQSYPG RSHYYWDEDS GLLFLKLKQK 780
 NEREKFAFCS MKGCERIKK ALIPKNAGVS DCTATAYPKF TERAVVDVPM PKKLFGSQLK 840
 TKDHFLEVMK ESSQHFPHL WNDPAYIEVD GKYPSSSEDG IQVVIDGNQ GRVVSHTSPR 900
 NSILQGPWQ LBNYVATIPD NSIVLMASKG RYVSRGPWTR VLEKLGDARG LKLEQMAFV 960
 GFKGSFRPIW VTLDTEHKA KIFQVVPFV VKKKKL

Seq ID NO: 452 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 261..2861

1 11 21 31 41 51
 GAGCTAGCGC TCAAGCAGAG CCCAGCGCGG TGCTATCGGA CAGAGCCTGG CGAGCGCAAG 60
 CGCGCGCGGG AGCCAGCGGG GCTGAGCGCG GCCAGGGTCT GAACCCAGAT TTCCAGACT 120
 AGCTACCACT CGCTTGCCG ACGCCCCGGG AGCTCGCGCG GCCTGGCGGT CAGCGACCAG 180
 ACGTCCGGGG CGCTGCGCT CCTGGCCCGC GAGGCGTGAC ACTGTCTCGG CTACAGACCC 240
 AGAGGAGACA CACTGCGCTC ATGGGAGCTG CTGGGAGGCA GGACTTCCTC TTCAAGCCAG 300
 TGCTGACCAT CAGCTGGCTC ACTCTGACCT GCTTCCCTGG GGCCACATCC ACAGTGGCTG 360
 CTGGGTGCCC TGACAGAGAG CCTGAGTTGC AACCTTGGAA CCCTGGCCAT GACCAAGACC 420
 ACCATGTGCA TATCGTCGAG GGCAAGACAC TGCTGCTCAC CTCTTCTGCC ACGGTCTATT 480
 CCATCCACAT CTCAGAGGGA GGCAAGCTGG TCATTAAAGA CCACGACGAG CCGATTGTTT 540
 TGCGAACCCG GCACATCCTG ATTGACAACG GAGGAGAGCT GCATGCTGGG AGTCCCTCT 600
 GCCCTTTCCA GGGCAATTTC ACCATCATT TGTATGGAAG GGCTGATGAA GGTATTTCAGC 660
 CGGATCCTTA CTATGGTCTG AAGTACATTG GGGTTGGTAA AGGAGGCGCT CTGAGTTGC 720
 ATGGACAGAA AAAGCTCTCC TGGACATTTC TGAACAAGAC CCTTCACCCA GGTGGCATGG 780
 CAGAGGAGAG CTATTTTTTT GAAAGGAGCT GGGGCCACCG TGGAGTTATT GTTCATGTCA 840
 TCAGACCCAA ATCAGGCACA GTCATCCATT CTGACCGGTT TGACACCTAT AGATCCAAGA 900
 AAGAGAGTGA ACGTCTGGTC CAGTATTGTA ACGCGGTGCC CGATGGCAGG ATCCTTCTCTG 960
 TTGCACTGAA TGATGAAGGT TCTCGAAATC TGGATGACAT GGCCAGGAAG GCGATGACCA 1020
 AATTGGGAAG CAACACCTTC CTGACCTTGG GATTTAGACA CCCTTGGAGT TTTCTAACTG 1080
 TGAAGGAAAT TCCATCATCT TCAGTGGGAG ACCATATTGA ATATCATGGA CATCGAGGCT 1140
 CTGCTGCTGC CCGGTGATTC AAATTGTTCC AGACAGAGCA TGGCGAATAT TTCAATGTTT 1200
 CTTTGTCCAG TGAGTGGGTT CAAGACGTGG AGTGGACGGA GTGGTTCGAT CATGATAAAG 1260
 TATCTCAGAC TAAAGGTGGG GAGAAAATTT CAGACCTCTG GAAAGCTCAC CCAGGAAAAA 1320
 TATGCAATCG TCCATTTGAT ATACAGGCCA CTACAATGGA TGGAGTTAAT CTCAGACCG 1380
 AGGTGTGCTA CAAAAAGGCG CAGGATTATA GGTTTGCTTG CTACGACCGG GGCAGAGCCT 1440
 GCCGAGAGTA CCGTGTACGG TTCTCTGTG GGAAGCTGTG GAGGCCCAAA CTCACAGTCA 1500
 CCATTGACAC CAATGTGAAC AGCACCATTG TGAACCTGGA GGATTAATGTA CAGTCATGGA 1560
 AACCTGGAGA TACCTGGTTC ATTGCCAGTA CTGATTACTC CATGTACCAG GCAGAAGAGT 1620
 TCCAGGTGCT TCCCTGACAGA TCCTGCGCCC CCAACCAGGT CAAAGTGGCA GGGAAACCAA 1680
 TGTAACCTGA CATCGGGGAG GAGATAGACG CGCTGGACAT GCGGCGCGAG GTTGGGCTTC 1740
 TGAGCCGGAA CATCATAGTG ATGGGGGAGA TGGAGGACAA ATGCTACCCC TACAGAAACC 1800
 ACATCTGCAA TTTCTTTGAC TTCGATACCT TTGGGGGCCA CATCAAGTTT GCTCTGGGAT 1860
 TTAAGSCAGC ACATTTGAGG GGCACGGAGC TGAAGCATAT GGGACAGCAG CTGGTGGGTC 1920
 AGTACCCGAT TCACCTCCAC CTGGCCGGTG ATGTAGACGA AAGGGGAGGT TATGACCCAC 1980
 CCACATACAT CAGGGACCTC TCCATCCATC ATACATTCTC TCGCTGGCTC ACAGTCCATG 2040
 GCTCCAATGG CTGTGTGATC AAGGACGTTG TGGGCTATAA CTCTTTGGGG CACTGCTTCT 2100
 TCACGGAAGA TGGGCGGAG GAACGCAACA CTTTTGACCA CTGTCTTGGC CTCTTGTCA 2160
 AGTCTGGAAC CCTCTCCCCC TCGGACCGTG ACAGCAAGAT GTGCAAGATG ATCAAGAGG 2220
 ACTCTACCC AGGGTACATC CCAAGGCCA GGCAAGACTG CAATGCTGTG TCCACCTTCT 2280
 GGATGGCCAA TCCCAACAAC AACCTCATCA ACTGTCCGCG TGCAGGATCT GAGGAAACTG 2340
 GATTTTGGTT TATTTTTCAC CACGTACCAA CGGGCCCCCT CGTGGGAATG TACTCCCCAG 2400
 GTTATTGAGA GCACATTCCA CTGGGAAAAT TCTATAACAA CCGAGCACAT TCCAACCTACC 2460
 GGGCTGGCAT GCTCATAGAC AACGGAGTCA AAACCAACGA GGCCTCTGCC AAGGACAAGC 2520
 GGGCTGCTCT CTCATCATC TCTGCCAGAT ACAGCCCTCA CCAGGACGCC GACCCGCTGA 2580
 AGCCCCGGA GCCCGCCATC ATCAGACACT TCATTGCCA CAAGAACCAG GACCACGGGG 2640
 CTGGCTGCG CGCGGCCGAT GTGTGGCTGG ACAGCTGCCA TTTAGAGGG GAGGCTCAGG 2700
 AAGGCTTCTT GCTTACAGGA ATGAAGGCTG GGGGCATTTT GCTGGGGGGA GATGAGGCG 2760
 CCTCTGGAAT GGCTCAGGGA TTCAGCCCTC CTGCGCGCTG CCGTCTGAGG CTGGTACTA 2820
 CGGGGTGCGC CTTTGTCTAC GTCTCTCTGG CCCACTCATG ATGAGAGAAT GTGGTCAGAG 2880
 GGGAGCAATG GGGCTTTGCTG CTTATGAGCA CAGAGGAATT CAGTCCCCAG GCAGCCCTGC 2940
 CTCTGACTCC AAGAGGGTGA AGTCCACAGA AGTGAGCTCC TGCCTTAGGG CCTCATTTGC 3000
 TCTTCATCCA GGGAACTGAG CACAGGGGGC CTCCAGGAGA CCCTAGATGT GCTCGTACTC 3060
 CCTCGGCGTG GGATTTTACA GCTGGAATA TAGAAAATAT CTAGCCCAAA GCCTTCATTT 3120

WO 02/086443

PCT/US02/12476

5
10
15
20
25
30

TAACAGATGG GGAAGTGGAG CCCCCAAGAT GGGAAAGAAC CACACAGCTA AGGGAGGGCC 3180
TGGGGAGCCC CACCTAGACC CTGCTGCCA CACCACATTG CCTCAACAAC CGGCCCCAGA 3240
GTGCCCAGGC ACTCTGAGG TAGCTTCTGG AAATGGGGAC AAGTCCCCTC GAAGGAAAGG 3300
AAATGACTAG AGTAGAATGA CAGCTAGCAG ATCTCTTCCC TCCTGCTCCC AGCGCACACA 3360
AACCCGCCCT CCCCTTGGTG TTGGCGGTCC CTGTGGCCTT CACTTTGTTT ACTACCTGTC 3420
AGCCCAGCCT GGGTGCACAG TAGCTGCAAC TCCCATTGG TGCTACCTGG CTCTCCTGTC 3480
TCTGAGCTC TACAGGTGAG GCCCAGCAGA GGGAGTAGGG CTCGCCATTG TTCTGGTAGG 3540
CCAATTGGC TGATCTTGGG TGTCTGAACA GCTATTGGGT CCACCCAGT CCCTTTCAGC 3600
TGCTGCTTAA TGCCCTGCTC TCTCCCTGGC CCACCTTATA GAGAGCCCAA AGAGCTCCTG 3660
TAAGAGGGAG AACTCTATCT GTGGTTTATA ATCTTGACAG AGGCACCAGA GTCTCCCTGG 3720
GTCTTGTGAT GAACCTACATT TATCCCCCTT CTGCCCCCAA CCACAAACTC TTTCTTCAA 3780
AGAGGGCCTG CCTGGCTCCC TCCACCCAAC TGACCCCATG AGACTCGGTC CAAGAGTCCA 3840
TTCCCCAGGT GGGAGCCAAC TGTCAGGGAG GTCTTTCCCA CCAACATCTT TTCAGCTGCT 3900
GGGAGGTGAC CATAGGGCTC TGCTTTTAAA GATATGGCTG CTTCAAAGGC CAGAGTCACA 3960
GGAAGGACTT CTTCCAGGGA GATTAGTGGT GATGGAGAGG AGAGTTAAAA TGACCTCATG 4020
TCCTTCTTGT CCACGGTTTT GTTGAGTTTT CACTCTTCTA ATGCAAGGGT CTCACACTGT 4080
GAACCACTTA GGATGTGATC ACTTTTCAAGT GGCCAGGAAT GTTGAATGTC TTTGGCTCAG 4140
TTCAATTTAA AAGATATCTT ATTTGAAAGT TCTCAGAGTT GTACATATGT TTCACAGTAC 4200
AGGATCTGTA CATAAAAGTT TCTTTCTCTA ACCATTCAAC AAGAGCCAAT ATCTAGGCAT 4260
TTTCTTGGTA GCACAAATTT TCTTATTGCT TAGAAAAATT TCCTCTCTGT TATTTCTGTT 4320
TGTAAAGACT AGTGAGTTA GGTCTTTAAG GAAAGCAACG CTCCTCTGAA ATGCTTGTCT 4380
TTTTTCTGTT GCCGAAATAG CTGGTCTCTT TTCGGGAGTT AGATGTATAG AGTGTTTGTA 4440
TGTAACACTT TCTGTAGGCT ATCACCATGA ACAAAGATAT ATTTTCTATT TATTTATTAT 4500
ATGTGCACCT CAAGAAGTCA CTGTGAGAGA AATAAAGAA TGTCTTAAAT GTCATGATTG 4560
GAGATGCTCT TTGCTATTGCT TGAAGGGGT GTACCTAGAG CCAAGGAAAT TGGCTCTGGT 4620
TTGAAAAAAT TTGCTGTTA TTATAGTAAA CATACAAAGG ATGTCAAAAA AAAAAAATAA 4680
AAAAAATAA AAAAAAATAA AA

Seq ID NO: 453 Protein sequence
Protein Accession #: Eos sequence

35
40
45
50

1 11 21 31 41 51
MGAAGRQDFL FKAMLTISWL TLTCPPGATS TVAAGCPDQS PELQFWNPGH DQDHHVHIGQ 60
GKILLTSSA TVYSIHSEG KGLVIKDHDE PIVLRTRHIL IDNGGELHAG SALCPFQGNF 120
TIILYGRADE GIQPDPIYGL KYIGVGKGGG LELHGQKKLS WTFLNKLTHP GGMAEGGYFF 180
ERSWGHGRVI VHVDPKSGT VIHSDFDFTY RSKKESERLV QYLNAPVDGR ILSVAVNDEG 240
SRNLDDMARK LHLGFRHPWS PLTVKGNPSS SVEDHIEYHG HRGSAAARVF 300
KLFQTEHGEY FNVLSSESWV QDVEWTEWFD HDKVSTKGG EKISDLWKAH PGKICNRPID 360
IQATTMDGVN LSTEVVYKKG QDVFACYDR GRACRSYRVR FLCGKVPVRPK LTVTIDTNVN 420
STILNLEDNV QSWKPGDTLV IASTDYSMYQ AEEFQVLPCR SCAPNQVKVA GKPMYLHIGS 480
EIDGVDMRAE VGLLSRNIIV MGEMEDKCPY YRNHNCFPD PDTFGGHIFK ALGFKAAHLE 540
GTBLKHMGRQ LVGQYPIHFH LAGDVDERGG YDPPYIIRDL SIHHTFSCRVC TVHGSNGLLI 600
KDVVGVNSLG HCFPTEDGPE ERNTPDHCLG LLVKSGLTLLP SDRDSKMKCM ITEDSYPGVI 660
PKPRQDCNAV STFWMANPNN NLINCAAAGS EBTGFWFIFH HVPTGPSVGM YSPGVSEHIP 720
LGKPYNNRAH SNYRAGMIID NGVKTTEASA KDKRPFLSII SARYSPHQDA DPLKPREPAI 780
IRHFIAVKNQ DHGAWLRRGD VWLDSCHFRG EAQEGFLLTG MKAGGILLGG DEAAAGMAQG 840
FSPPCRCLLK LVTGSPFAH VSLAHS

Seq ID NO: 454 DNA sequence
Nucleic Acid Accession #: NM_013282.2
Coding sequence: 85..2466

55
60
65
70
75
80
85

1 11 21 31 41 51
CGACTCCTTA GAGCATGGCA TGGCTCAGAG GTGCTGGTAA AACTGATGGG GGTTTTGTCT 60
GTCCCTCCCC TCAGCGCCGA CACCATGTGG ATCCAGGTTT GGACCATGGA CGGGAGGCAG 120
ACCCACACGG TGGACTCCTG GTCCAGGCTG ACCAAGGTGG AGGAGCTGAG CGCGAAGATC 180
CAGGAGCTGT TCCAGCTGAT GCCAGGCTGT CAGAGGCTGT TCTACAGGGG CAAACAGATG 240
GAGGACGGCC ATACCTCTTT GACTACGAG GTCCGCTCTG ATGACACCAT CCAGCTCCTG 300
GTCCGCCAGA GCCTCGTGCT CCCCCACAGC ACCAAGGAGC GGGACTCCGA GCTCTCCGAC 360
ACCGACTCCG GCTGCTGCTT GGGCCAGAGT GAGTCAGACA AGTCCTCCAC CCACGGCGAG 420
CGGCGCGCGG AGACTGACAG CAGGCCAGCC GATGAGGACA TGTGGGATGA GACGGAATTG 480
GGGCTGTACA AGGTCAATGA GTACGTCGAT GCTCGGGACA CGAACATGGG GCGGTGGTTT 540
GAGGCGCAGG TGGTCAGGGT GACGCGGAAG GCCCCTCCC GGGACGAGCC CTCGAGCTCC 600
ACGTCCAGGC CGCGCTGGA GGAGGACGTC ATTTACCAGC TGAATACGA CGACTACCGG 660
GAGAACGGCG TGGTCCAGAT GAATCCAGG GACGTCGAG CGCGCGCCCG CACCATCATC 720
AAGTGGCAGG ACCTGGAGGT GGGCCAGGTG GTCATGCTCA ACTACAACCC CGACAACCCC 780
AAGGAGCGGG GCTTCTGGTA CGACGCGGAG ATCTCCAGGA AGCGCGAGAC CAGGACGGCG 840
CGGGAACCTC AGCCCAACGT GGTGCTGGGG GATGATTCTC TGAACGACTG TCGGATCATC 900
TTCTGGGACG AAGTCTTCAA GATTGAGCGG CCGGGTGAAG GGAGCCCATG GGTGACAAAC 960
CCCATGAGAC GGAAGAGCGG CCGTCTCTGC AAGCACTGCA AGGACGAGT GAACAGACTC 1020
TGCCGGGTCT GCGCTGCCA CTTGCCATC TACTGCCTGG ACCCGCCCTC CAGCAGTGT 1080
TGCGATGAGT GCGACATGGC CTGCCATC TATCCGCTG ATGCCAGCGA GGTGGTACTG 1140
CCGAGCGAGG ACAGTGGTA CTGCCCTGAG TGCCGGAATG ATGCCAGCGA GGTGGTACTG 1200
GCGGGAGAGC GGCTGAGAGA GAGCAAGAAG AAGCGCAAGA TGGCTCGGC CACATCGTCC 1260
TCACAGCGGG ACTGGGCA GGCATGGCC TGTGTGGGCC GCACCAAGGA ATGTACCATC 1320
GTCCCGTCCA ACCACTACGG ACCCATCCC GGGATCCCCG TGGGCACCAT GTGGCGGTTT 1380
CGAGTCCAGC TCAGCGAGTC GGGTGTCCAT CGGCCCCACG TGGCTGGCAT ACACGGCCGG 1440
AGCAACGAGC ATGCAATCTC CTAAGTCTCT GCGGGGGGCT ATGAGGATGA CGTGGACCAT 1500
GGGAATTTT TCACATACAC GGGTAGTGGT GGTGAGATC TTTCCGCAA CAAGAGGACC 1560
GCGGAACCTT CTTGTGATCA GAAACTCAC AACACCAACA GGGCGCTGGC TCTCAACTGC 1620
TTTGCTCCCA TCAATGACCA AGAAGGGGCC GAGGCCAAG ACTGGCGGTC GGGGAAGCGG 1680
GTGAGGTTGG TGCAGAAATG CAAGGGTGGC AAGAATAGCA AGTACGCCCC CGCTGAGGGC 1740
AACCGCTACG ATCGGCTCTA CAAGGTTGTG AAATACTGGC CCGAGAAGGG GAAGTCCGGG 1800
TTTCTGTTGT GCGCTACCT TCTGCGGAGG GACGATGATG AGCCTGGCCC TTGGACGAAG 1860
GAGGGGAAGG ACCGATCAA GAAGCTGGGG CTGACCATGC AGTATCCAGA AGGCTACCTG 1920

	GAAGCCCTGG	CCAAACCAGA	GCGAGAGAAG	GAGAACAGCA	AGAGGGAGGA	GGAGGAGCAG	1980
	CAGGAGGGGG	GCTTCGGGTC	CCCCAGGACG	GGCAAGGGCA	AGTGGAAAGCG	GAAGTCGGCA	2040
	GGAGGTGGCC	CGAGCAGGGC	CGGGTCCCCG	CGCCGGACAT	CCAAGAAAAC	CAAGGTGGAG	2100
5	CCCTACAGTC	TCACGGCCCA	GCAAGAGCAG	CTCATCAGAG	AGGACAAGAG	CAACGCCAAG	2160
	CTGTGGAATG	AGGTCTCGGC	GTCACTCAAG	GACCGGCCGG	CGAGCGGCAG	CCCGTTCAG	2220
	TTGTTCCCTGA	GTAAGGTGGA	GGAGACGTTT	CAGTGTATCT	GCTGTCAAGG	GCTGGTGTTC	2280
	CGGCCCATCA	CGACCGGTGT	CCAGCACAAC	GTGTGCAAGG	ACTGCCTGGA	CAGATCCTTT	2340
	CGGGCAGAGG	TGTTCAAGTC	CCCTGCCTGC	CGCTACGACC	TGGGCCGCGG	CTATGCCATG	2400
10	CAGGTGAACC	AGCCTCTGCA	GACCGTCCTC	AACAGCTCTT	TCCCGCGCTA	CGGCAATGGC	2460
	CGGTGATCTC	CAAGCACTTC	TCGACAGGCG	TTTTGCTGAA	AACGTGTGCG	AGGGCTCGTT	2520
	CATCGGCACT	GATTTTGTTC	TTAGTGGGCT	TAACTTAAAC	AGGTAGTGTG	TCCTCGTTTC	2580
	CCTAAAAAGG	TTTGTCTTCC	TTTTTTTTTA	TTTTTATTTT	TCAAATCTAT	ACATTTTCAG	2640
	GAATTTATGT	ATCTCTGGCTA	AAAGTTGGAC	TTCTCAGTAT	TGTGTTTAGT	TCITTTGAAA	2700
15	CATAAAGCC	TGCAATTTCT	CGACAAAACA	ACACAAGATT	TTTTAAAGAT	GGAAATCAGAA	2760
	ACTACGTGGT	GTGGAGGCTG	TTGATGTTTC	TGGTGTCAAG	TTCTCAGAAG	TTGCTGCCAC	2820
	CAACTCTTTA	AGAAAGGCGAC	ATGATCAGTC	CTTCTTAGGG	GTTCTGGCCC	CCAAGGTCAG	2880
	AGCAAGCATC	TTCTCTACAG	CATTTTGTCA	TCTAAAGTCC	AGTGACATGG	TTCCCGTGG	2940
	TGGCCCGTGG	CAGCCCGTGG	CATGGCGTGG	CTCAGCTGTC	TGTTGAAGTT	GTTGCAAGGA	3000
20	AAAGAGGAAA	CATCTCGGGC	CTAGTTCAAA	CCTTTGCCCTC	AAAGCCATCC	CCCACCGAGC	3060
	TGCTTAGCGT	CTGAGATCCG	CGTGAAAAGT	CCTCTGCCCA	CGAGAGCAGG	GAGTTGGGGC	3120
	CACGCAGAAA	TGGCCTCAAG	GGGACTCTGC	TCCACGTGGG	GCCAGGCGTG	TGACTGACGC	3180
	TGTCCGACCA	AGGCGGCCAC	GGACGGACGC	CAGCACACGA	AGTCACGTGC	AAGTGCCTTT	3240
	GATTCGTCCG	TTCTTTCTAA	AGACGACAGT	CTTTGTTGTT	AGCACTGAAT	TATTGAAAAA	3300
25	GTCAACCAGA	TTCTAGAAAC	TGCGGTCTATC	CAGTTCTTCC	TGACACCGGA	TGGGTGCTTG	3360
	GGAAACGTTT	GAGCCTTATA	GATCAATTTAC	ATTCAATTTT	TTTAACCTAG	CAAGTGAGAA	3420
	CTTACAAGAG	GGTTTTTTTT	TAATTTTTTT	TTCTCTTAAT	GAACACATTT	TCTAAATGAA	3480
	TTTTTTTTGT	AGTTACTGTA	TATGTACCAA	GAAAGATATA	ACGTTAGGGT	TTGGTTGTTT	3540
	TTGTTTTTGT	ATTTTGTTC	TTTTGAAAGG	GTTTGTAAAT	TTTTCTAATT	TTACCAAAAT	3600
30	TGTCAGCCTA	TACCTCAATA	AAACAGGGAT	ATTTTAAATC	ACATACCTGC	AGACAAACTG	3660
	GAGCAATGTT	ATTTTTAAAG	GGTTTTTTTC	ACCTCCTTAT	TCTTAGATTA	TTAATGTATT	3720
	AGGGAAGAAAT	GAGACAATTT	TGTGTAGGCT	TTTTCTAAAG	TCCAGTACTT	TGTCCAGATT	3780
	TTAGATTCTC	AGAATAAATG	TTTTTCACAG	ATTGAAAAAA	AAAAAAA		

Seq ID NO: 455 Protein sequence
Protein Accession #: NP_037414.2

	1	11	21	31	41	51	
40	MWIVRTMDG	RQTHTVDSL	RLTKVBELRR	KIQELFHVPE	GLQRLFYRGK	QMEDGHTLFD	60
	YEVRNLDTIQ	LLVRQSLVLP	HSTKERDSEL	SDTDGCGCLG	QSESDKSSTH	GEAAAEETDSR	120
	PADEDMWDET	ELGLYKVNEY	VDARDTNMGA	WFEAQVVRVT	RKAPSRDEPC	SSTSRPALBE	180
	DVIYHVKKYD	YPENGVMQMN	SRDVRARART	IIKWQDLEVG	QVVMNLNYPD	NPKERGFWDY	240
	AEISRKRETR	TLRSLYANVV	LGDDSLNDCR	IIFVDEVFKI	ERPGESEPMV	DNFMRRKSGP	300
45	SKCHKRQDVN	RLCRVCACHL	CGGRQDPDKQ	LMCDECDMAF	HIYCLDPPLS	SVPSSEDEWYC	360
	PECRNDASEV	VLAGERLRES	KKKAOMASAT	SSSQRDWKGK	MACVGRTEKEC	TIVPSNHYGP	420
	IFGIPVGTMW	RFRVQVSESG	VHRPHVAGIH	GRSNDGAYSL	VLAGGYEDDV	DHGNFFTYTG	480
	SGGRDLGSMK	RTAEQSCDQK	LTNTNRALAL	NCFAPINDQE	GAEAKDWRSG	KPVRVVRNVK	540
	GGKNSKYAFA	EGNRYDAGYK	VVKYWPEKKG	SGFLVWRVLL	RRDDDEPGPW	TKEGKDRIKK	600
50	LGLTMQYPEG	YLEALANRER	EKENSKREEE	EQQEGGFASP	RTGKGKWKRK	SAGGGPSRAB	660
	SPRRTSKTKT	VEFYSLTAQQ	SSLIREDKSN	AKLWNEVLAS	LKDRPASGSP	FQLFLSKVBE	720
	TFQCICCOEL	VFRPITTVCO	HNVCCKCLDR	SFRAQVFSFC	ACRYDLGRSY	AMQVNQLQT	

Seq ID NO: 456 DNA sequence
Nucleic Acid Accession #: NM_001200.1
Coding sequence: 325..1514

	1	11	21	31	41	51	
60	GGGGACTTCT	TGAACTTGCA	GGGAGAATAA	CTTGCGCACC	CCACTTTGCG	CCGGTGCCTT	60
	TGCCCCAGCG	GAGCCTGCTT	CGCCATCTCC	GAGCCCCACC	GCCCCCTCAC	TCCTCGGCTT	120
	TGCCCCAGAC	TGAGACGCTG	TTCCAGCGT	GAAAGAGAG	ACTGCGCGGC	CGGCACCCGG	180
	GAGAAGGAGG	AGGCAAGAA	AAGGAACGGA	CATTGCGTCC	TTGCGCCAGG	TCCTTTGACC	240
	AGAGTTTTTC	CATGTGGACG	CTCTTTCAAT	GGACGTGTCC	CCGCGTGCTT	CTTAGACGGA	300
65	CTGCGGTCTC	CTAAGGTGCG	ACCATGTTGG	CCGGGACCCG	CTGTCTTCTA	CGGTGTGCTG	360
	TTCCCCAGGT	CCTCTGCGGC	GGGCGGCTG	GCCTCGTTCC	GGAGCTGGGC	CGCAGGAAGT	420
	TGCGGCGCGC	GTCGTGCGGC	CGCCCTCAT	CCCAGCCCTC	TGACGAGGTC	CTGAGCGAGT	480
	TCGAGTTGCG	GCTGCTCAGC	ATGTTGCGCC	TGAAACAGAG	ACCCAACCCC	AGCAGGGACG	540
	CCGTGCTGCC	CCCTTACATG	CTAGACCTGT	ATCGCAGGCA	CTCAGGTCAG	CCGGGCTCAC	600
70	CCGCCCCAGA	CCACCGGTTG	GAGAGGGCAG	CCAGCCGAGC	CAACACTGTG	CGCAGCTTCC	660
	ACCATGAAGA	ATCTTTGGAA	GAACACACAG	AAACGAGTGG	GAAAAACAAC	CGGAGATTCT	720
	TCITTAATTT	AAGTTCTATC	CCACGGGAGG	AGTTTATCAC	CTCAGCAGAG	CTTCAGGTTT	780
	TCCGAGAACA	GATGCAAGAT	GCTTTAGGAA	ACAATAGCAG	TTTCCATCAC	CGAATTAATA	840
	TTTATGAAAT	CATAAAACCT	GCAACAGCCA	ACTCGAAATT	CCCCGTGACC	AGACTTTTGG	900
75	ACACCAAGTT	GGTGAATCAG	AATGCAAGCA	GGTGGGAAG	TTTTGATGTC	ACCCCGCTG	960
	TGATGCGGTG	GACTGCACAG	GGACACGCCA	ACCATGGATT	CGTGGTGGAA	GTGGCCCACT	1020
	TGGAGGAGAA	ACAAGGTGTC	TCCAAGAGAC	ATGTTAGGAT	AAGCAGGTCT	TTGCACCAAG	1080
	ATGAACACAG	CTGTCTACAG	ATAAGGCCAT	TGCTAGTAAC	TTTTGGCCAT	GATGGAAGAA	1140
	GGCATCCTCT	CCACAAAAGA	GAAAAACGTC	AAGCCAAACA	CAAAACAGCG	AAACGCCTTA	1200
80	AGTCCAGCTG	TAAGAGACAC	CCTTTGTACG	TGGACTTCAG	TGACGTGGGG	TGGAATGACT	1260
	GGATTGTGGC	TCCCGCGGGG	TATCACGCCT	TTTACTGCCA	CGGAGAAATG	CCTTTTCCTC	1320
	TGCTGTATCA	TCTGAATCC	ACTAATCATG	CCATTGTTCA	GACGTTGGTC	AACTCTGTTA	1380
	ACTCTAAGAT	TCCTAAGACA	TGCTGTGTCC	CGACAGAACT	CAGTGCTATC	TCGATGCTGT	1440
	ACCTTGACGA	GAATGAAAAG	GTTGTATTAA	AGAAGTATCA	GGACATGTTT	GTGGAGGGTT	1500
85	GTGGGTGTCG	CTAGTACAGC	AAAATTAAAT	ACATAAATAT	ATATATA		

Seq ID NO: 457 Protein sequence
Protein Accession #: NP_001191.1

	1	11	21	31	41	51	
5	MVAGTRCLLA	LLLPPVLLGG	AAGLVPELGR	RKPAAASSGR	PSSQPSDEVL	SSEFELRLLSM	60
	PGLKQRPPTS	RDVAVPPYML	DLYRRHSGQP	GSPAPDHRLE	RAASRANTVR	SFHHEESLEE	120
	LPETSGKTR	RFFFNLSIP	TEEFITSDEL	QVFRQMQDA	LGNSSPFHR	INIYEIKPA	180
	TANSKFPVTR	LLDT					

Seq ID NO: 458 DNA sequence
Nucleic Acid Accession #: NM_001999.2
Coding sequence: 1..8736

	1	11	21	31	41	51	
15	ATGGGGAGAA	GACGGAGGCT	GTGTCTCCAG	CTCTACTTCC	TGTGGCTGGG	CTGTGTGGTG	60
	CTCTGGGCGC	AGGGCACGGC	CGGCCAGCCT	CAGCCTCCTC	CGCCCAAGCC	GCCCGGGCCC	120
	CAGCCGCGCG	CGCAACAGGT	TCGGTCCGCT	ACAGCAGGCT	CTGAAGGCGG	GTTTCTAGCG	180
	CCCGAGTATC	GCGAGGAGGG	TGCCGAGTGT	GCCAGCCGCG	TCCGCGGCGG	AGGACAGCAG	240
20	GACGTGCTCC	GAGGGCCCAA	CGTGTGCGGC	TCCAGATTCC	ACTCCTACTG	CTGCCCTGGA	300
	TGGAAGACAG	TCCCTGGAGG	AAACCACTGC	ATTGTCCCGA	TTTGTAGAAA	TAGTTGTGGA	360
	GATGGATTTC	GTTCCCGTCC	TAACATGTGT	ACTTGTTCCT	GTGGGCAAAAT	ATCATCAACC	420
	TGTGGATCAA	AATCAATTCA	GCAGTGCAGT	GTGAGATGCA	TGAATGGTGG	GACCTGTGCA	480
	GATGACCACT	GCCAGTGCCA	GAAAGGATAT	ATTGGAACCT	ATTGTGGACA	ACCTGTCTGT	540
25	GAAAATGGAT	GTGAGATGG	TGGACGTTGC	ATCGCCCAAC	CGTGTGCTTG	TGTTTATGGG	600
	TTCACCTGGT	CACAGTGTGA	AAGAGATTAC	AGGACAGGCC	CGTGTTCAC	TCAGGTCAAC	660
	AAACAGATGT	GCCAGAGGCA	GCTGACAGGC	ATTGTCTGCA	CGAAGACTCT	GTGCTGTGCC	720
	ACCACTGGAG	GGGGCTGGGG	CCATCCCTGT	GAGATGTGTC	CAGCCAGGCC	TCAGCCCTGC	780
	CGACGGGGTT	TCATCCCAAA	CATCCGCACT	GGAGCTTGCC	AAGATGTGTA	TGAATGCCAG	840
30	GCTATCCAG	GGATATGCCA	AGGAGGAAAC	TGTATCAATA	CAGTGGGCTC	TTTGAATGTC	900
	AGATGCCCTG	CTGGTCAAAA	ACAGAGTGAA	ACTACTCAGA	AATGTGAAGA	CATTGATGAG	960
	TGCAGCATCA	TTCTCTGGAT	ATGTGAAACT	GGTGAATGTT	CCAACACCGT	GGGAAGCTAT	1020
	TTTGTGTTT	GTCACCGTGG	ATATGTAACC	TCAACAGATG	GCTCTCGATG	CATCGATCAG	1080
	AGAACAGGCA	TGTGTTTCTC	GGGCTTGGTG	AATGGCCGCT	GTGCACAAGA	GCTCCCGGGG	1140
35	AGAATGACGA	AAATGCAGTG	CTGCTGTGAG	CCTGGCCGCT	GCTGGGGCAT	CGGAACCAT	1200
	CCTGAAGCCT	GTCCTGTGAG	AGGTTCTGAG	GAATATCGCA	GACTTTGCAT	GGATGGACTT	1260
	CCAATGGGAG	GAATCTGGAG	GAGTGTCTGT	TCCAGACCTG	GAGGCACCTG	GGGAAATGGC	1320
	TTTGCCCAAA	GTGGCAATGG	CAATGGCTAT	GGCCACAGGAG	GGACAGGCTT	CATCCCATC	1380
	CTGGAGGCA	ATGCTTTTTC	TCTGTGGCTT	GGGGGAGCCG	GTGTGGGGGG	CGGGGACAG	1440
40	GGACCTATCA	TCACTGDACT	AACAATTCTG	AACCAGACAA	TAGATATCTG	TAAGCATCAT	1500
	GCTAACCTTT	GTTTAAATGG	ACGCTGTATA	CCAACCTGCT	CAAGCTACCG	ATGTGAATGC	1560
	AACATGGGTT	ATAAGCAGGA	TGCAAAATGGA	GATTGTATAG	ATGTTGATGA	ATGCACATCA	1620
	AATCCCTGCC	CTAATGGAGA	TTGTGTTAAC	ACACCTGGTT	CCTATTATTG	TAAATGTCAT	1680
	GCTGGATTCC	AGAGGACTCC	TACCAAGCAA	GCATGCATTG	ATATTGATGA	GTGCATCCAG	1740
45	AATGGGGTTC	TTTGTAAAAA	CGGTCCGATG	GTGAACCTCAG	ATGGAAGTTT	CCAGTGCAAT	1800
	TGCAATGCCG	GCTTTGAATT	AACACAGAT	GGAAAAAAT	GTGTTGATCA	TGATGAATGT	1860
	ACAACTACCA	ACATGTGTTT	GAATGGAATG	TGCATCAATG	AAGATGGCAG	CTTCAAGTGC	1920
	ATCTGCAAA	CAGGATTTGT	CTTGGCTCCA	AATGGGCGTT	ACTGTACTGA	TGTTGATGAA	1980
	TGCCAGACCC	CAGGAATCTG	CATGAATGGG	CACCTGCATCA	ACAGTGAAGG	GTCTTCCGCG	2040
50	TGTGACTGTG	CCCCAGGGCT	GGCTGTGGGC	ATGGATGGAC	GTGTGTGTGT	TGATACTCAC	2100
	ATGCGCAGTA	CCTGCTATGG	AGGAATCAAG	AAAGGAGTGT	GTGTGCGTCC	TTTCCCGGGT	2160
	GCAGTGACCA	AGTCCGAATG	CTGCTGTGCC	AATCCAGACT	ATGGTTTTGG	AGAACCCTGC	2220
	CAGCCATGCC	CTGCAAAAAA	TTCAGCTGAA	TTCCACGGCC	TTTGTAGTAG	TGGAGTAGGT	2280
	ATCACTGTGG	ATGGAAGAGA	TATCAATGAA	TGTGCTTTGG	ATCCTGATAT	ATGTGCCAAT	2340
	GGGATTGTGT	AAACTTACG	TGGTAGTTAC	CGTTGTAATT	GCAACAGTGG	CTATGAACCA	2400
55	GATGCTCTG	GAGAAACTGT	TATTGACATT	GATGAATGTT	TAGTAAACAG	ACTGCTTTGT	2460
	GATAACGGAT	TGTGCCGAAA	CACGCCAGGA	AGTTACAGCT	GTACGTGCCC	ACCAGGGTAT	2520
	GTGTTTCAGGA	CTGAGACAGA	GACCTGTGAA	GATATAAATG	AATGTGAAAG	CAACCCATGT	2580
	GTCAATGGGG	CTGCAGAGAA	CAACCTTGGA	TCTTTCAATT	GTGAATGTTT	GCCCGGCAGC	2640
	AAACTCAGCT	CCACAGGATT	GATCTGTATT	GACAGCCTGA	AGGGGACCTG	TTGGCTCAAC	2700
60	ATCCAGGACA	GCGCTGTGTA	GTGAAATATT	AATGGAGCCA	CTCTGAAATC	TGAATGCTGT	2760
	GCCACCCTCG	GAGCCGCTCG	GGGGAGCCCC	TGTGAGCGGT	GTGAACTAGA	TACAGCTTGC	2820
	CCAAGAGGCG	TTGCCAGGAT	TAAAGGTGTT	ACGTGTGAGG	ATGTTAATGA	GTGTGAGGTG	2880
	TTCCCTGGCG	TTTGTCCAAA	TGGACGCTGT	GTCAACAGTA	AGGGATCTTT	TCATTGCGAG	2940
65	TGCCCTGAAG	GCCTTACGTT	GGATGGGACT	GGCCGTGTAT	GTTTGGATAT	TCGCATGGAG	3000
	CAGTGTACT	TGAAGTGGGA	TGAAGATGAA	TGCATCCACC	CCGTTCCTGG	AAAGTTCCGC	3060
	ATGGATGCCT	GCTGCTGTGC	TGTGCGGGCG	GCTTGGGGCA	CCGAGTGTGA	GGAGTGCCCC	3120
	AAACCTGGCA	CCAAGGAATA	CGAGACACTG	TGCCCCCGCG	GGGCTGGCTT	TGCTAACCGA	3180
	GGGATGTTC	TACTTGGGCG	GCCATTTTAC	AAAGACATCA	ATGAATGCAA	AGCATTTCCT	3240
70	GGGATGTGCA	CTTATGGGAA	GTGCAGAAAT	ACAATCGGAA	GCTTCAAATG	CCGTTGCAAT	3300
	AGTGGCTTTG	CTCTAGACAT	GGAGGAAAGA	AACCTGCACG	ACATCGACGA	GTGCAGGATT	3360
	TCTCCTGACC	TCTGTGGCAG	TGGAATCTGC	GTCAATACAC	CGGGCAGCTT	TGAGTGCGAG	3420
	TGCTTGAAG	GCTATGAAAG	TGGCTTCATG	ATGATGAAGA	ACTGCATGGA	CATTGACGGA	3480
	TGTGAACGTA	ACCCTCTCCT	TTGTAGGGGT	GGCACCTGTG	TGAACACTGA	GGGCACTTGT	3540
75	CAGTGTGACT	GCCCACTGGG	ACACGAGCTG	TCACCATCCC	GTGAGGACTG	TGTGGATATT	3600
	AATGAATGCT	CCCTGAGTGA	CAATCTCTGC	AGAAATGGAA	AATGTGTGAA	CATGATTGGA	3660
	ACCTATCAGT	GCTCTTGCAA	TCCTGGATAT	CAGGCTACGC	CAGACCCGCA	GGGCTGTACA	3720
	GATATTGATG	AATGTATGAT	AATGAACGGA	GGCTGTGACA	CCCAGTGCAC	AAATTACAGG	3780
	GGAGAGTACG	AATGCAGCTG	CAGTGAGGGT	TATGCCCTGA	TGCCAGATGG	GAGATCGTGT	3840
80	GCAGACATTG	ATGAATGTGA	AAACAATCCT	GATATCTGTG	ATGGCGGCCA	GTGTACCAAC	3900
	ATTCTGGAG	AGTATCGCTG	CCTCTGCTAT	GATGGCTTCA	TGGCTTCCAT	GGACATGAAA	3960
	ACATGCATTG	ATGTCAATGA	ATGTGACCTA	AATTCAAATA	TCTGCATGTT	TGGGGAATGT	4020
	GAGAACACAA	AGGGATCCTT	CATTTGCCAC	TGTCAGCTGG	GTTACTCAGT	GAAGAAGGGG	4080
	ACCACAGGAT	GTACAGATGT	GGATGAGTGT	GAAATGGTGT	CTCATAACTG	CGACATGCAT	4140
85	GCCTCATGTC	TGAATATCCC	AGGAAGCTTC	AAAGTGTAGT	GCAGAGAAGG	CTGGATTGGA	4200
	AACGGCATCA	AGTATATGGA	TCTGGAACGA	TGTTCTAATG	GAACCCACCA	GTGTAGCATC	4260
	AATGCTCAGT	GTGTAAATAC	CCCGGGCTCA	TACCGCTGTG	CCTGCTCCGA	AGGTTTCACT	4320
	GGTGATGGCT	TTACCTGCTC	AGATGTTGAT	GAGTGTGCAG	AAAACATAAA	CCTCTGTGAG	4380

	AACGGACAGT	GCCTTAAATGT	CCCGGGTGCA	TATCGCTGCG	AGTGTGAGAT	GGGCTTCAC	4440
	CCAGCCTCAG	ACAGCAGATC	CTGCCAAGAT	ATTGATGAAT	GCTCCTTCCA	AAACATTTGT	4500
	GTCTCTGGAA	CATGTAATAA	CCTGCCTGGA	ATGTTTCATT	GCATCTGCGA	TGATGGTTAT	4560
5	GAATTTGGACA	GAACAGGAGG	GAACCTGTACA	GATATTGATG	AGTGTGCAGA	TCCTATAAAC	4620
	TGTGTCAATG	GCCTATGTGT	CAACACGCCT	GGTCGCTATG	AGTGTAACTG	CCCACCCGAT	4680
	TTTCAGTTGA	ACCCAATCTGG	TGTGGGTTGT	GTGGACAACC	GTGTGGGCAA	CTGCTACCTG	4740
	AAGTTTGGAC	CTCGAGGAGA	TGGGAGTCTG	TCTTGCAACA	CCGAGATCGG	GGTGGGCGTC	4800
	AGTCGCTCTT	CATGCTGCTG	CTCTCTGGGA	AAGGCCTGGG	GAAACCCCTG	TGAGACATGC	4860
10	CCCCCTGTCA	ATAGCACTGA	ATATTACACC	CTGTGTCCCG	GAGGTGAAGG	CTTCAGACCT	4920
	AACCCCATCA	CAATCATTTT	AGAAGACATT	GACGAATGCC	AGGAGTTACC	AGGTCTCTGC	4980
	CAGGGTGGAA	ACTGCATCAA	CACTTTGGG	AGCTTCCAGT	GTGAGTGCCC	ACAAGGCTAC	5040
	TACCTCAGCG	AGGATACCCG	CATCTGTGAG	GATATTGATG	AGTGTTTTGC	ACATCCTGGT	5100
	GTGTGTGGGC	CTGGGACCTG	CTATAACACC	CTGGGAAATT	ACACCTGCAT	TTGCCCACT	5160
15	GAGTACATG	AGGTCAATGG	AGGCCACAAC	TGCATGGACA	TGAGAAAAAG	CTTTTGCTAC	5220
	CGAAGCTATA	ATGGAACAC	TTGTGAGAAT	GAGTTGCCCT	TCAATGTGAC	AAAAAGGATG	5280
	TGCTGCTGCA	CATATAATT	GGCAAAAGCT	GGGAACAAC	CTTGTGAACC	ATGCCCACT	5340
	CCAGGAACAG	CTGACTTTAA	AACCATATGT	GGAAATATTC	CTGGAATCAC	CTTTGACATT	5400
	CACACAGGAA	AAGCTGTGTA	CATTGTATGA	TGTAAGAGAG	TTCCAGGCAT	TTGTGCAAA	5460
20	GGTGTGTGCA	TTAACCATG	TGGCAGTTTC	CGCTGTGAAT	GCCTACAGG	ATTGAGTTAC	5520
	AATGACCTGC	TGTTGGTTTG	TGAAGATATA	GATGAGTGCA	GCAATGGTGA	TAATCTCTGC	5580
	CAGCGGAATG	CAGACTGCAT	CAATAGTCCT	GGTAGTTACC	GCTGTGAATG	TGCCGCGGGT	5640
	TTCAAACCTT	CACCAATGG	GGCCTGTGTA	GATCGCAATG	AATGTTTAGA	AATTCCTAAC	5700
	GTTTGCAGTC	ATGGCTTGTG	TGTTGATCTG	CAAGGAAATT	ACCAAGTCAT	CTGCCACAA	5760
25	GGCTTTAAGG	CTTCTCAGGA	CCAGACCATG	TGCATGGATG	TTGATGAGTG	CGAGCGGCAC	5820
	CCATGTGGAA	ATGGAACCTG	TAAAAACACC	GTGGATCCCT	ATAACTGTCT	GTGCTACCCA	5880
	GGGTTTGAAC	TCACCTATA	TAATGATTGC	CTGGACATAG	ATGAGTGACG	TTCCTTTTTT	5940
	GGTCAGGTGT	GCAGAAATGG	ACGTTGTTTT	AATGAAATGG	GTTCCTTCAA	GTGTCTATGT	6000
	AACGAAGGTT	ATGAACATTAC	CCCAGATGGC	AAAACTGTA	TAGACACTAA	TGAGTGTGTC	6060
30	GGCCTTCCCG	GCTCTTGCTC	TGCTGGTACC	TGTCAGAAAT	TGGAGGGATC	CTTCAGATGC	6120
	ATCTGTCCCC	CAGGGTATGA	AGTAAAGAGC	GAGAACTGCA	TTGATATAAA	TGAATGTGAT	6180
	GAAGATCCCA	ACATTTGTCT	TTTTGGTTCC	TGTACTAATA	CTCCAGGGGG	CTTCCAGTGC	6240
	CTCTGCCCCC	CTGGCTTTGT	ACTATCTGAT	AATGGACGGA	GATGCTTTGA	TACTCGCCAG	6300
	AGCTTCTGCT	TCACAAATTT	TGAAAATGGA	AAGTGTCTCT	TACCCAAAGC	TTTCAACACC	6360
35	ACAAAAGCAA	ATGGTACATG	TAGTAAGATG	CCAGGAGAGG	GCTGGGGGGA	CCCCTGTGAG	6420
	CTGTGCCCCA	AAGACGATGA	AGTTGCATTT	CAGGATTTGT	GTCCATATGG	CCATGGAACT	6480
	TGCCCTAGTC	TTCAATGATAC	ACGTGAAGAT	GTCAATGAGT	GTCTTGAGAG	CCCAGGCATT	6540
	TGTTCAAATG	GTCAATGTAT	CAACACCGAC	GGATCTTTTC	GCTGTGAATG	TCCAATGGGC	6600
	TACAACCTGT	ACTACACTGG	AGTACGCTGT	GTGGATCTG	ATGAGTGTC	AATCGGCAAT	6660
40	CGGTGTGAA	ATGGTACATG	CACCAATGTT	ATTGGGAGTT	TTGAATGCAA	TTGCAATGAA	6720
	GGCTTTGAGC	CAGGGCCCAT	GATGAATTTG	GAAGATATCA	ACGAATGTGC	CCAGAACCCA	6780
	CTGTGTGATG	CTTACGCTG	CATGAACACT	TTTGGGTCC	ATGAATGCAC	GTGCCCGATT	6840
	GGCTATGCCC	TCAGGGAAGA	TCAAAAGATG	TGCAAGATC	TGGATGAATG	TGCTGAAGGG	6900
	TTACACGAT	GTGAATCTAG	GGGCATGATG	TGTAAGAATC	TAATCGGCAC	CTTCATGTGC	6960
45	ATCTGCCCTC	CTGGAATGGC	CCGAAGGCC	GATGGAGAGG	GCTGTGTAGA	TGAAAATGAA	7020
	TGCGAGGACA	AGCCAGGAAT	CTGTGAAAAT	GGACGTTGTG	TAAACATTAT	TGGAAGCTAT	7080
	AGATGTGAGT	GTAATGAAGG	ATTCCAGTCA	AGTTCTTCAG	GCACTGAATG	CCTTGACAAT	7140
	CGACAGGGTC	TCTGCTTTGC	AGAGGTACTG	CAGACAATAT	GTCAAATGGC	ATCCAGTAGT	7200
	CGCAATCTGG	TCACATAAGT	AGAATGCTGC	TGTGATGGTG	GGCGAGGCTG	GGGCCACCA	7260
50	TGCGAGCTTT	GCCCACTTCC	TGGAACCTGC	CAGTACAAAA	AGATATGTCC	TCATGGCCCA	7320
	GGATATACAA	CTGATGGAAG	AGATATTGAT	GAATGTAAGG	TAATGCCAAA	CCTCTGCACC	7380
	AATGTCTAGT	GCATCAATAC	CATGGGCTCA	TTCCGATGCT	TCTGCAAGGT	TGGCTACACC	7440
	ACAGACATCA	GTGGAACCTC	TTGTATAGAC	CTTGATGAAT	GCTCCCAGTC	CCCGAAACCA	7500
	TGCAACTACA	TCTGCAAGAA	CACGTGAGGG	AGTTATCAGT	GTTCTATGTC	GAGGGGGTAT	7560
55	GTCTTGCAAG	AGGATGGAAA	GACATGCAAA	GACCTTGATG	AATGTCAAAC	AAAGCAGCAT	7620
	AACTGCCAGT	TCCTCTGTGT	CAACACCTTG	GGGGGGTTTA	CCTGTAAATG	TCCACCTGGT	7680
	TTTACACAGC	ATCACACTGC	TTGTATCGAC	AACAACGAAT	GTGGGTCTCA	ACCTTTGCTT	7740
	TGTGGAGGAA	AGGGAATCTG	TCAAAACACT	CCAGGCAGTT	TCAGCTGTGA	ATGCCAAAGA	7800
	GGGTTCTCTC	TTGATGCCAC	CGGACTGAAC	TGTGAAGATG	TTGATGAATG	TGATGGGAAC	7860
60	CACAGGTGCC	AACACGCTG	CCAGAACATC	CTGGGTGGCT	ACAGATGTGG	CTGCCCCCAA	7920
	GGCTACATCC	AGCACTACCA	GTGGAATCAG	TGTGTGCGAT	AGAATGAATG	CTCCAATCCC	7980
	AATGCCCTGT	GCTCTGCTTC	CTGCTACAAC	ACCCTGGGGA	GTTACAAGTG	CGCCTGCCCC	8040
	TCGGGGTTCT	CCTTCGACCA	GTCTCTCAGT	GCCTGCCACG	ACGTGAATGA	GTGCTCGTCC	8100
	TCCAAGAAC	CCTGCAATTA	CGGCTGCTCT	AACACGGAGG	GGGGCTACCT	CTGTGGCTGC	8160
65	CCCCCTGGGT	ATTACAGAGT	GGGACAAGGC	CACGTGTGCT	CAGGAATGGG	ATTTAACAAG	8220
	GGGCAGTACC	TGTCACCTGGA	TACAGAGGTC	GATGAGGAAA	ATGCTCTGTC	CCCAGAAGCA	8280
	TGCTACGAGT	GCAAAATCAA	CGGCTATCCT	AAGAAAGACA	GCAGGCAGAA	GAGAAGTATT	8340
	CATGAACCTG	ATCCCACTGC	TGTTGAACAG	ATCAGCCTAG	AGAGTGTGCA	CATGGACAGC	8400
	CCGCTCAACA	TGAAGTTCAA	CCTCTCCCAC	CTCGGCTCTA	AGGAGCACAT	CCTGGAACCTA	8460
70	AGGCCCGCCA	TCCAGCCCTT	CAACAACCA	ATCOGTTATG	TCATCTCTCA	AGGGAACGAT	8520
	GACAGGCTCT	TCCGATCCCA	CCAAAGGAAT	GGGCTCAGCT	ACTTGACAC	GGCCAAGAAG	8580
	AAGCTCATGC	CCGGCACATA	CACACTGGAA	ATCACTAGCA	TCCCTCTCTA	CAAGAAGAAG	8640
	GAGCTTAAGA	AACGTGAAGA	GAGCAATGAG	GATGACTACC	TCCTAGGGGA	GCTTGGGGAG	8700
	GCTCTCAGAA	TGAGGCTGCA	GATTCAAGCT	TATTAACCGT	TCACAGACTT	GGGCCAGGC	8760
75	TCAAATCCTA	GCACAGCCAG	TCTGCAGAAG	CATTTGAAAA	GTCAGGACT	AATTTTAAAG	8820
	AGGAAAAATA	ATAATAACTC	TTGTTTCTTT	CCTCCCTGTC	TTAGACTTTG	AATGTTGACC	8880
	CTCACAGGGA	GGGATAATTT	AGACTCTGGT	ATGGCCAAAG	ATTTGAGCTC	AAAGGCAACC	8940
	TGTTGTTACTG	TATTTTATAT	ATAACTTCAT	TTTAAATAT	ATTTAAAGAA	ACCTAAATGT	9000
	TCAAGATATG	ACTAAATGCA	CAAAAATAAT	GTGAGCTTTT	TTTTTTTTTT	TTTTTTTTTT	9060
80	CCTGTTAGCA	GTCTGTAAAC	CTTTGGGTAT	TTTGCTATAG	TTGCTAATTA	AAAAATATA	9120
	GATGTTTATT	TATTTTAAAT	GCAGTAATAT	ATGGAGAAAT	GAACAACTA	TGTAACAAA	9180
	AAGGGAAACT	CACPTGTTTT	TCTTTAGATT	TATAAATTTG	AGCTATTTTT	TTTAGAGGTG	9240
	CTTTTTAAAA	ATCCAATAGA	TACAAGAGAT	GTTCCTTTTG	GTTCCTTGCC	AGTCATCCAG	9300
	CTGATACACA	CCTGATCGAT	TTTAAAGAAA	GCCACACAGA	GCTGAATCGG	GCAGTGCTAA	9360
	TCATATATTT	AAAAGACATG	AATGTCATTA	GATCCTTTAT	AACGTAGATC	GAAGCCAAAG	9420
85	CAGCTCATTT	GTGACACAT	TTCATATCAC	CAGACACACC	AGGCAACAGA	AGTTGAAGCA	9480
	CAACCACTGT	AGCAAAATAC	CTTGACTGCT	TGTGAGACCA	TTAGCATTTG	AGGCCAAACC	9540
	GTACTGTATT	TCCCTCTCAT	AACCTCAAGG	AACCATATGT	GCTACCCACA	ACACCTCAT	9600

WO 02/086443

PCT/US02/12476

5
10

```

CTTACCCAGG GTGCGCTGCG TCCTCATGGT ACTGTAGGCA GCTGAAGAAC CGCCGTTCCC 9660
TTGAAAGGGA ACACCTGGCA TTCTGTGGTG TTCTGATGCTG TCTTAATAAA TGGTGCATTT 9720
ATTATGTTCA AGTTATTTCG GGAATGCCAT ATGTGCAAAAC AAATCATGCA ATGCAGCCAA 9780
GGAATATATG TTGTTGTTGT TGTTTTAAAC CCATTTTTTT TTTAGATTTT TCATTAAATAC 9840
TGTAGTTATA CACCATATGC CTCATTTTAT CATAGCCTAT TGTGTATGAA AGATGTTTGT 9900
ACAATGAATT GATGTTTAGT TTGCTTTAGT CATTTAAGAAA GATATTGTAC CAGGATGTGC 9960
TATTAAGAGC ACATATCCAT TATTCTTCTC AACCCAAAGAA CCTGTTTCTT GGACCAAGTGA 10020
CCAAACCTCA TATGTGAAAT GGCCAAAGCA CATGCAGGCT CCTGGTTGTT CCTCTCAAAC 10080
CTGTGCTGAC CAAAGATTAG TAACCAAGTA TACCAGATAT TTTGAGGTTT TATTGTTTTT 10140
TTAATAACTA AAAAAAACT CGTGCC

```

Seq ID NO: 459 Protein sequence
Protein Accession #: NP_001990.1

15
20
25
30
35
40
45
50
55
60
65

```

1 11 21 31 41 51
MGRRRRLCLQ LYPLWLGCVV LWAQGTAGQP QPPPKPPRP QPPPPQVRS TAGSEGGFLA 60
PEYREEGAAY ASRVRRRQSQ DVLRRPNVCG SRPHSYCCPG WKTLPGNQNC IVPICRNSCG 120
DGFCSRPNMC TCSSGQ18ST CGSKSIQCCS VRMCNMGTC A DDHCQCGKY IGTYCGQPV 180
ENGCGNGGRC IAQPCACVYG FTGPQCERDY RTGPFCTQVN NQMCQQLTG IVCTKTLCCA 240
TTGRAWGHPC EMCFAQPPQC RRGFIPNIRT GACQDVDEQ AIPIGCGGN CINTVGSFEC 300
RCPAGHKQSE TTQCEDIDE CSIIPGICET GECSNTVGSY FCVCPRGYVT STDGSRCIDQ 360
RTGMCPSGLV NGRCAQELPG RMTKMQCCCE PGRCNIGITI PEACPVRSSE BYRRLCMDGL 420
PMGGIPGSAG SRPGGTGGNG FAPSGNGNGY GPGGTGFPI PGGNGFSPGV GGAGVGAGGQ 480
GPIITGLTIL NQTIDICKHH ANLCINGRCI PTVSSYRCEC NMGYKQDANG DCIDVDECTS 540
NPCTNGDCVN TPGSYCKKCH AGFQRTPTKQ ACIDIDEQI NGVLCKNGRC VNSDGSFQCI 600
CNAGFELTID GKNVVDHDEC TTNMCLNGM CINEDGSPKC ICKPGFVLAP NGRYCTDVDE 660
CQTGICMNG HNCINSEGSFR CDCPGLAVG MDGRVCVDTH MRSTCYGGIK KGVVVRPFPG 720
AVTKSECCCA NPDYGFGEPC QCPAKNSAE FHGLCSSGVG ITVDGRDINE CALDPDICAN 780
GICENLRGSY RCNCNSGYEP DASGRNCIDI DECLVNRLLC DNGLCRNTPG SYSTCPPGY 840
VFRTEETCE DINECESNPC VNGACRNLG SFNCECSPGS KLSSTGLICI DSLKGTICWL 900
IQDSRCEVNI NGATLKSECC ATLGAAWGSF CERCELDTAC PRGLARIKGV TCEDVNECEV 960
FPGVCFNNG YALMPDGSRF CPEGLTLDGT GRVCLDIRME QCYLKWDEDE CIHPVPGKFR 1020
MDACCAVGA AWGTCECECP KPGTKEYETL CPGAGFANR GDVLITGRFFY KDINECKAFP 1080
GMCTYGKCRN TIGSFKCRCN SGFALDMEER NCTDIDECRI SPDLCSGIC VNTPGSFECE 1140
CFEGYESGFM MMKNCMDIDG CERNPLLCRG GTCVNTGSGF QDCDPLGHEL SPSREDCVDI 1200
NECSLSDNLC RNRKCVNMIG TYQCSNPGY QATPDRQGCT DIDECEMIMG GCDTQCTNSE 1260
GSYECSCSEG YALMPDGSRF ADIDECENNP DICDGGQCTN IPGEYRCLCY DGFMAISDMK 1320
TCIDVNECDL NSNICMFGEIC ENTKGSPICH CQLGYSVKKG TTGCTDVDECE SIGAHNCMDH 1380
ASCLNIPGSF KCSREBGWIG NGIKCIDLDE CSNGTEQCSI NAQCVNTPGS YRCACSEGT 1440
GDGFTCSVDV ECAENINLCE NGQCLNPGA YRCECEMGFT PASDSRSCQD IDECSFONIC 1500
VSGTGNLPG MFHCICDDGY ELDRGTGNGT DIDECADPIN CVNGLCVNTP GRYECNCPD 1560
FQLNPTGVGC VDNRVGNCYL KPFPRGDSGL SCNTEIGVGV SRSSCCSLG KAWGNPCET 1620
PPVNSTEYIT LCPGEGEGRP NPITILEDI DECQELPGLC QGNGCINTFG SPQCECPQGY 1680
YLSEDTRICE DIDECEFAHPG VCGPPTCYNT LGNYTCICFP BYMQVNGGHN CDMRKSFCY 1740
RSYNGTTCEN ELPPNVTKRM CCCTYNVGA GKNKPECPPT PGTADEFKIC GNIPGFTFDI 1800
HTGKAVDIDE CKEIPGICAN GVCINQIGSF RCECPTGFSY NDLLLVCEDE DECSNGDNLC 1860
QRNADCNISF GSYRCECAAG PKLSPNGACV DRNECLEIPN VCSHGLCVDL QGSYQICHN 1920
GFKASQDQTM CNDVDECERH PCNGNCTKNT VGSYNLCYFP GFELTHNNDL LDIDECSFF 1980
QVCRNGRCF NEIGSFKCLC NBYELTPDG KNCIDTNECV ALPGSCSPGT CQNLGSSFR 2040
ICPPGYEVKS ENCIDINECD EDPNCLFSG CTNTPGGFCQ LCPGFLVSD NGRRCFDTRQ 2100
SPCFPTNFENG KCSVPKAFNT TRAKCCSKM PEGEGWDPE LCPKDEEVAF QDLCPYGHGT 2160
VPSLHDTRED VNECLSPGI CSNGQCINTD GSFRCECPMG YNLDTYGVRC VDTDECSIGN 2220
PCNGNCTNMT IGSPECNCE GFEPGPMNC EDINECAQNP LLALCALCMNT FGSYECTCFI 2280
GYALREDQNM LHDCECAEG LHDCEGRMM CKNLIGTFMC ICPPGMARRP DGEGVDENE 2340
CRTKPGICEN GRCVNIIGSY RCECNEGFQS SSSGTECLDN RQGLCFAEVL QTICQMASSS 2400
RNLVTKSECC CDGGRGWGHQ CELCPLPGTA QYKICPHGP GYTDTGRDID ECKVMPNLCT 2460
NGQCTNMTGS FRCPCKVGYT TDISGTSCID LDECSQSPKP CNYICKNTEG SYQCSCPRGY 2520
VLQEDGKCTK DLDCEQTKQH NCQFLCVNTL GGFTCKCPGP FTQHTTACID NNECGSQPLL 2580
CGGKIGICNT PGSFSCQCR PGLSDATGLN CEDVDECDGN HRCQHGQNI LGGYRCGCPQ 2640
GYIQHYQWQ CVDNECSNP NACGSASCYN TLGSYKACP SGFSFDQFSS ACHDVNECSS 2700
SKNPNYGCSS NTEGGYLCG PPGYYRVGQG HCVSGMGFNK GQYLSLDTEV DEENALSPEA 2760
CYECKINGYP KKDQRKRSI HEPDPTAVEQ ISLESVDMS PVMNMFNLH LGSKEHILEL 2820
RPAIQPLNTH TRYVISQND DSVFRIHQRN GLSYLHAKK KLMPGTITLE ITSIPLYKKK 2880
ELKLEESNE DDYLLGELGE ALNRLQIQL Y

```

Seq ID NO: 460 DNA sequence
Nucleic Acid Accession #: NM_013372.1
Coding sequence: 63..617

70
75
80
85

```

1 11 21 31 41 51
GCGGCCGCAC TCAGCGCCAC GCGTCGAAAG CGCAGGCCCC GAGGACCCGC CGCACTGACA 60
GTATGAGCCG CACAGCCTAC ACGGTGGGAG CCTCTGCTCT CCTCTGGGG ACCCTGCTGC 120
CGGCTGCTGA AGGGAAGAAC AAGGGTCCC AAGGTGCCAT CCCCCGCCA GACAAGGCC 180
AGCACATGA CTCAGAGCAG ACTCAGTCGC CCCAGCAGCC TGGCTCCAGG AACCGGGGG 240
GGGCGCAAGG GCGGGGCACT CCATGCGCCG GGGAGGAGST GCTGGAGTCC AGCCAGAGG 300
CCCTGCATGT GACGGAGCGC AAATACCTGA AGCAGACTG GTGCAAAACC CAGCCGCTTA 360
AGCAGACCAT CCAGAGGAA GGCTGCAACA GTGCGACCAT CATCAACCCG TTCTGTTAGC 420
GCCAGTGCAA CTCTTTCTAC ATCCCCAGGC ACATCOGGAA GGAGGAAGGT TCCTTTCA 480
CTGTCTCTCT CTGCAAGCCC AAGAAATTCA CTACCATGAT GGTCACTC AACTGCCCTG 540
AACTACAGC ACCTACCAAG AAGAAGAGAG TCACACGTGT GAAGCAGTGT CGTTGCATAT 600
CCATCGATTG GGATTAAGCC AAATCCAGGT GCACCCAGCA TGTCCTAGGA ATGCAGCCCC 660
AGGAAGTCCC AGACCTAAAA CAACCAGATT CTACTTGGC TTAACCTAG AGGCCAGAAG 720
AACCCCGAC TGCCTCTCGG CAGGAGCCTG CTTGTGCGTA GTTCGTGTGT ATGAGTGTGG 780
ATGGGTGCT GTGGGTGTTT TTAGACACCA GAGAAAACAC AGTCTCTGCT AGAGAGCACT 840
CCCTATTTTG TAAACATATC TGCTTTAATG GGGATGTACC AGAAACCCAC CTCACCCCGG 900

```

CTCACATCTA AAGGGGCGGG GCCGTGGTCT GGTTCGACT TTGTGTTTTT GTGCCCTCCT 960
GGGGACGAGA ATCTCCTTTC GGAATGAATG TTCAATGGAAG AGGCTCCTCT GAGGGCAAGA 1020
GACCTGTTTT AGTGTCTGCAT TCGACATGGA AAAGTCCTTT TAACCTGTGC TTGCATCCTC 1080
5 CTTTCTCCTCT CCTCCTCACA ATCCATCTCT TCTTAAGTTG ATAGTGACTA TGTCACTCTA 1140
ATCTCTTGTG TGCCCAAGGTT CCTAAATTAA TTCACCTAAC CATGATGCAA ATGTTTTTCA 1200
TTTTGTGAAG ACCCTCCAGA CTCTGGGAGA GGCTGGTGTG GGCAAGGACA AGCAGGATAG 1260
TGGAGTGAGA AAGGGAGGGT GGAGGGTGAG GCCAAATCAG GTCCAGCAAA AGTCAGTAGG 1320
GACATTGCAG AAGCTTGAAA GGCCAATACC AGAACACAGG CTGATGCTTC TGAGAAAGTC 1380
10 TTTTCTTAGT ATTTAACAGA ACCCAAGTGA ACAGAGGAGA AATGAGATTG CCAGAAAGTG 1440
ATTAACCTTG GCCGTGCAAA TCTGCTCAAA CCTAACACCA AACTGAAAAC ATAAATACTG 1500
ACCACTCCTA TGTTCGAGCC CAAGCAAGTT AGCTAAACCA AACCAACTCC TCTGCTTTGT 1560
CCCTCAGGTG GAAAGAGAGG GTAGTTTAGA ACTCTCTGCA TAGGGGTGGG AATTAATCAA 1620
AAACCKCAGA GGCTGAAATT CCTAATACCT TTCCTTTATC GTGGTTATAG TCAGCTCATT 1680
15 TCCATTCCAC TATTTCCCAT AATGCTTCTG AGAGCCACTA ACTTGATTGA TAAAGATCCT 1740
GCCTCTGCTG AGTGTACCTG ACAGTAAGTC TAAAGATGAR AGAGTTTAGG GACTACTCTG 1800
TTTTAGCAAG ARATATTTTG CCGGTCTTTT TGTTTAACT ATTGTGAGGA GATTGGGCTA 1860
RAGAGAGAGC GACGAGAGTA AGGAAATAAA GGGRATTGCC TCTGGCTAGA GAGTAAGTTA 1920
GGTGTATAA CCTGTGAGAA ATGTAAGGGA TATGACCTCC CTTTCTTAT GTGCTCACTG 1980
20 AGGATCTGAG GGGACCTGT TAGGAGAGCA TAGCATCATG ATGTATTAGC TGTTCATCTG 2040
TCTACTGTTG GATGACATA ACTATTGTAA CTATTTCAGTA TTTACTGGTA GGCACCTGTC 2100
TCTGATTAAA TGTTCGCTAC TGGCAATGGC TACTTAGGAT TGATCTAAGG GCCAAAGTGC 2160
AGGTTGGGTG AACTTTATG TACTTTGGAT TTGGTTAAAC TGTTTCTTC AAGCCTGAGG 2220
TTTTATATAC AACTTCCCTG AATACTCTT TTGCTTGTG TCTTCTCAGC CTCCTAGCCA 2280
25 AGTCTATGT AATATGGAAG ACAAACACTG CAGACTTGAG ATTCACTGTC CGATCAAGGC 2340
TCTGGCATTG AGAGAACCTT TGCAACTCGA GAAGCTGTTT TTATTTCTGT TTTGTTTTGA 2400
TCCAGTGTCT TCCCATCTAA CAACATAACA GGAGCCATT CAAGGCGGGA GATATTTTAA 2460
ACACCCAAAA TGTGGGTCT GATTTTCAAA CTTTAAACT CACTACTGAT GATTCTCAGC 2520
CTAGGCGAAT TGTGCTAAG ACATAGTGTG TGTGTTTTGT ATACACTGTA TGACCCCAAC 2580
30 CCAATCTTT GTATTGTCCA CATCTCCAA CAATAAAGCA CAGAGTGGAT TTAATTAAGC 2640
ACACAAATGC TAAGGCAGAA TTTTGAGGGT GGGAGAGAG AAAAGGGAAA GAAGCTGAAA 2700
ATGTAAAAAC ACACAGGGA GGAATAATGA CATTGAGAAC CAGCAAAAC TGAATTTCTC 2760
TTGTTGTTTT AACTCTGCA CAAGAATGCA ATTCGTTAA TGGAGATGAC TTAAGTTGGC 2820
AGCAGTAATC TCTTTTAGG AGCTTGTAAC ACAGCTTGAC ACATAAGTGC AGATTGGCT 2880
35 CAAGTAAAGA GAATTTCTC AACACTAAT TCACTGGGAT AATCAGCAGC GTAACTACCC 2940
TAAAGCATA TCACTAGCCA AAGAGGGAAA TATCTGTTCT TCTTACTGTG CCTATATTAA 3000
GACTAGTACA AATGTGGTGT GTCTTCCAAC TTTTATTGAA AATGCCATAT CTATACCATA 3060
TTTTATTCCA GTCACTGATG ATGTAATGAT ATATTTTTTC ATTATTATAG TAGAATATT 3120
TTATGGCAAG ATATTGTGG TCTGTATCAT ACCTATTAAA ATAATGCCAA ACACCAATA 3180
40 TGAATTTTAT GATGTACACT TTGTGCTTGG CATTAAGAGA AAAAACAACA CATCCTGGAA 3240
GTCTGTAAGT TGTTTTTTGT TACTGTAGGT CTTCAAAGTT AAGAGTGTA GTGAAAAATC 3300
TGGAGGAGAG GATAATTTCC ACTGTGTGGA ATGTGAATAG TTAATGAAA AGTTATGGTT 3360
ATTTAATGTA ATTATTCTT CAAATCCTTT GGTCACCTGT ATTTCAAGCA TGTTTTCTTT 3420
TTCTCTTTA TATGACTTTC TCTGAGTTGG GCAAAGAAGA AGCTGACACA CCGTATGTTG 3480
45 TTAGAGTCTT TTATCTGCTC AGGGGAAACA AAATCTTGAC CCAGCTGAAC ATGTCTTCTC 3540
GAGTCAGTGC CTGAATCTTT ATTTTTTAAA TTGAATGTTT CTTAAAGGTT AACATTTCTA 3600
AAGCAATATT AAGAAAGAT TTAATGTTA TTTTGAAGA CTTACGATG ATGTATACAA 3660
ACGAATAGCA GATAATGATG ACTAGTTTAC ACATAAAGTC CTTTAAAGGA GAAAACTCAA 3720
AATGAAAAGT GATATTGTAAG AACATTTATA AGTGATCAGT TAATGCCCTA GAGTGAAGT 3780
50 AGTTCTATTG ACATCTCTCA AGATATTTAA TATCAACTGC ATTAGTATT ATGTCTGCTT 3840
AAATCATTTA AAAACGGCAA AGAATTATAT AGACTATGAG GTACCTTGCT GTGTAGGAGG 3900
ATGAAAGGGT AGTTGATAGT CTCATAAAAC TAATTTGGCT TCAAGTTTCA TGAATCTGTA 3960
ACTAGAATTT AATTTTCAAC CCAATAATGT TCTATATAGC CTTTGCTAAA GAGCACTAA 4020
TAAATTAAC CTATCTTTC AAAAAAAA

Seq ID NO: 461 Protein sequence
Protein Accession #: NP_037504.1

1 11 21 31 41 51
60 MSRTAYTVGA LLLLLGLTLP AAEKKKKSQ GAIPPPDKAQ HNDSEQTQSP QPGSRNRGR 60
GQGRGTAMPG EVLESSQEA LHVTERKYLK RDWCKTQPLK QTIHEEGCNS RTIINRFCYG 120
QCNFPYIPRH IRKEGSPQS CSFCKPKKFT TMMVTINCPE LQPPTKKKRV TRVKQCRIS 180
IDLD

Seq ID NO: 462 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..2733

1 11 21 31 41 51
70 ATGAAAGTTG GAGTGCTGTG GCTCATTCTT TTCTTCACCT TCACTGACGG CCACGGTGGC 60
TTCTGGGGA AAAATGATGG CATCAAAACA AAAAAGAAG TCAATGTGAA TAAGAAAAA 120
CATCTAGGCC CAGTCGAAGA ATATCAGCTG CTGCTTCAGG TGACCTATAG AGATTTCAAG 180
75 GAGAAAGAG ATTTGAGAAA TTTTCTGAAG CTCTTGAAGC CTCCATTATT ATGGTCACAT 240
GGGCTAATTA GAATTATCAG AGCAAAGGCT ACCACAGACT GCAACAGCCT GAATGGAGTC 300
CTGCACTGTA CCTGTGAAGA CAGCTACACC TGGTTTCTCT CCTCATGCCCT TGATCCCCAG 360
AACTGCTACC TTCAACAGGC TGGAGCACTC CCAAGCTGTG AATGTCTCT CAACAACCTC 420
AGCCAGAGTG TCAATTTCTG TGAGAGAAACA AAGATTGGG GCACTTTCAA AATTAATGAA 480
80 AGGTTTACCA ATGACCTTTT GAATTCATCT TCTGCTATAT ACTCCAATA TGCAATGGA 540
ATTGAAATCT AACCTTAAAG AGCATATGAA AGAATTCAAG GTTTTGAGTC GGTTCAGGTC 600
ACCAATTTTC GAAATGGAAG CATCGTTGCT GGGTATGAAG TTGTTGGCTC CAGCAGTGCA 660
TCTGAATCTG TGTAGCCAT TGAACATGTT GCCGAGAAGG CTAAGACAGC CCTTCACAAG 720
CTGTTTCCAT TAGAAGACGG CTCTTTCAGA GTGTTGCGAA AAGCCGAGTG TAATGACATT 780
85 GTCTTTGGAT TTGGTCCAA GGATGATGAA TATACCTGCT CCTGCAGCAG TGGCTACAGG 840
GGAACATCA GACCAAGTG TGAGTCTCT GGGTGGCAGG TCACTAGGGA GACTTGTGTG 900
CTCTCTCTGC TTGAAGAAT GAACAAGAAT TTCAGTATGA TTGTAGGCAA TGCCACTGAG 960
GCAGCTGTGT CATCTTCTGT GCAAAATCTT TCTGTATCA TCGGCAAAA CCCATCAACC 1020

	ACAGTGGGGA	ATCTGGCTTC	GGTGGTGTG	ATTCTGAGCA	ATATTTTCATC	TCTGTCACTG	1080
	GCCAGCCATT	TCAGGGGTGTC	CAATTCAACA	ATGGAGGATG	TCATCAGTAT	AGCTGACAAT	1140
	ATCCTTAATT	CAGCCTCAGT	AACCAACTGG	ACAGTCTTAC	TGCGGGAAGA	AAAGTATGCC	1200
5	AGCTCACGGT	TACTAGAGAC	ATTAGAAAAC	ATCAGCACTC	TGGTGCCTCC	GACAGCTCTT	1260
	CCTCTGAATT	TTTCTCGGAA	ATTCATTGAC	TGGAAGGGGA	TTCCAGTGAA	CAAAAGCCAA	1320
	CTCAAAAGGG	GTTACAGTCA	TCAGATTAAA	ATGTGTCCCC	AAAATACATC	TATTTCCCAT	1380
	AGAGGCGGTG	TGTTAATTGG	GTCAGACCAA	TTCCAGAGAT	CCCTTCCAGA	AACTATTATC	1440
	AGCATGGCCT	CGTTGACTCT	GGGGAACATT	CTACCCGTTT	CCAAAATGG	AAATGCTCAG	1500
10	GTCAATGGAC	CTGTGATATC	CACGGTTATT	CAAACTATT	CCATAAATGA	AGTTTTCCTA	1560
	TTTTTTTCCA	AGATAGAGTC	AAACCTGAGC	CAGCCTCATT	GTGTGTTTTG	GGATTTCAGT	1620
	CATTTCAGT	GGAACGATG	AGGCTGCCAC	CTAGTGAATG	AAACTCAAGA	CATCGTGACG	1680
	TGCCAATGTA	CTCACTTGAC	CTCCTTCTCC	ATATTGATGT	CACCTTTTGT	CCCTCTACA	1740
	ATCTTCCCG	TTGTAATAATG	GATCACCTAT	GTGGGACTGG	GTATCTCCAT	TGGAAGTCTC	1800
15	ATTTTATGCC	TGATCATCGA	GGCTTTGTTT	TGGAAGCAGA	TAAAAAAAG	CCAAACCTCT	1860
	CACACACGTC	GTATTGTGAT	GGTGAACATA	GGCCTGTCCC	TCTTGATTGC	TGATGTCTGG	1920
	TTTATTGTTG	GTGCCACAGT	GTGACCAACG	GTGAACCCCT	CTGGAGTCTG	CACAGCTGCT	1980
	GTGTTCTTTA	CACACTTCTT	CTACCTCTCT	TTGTTCTTCT	GGATGCTCAT	GCTTGGCATC	2040
	CTGCTGGCT	ACCGGATCAT	CTCCTGTTC	CATCACATGG	CCCAGCATTT	GATGATGGCT	2100
20	GTGGAATTTT	GCCTGGGTTA	TGGGTGCCCT	CTCATATAT	CTGTCTTAC	CATTGCTGTC	2160
	ACGCAACCTA	GCAATACCTA	CAAAAGGAAA	GATGTGTGTT	GGCTTAACTG	GTCCAATGGA	2220
	AGCAAACCA	TCTTGTCCCT	GCACCTGGCTA	TTGTGGCTGT	GAACCTCGTT	TTCTTGAAG	2280
	GTGGTGCTGC	TAGTCTCTAC	AAAGCTCTGG	AGGCCGACTG	TGGGGGAAAG	ACTGAGTCGG	2340
	GATGACAAGG	CCACTCATCT	CCGCTGGGG	AAGAGCTCC	TCATTCTGAG	CCCTCTGCTA	2400
25	GGGCTCACT	GGGCTTTGG	AATAGGAACA	ATAGTGGACA	GCCAGAATCT	GGCTTGGCAT	2460
	GTATTATTTG	CTTTACTCAA	TGCATTCCAG	GGATTTTTTA	TCTTATGCTT	TGGAATACTC	2520
	TTGGACAGTA	AGCTGCGACA	ACTTCTGTTT	AACAAGTTGT	CTGCCTTAAG	TTCTTGAAG	2580
	CAAAACAGAA	AGCAAACTC	ATCAGATTTA	TCGTCCAAAC	CCAAATTCTC	AAAGCCTTTC	2640
30	AACCCACTGC	AAACAAAGG	CCATTATGCA	TTTTCTCATA	CTGGAGATTG	CTCCGACAA	2700
	ATCATGCTAA	CTCAGTTTGT	CTCAATGAA	TAA			

Seq ID NO: 463 Protein sequence
Protein Accession #: Eos sequence

	1	11	21	31	41	51	
35	1	11	21	31	41	51	
	MKVGVWLWIS	FFTPTDGHGG	FLGKNDGIKT	KKELIVNKKK	HLGPVBEYQL	LLQVITYRDSK	60
	EKRDLNLFK	LLKPLFLWSH	GLIRIIRAKA	TTDCNSLNGV	LQCTCEDSYT	WPPPSCLDPQ	120
	NCYLHTAGAL	PSCECHLNNL	SQSVNFCERT	KIWGTFKINE	RPTNDLLNSS	SAIYSKYANG	180
	IBIQLKKAYE	RIQGFESQVQ	TQPRNGSIVA	GVEVVGSSSA	SELLSAIEHV	AEKAKTALHK	240
40	1	11	21	31	41	51	
	LPFLEDGSPR	VFGKAQCNDI	VFGFGSKDDE	YTLPCSSGYR	GNITAKCESS	GWQVIRETCV	300
	LSLLEELNKN	FSMIVGNATE	AAVSSFVQNL	SVIIRQNPST	TVGNLASVVS	ILSNISLSSL	360
	ASHFRVSNST	MEDVISIADN	ILNSASVTNW	TVLLREEKYA	SSRLLETLEN	ISTLVPPAL	420
	PLNFSRKFID	WKGIFVNSQ	LKRGYSYQIK	MCPQNTSIPI	RGRVLIGSDQ	FQRLPETII	480
45	1	11	21	31	41	51	
	SMASLTGLNI	LVSKNGNAQ	VNGPVIISTVI	QNYISINEVFL	FFSKIESNLS	QPHCVWFDFS	540
	HLQWNDAGCH	LVNETQDIVT	CQCTHLTSFS	ILMSFPVPST	IFPVVKWITY	VGLGISIGSL	600
	ILCLIIIEALF	WKQIKKSQTS	HTRRICMVNI	ALSLLIADVW	FIVGATVDTT	VNPSGVCTAA	660
	VFPTTFEYFL	LEFFWMLMGI	LLAYRIILVF	HMAQHLMA	VGFCGLGYCP	LIISVITIAV	720
	TQPSNTYKRL	KGTLNWSNG	SKPLLAFFVP	ALAIVAVNFV	VLLVLVTLKW	RPTVGERLSR	780
50	1	11	21	31	41	51	
	DDKATIIIRVG	KSLILLTPLL	GLTWGFGIGT	IVDSQNLAWH	VIFALLNAFG	GFFILCFGL	840
	LDSKLRLQLF	NKLSALSSWK	QTERQNSDDL	SAKPKFSKFP	NPLQNKGHYA	FSHTGDSSDN	900
	IMLTQFVSNE						

Seq ID NO: 464 DNA sequence
Nucleic Acid Accession #: AB035089.1
Coding sequence: 9845..10219

	1	11	21	31	41	51	
60	1	11	21	31	41	51	
	GGGCATGCGC	CCATCGGGGA	AAATCCATAG	TGCAGATAAA	GCAAGGAGGA	AGAAGAAGGA	60
	CAGTTCTAGT	AAAAGGGAGA	ACATCAATAT	AGGATGTTTC	TTAGCAATAG	AAAAAGAAGG	120
	CCAAGAGGAA	TTAGGGAGAG	AGTTATAAGA	GATCAGCAAG	GGGACAGGGT	TAGATTGGGT	180
	TTGGTTTGAA	AGCATACAGT	AAATATGATG	TCTGTCCCTG	GCAGTGTGGG	CAGAGTAGGA	240
	AGGAGGAAGG	GAGGCAAGAG	ATAATATCAT	TTTCTCTGTG	CTCCAACGTG	ACTTACATAT	300
65	1	11	21	31	41	51	
	GAGACTATTT	CCCTCTCTCG	TTTTCAAACC	TTACTGGAGT	TGTTTTCCCT	ATGAAAAACC	360
	AAGAAAGGAA	AGCTAGTTAG	TCTTGTCTCG	AGGTTGTTCA	ATGTATACAT	ATCTATATCT	420
	GTAGACAGAA	TCCTTGGGAA	TACAGTAATT	GACATATATT	CTGTATTATT	ATGCTTGAAA	480
	AATCTCCTCC	ACTAACCACT	TTCCCTATAG	ATTGCCACAA	GCACATAATA	AGAAACAATA	540
	AATAAAATGT	TCTCTTGACT	TTGTTACTTA	ACAATGCTGA	GAAAACTTTA	CAGCCTTCAT	600
70	1	11	21	31	41	51	
	AAGGAAAGTA	GGTCCAGGAA	AATCTAGGAG	ATATTCTTTA	ACCAATCTAT	AAAGGCATTA	660
	GTAATGACAG	GATATTTCCT	GAAAGTGTA	TTTCCCATG	AGGATTGTTT	TTTAATTTCT	720
	GGATTCTCGG	AGCCAATGAA	GTGGGTGAT	GTTTATGAAA	TATCAAGAGA	CATAAGTTGG	780
	CAAGTGTTCA	TATGCAAAAA	CTTCTTGGA	TTTCTGAGTT	CTCTGTGGCA	ATATATGACA	840
	TCAGGATATG	TCCAGTCTCA	CACACCAGGA	TATGTCCTTT	CTAGCCTGTC	TATCACATGC	900
75	1	11	21	31	41	51	
	TAGGAGAACT	ATTTAGGAAC	AGAAAAAAT	GCCTGAAATG	ATTTCTCATT	TGAACCTCAT	960
	CAGCTTTTCT	CTAAATTTAA	GCAAACTCCT	GGTCATTTTC	AGTTAGTACC	TTTCCTTAAG	1020
	TTCAACCTTC	AGGGCAAAAC	TCCGTGCCTC	AGACGTTTAG	CCATAGTCTG	AAATTCTCTT	1080
	CCATAGATTG	GTCCCTCTGA	ACCCGGTTT	GTCTCAGCTT	GTTATCCTGT	TTTTTCTTCT	1140
	CCTCCATTCC	CAGGATGAGC	TTGTGTGCTC	TGTCCTATGA	GACATTAGAT	TCCTTTTCTT	1200
80	1	11	21	31	41	51	
	TGGTACCCGA	GTAATTCAT	CCTACTCCAA	TAGAGGAAGG	TCCATTTTGT	TCTTATAGCG	1260
	CTGGATGCGA	ACTCAATCTA	GAAGACCATT	ATTCATTTTT	GGAATTTCTT	ATCTCAGATA	1320
	TTTCTCTTCT	TTTCTTTTTC	TTCTATCTTT	GGATTTTITAG	TCCATCAACG	CCCCATTAGT	1380
	CTATTCCCGG	ACTTCAATCA	GGGAACCTAT	ACCTCTTAAA	CTCATTGAGA	GACTCAAAAC	1440
	ATATATATTG	ATACAGGAGA	CCTAAGAAGA	GCATGTCTTG	GGGGTTGAGG	AAACAGGCAG	1500
85	1	11	21	31	41	51	
	GTGAGAAAT	TCCAGATTGG	AAACACAGCT	TCCTTTCTCC	CATCCAGCCC	CTACTTTCAG	1560
	CCTATGTGTT	CTTGGCACTG	TGTTGTAGAT	AAATCTCCCT	TGACTTTTGT	ATGTGCTGAG	1620
	AAAACAAACT	CACGGCTGGT	GTTAAAAAGG	GCCTATGACA	ATACCAAGTG	TTGGGGAGAA	1680
	TGTGGAGAAA	TCAGAACTCT	ATTCAACGTC	GGTTGGAATG	CACACTTGTG	CAGAAATCTA	1740

5

10

15

20

25

30

35

40

45

50

55

60

65

70

75

80

85

TGGAGAAAGAG TCTGGCATT TCTCRAAATG TTAACCTGGA TTTACCATAT GACCAGCGA 1800
 TTTTCATTAT AGGTTTATAC TCAAAAGAAA TGAAGAAATA TGCCATGCAA AAAAATGTAC 1860
 ATGAAAGGTT ACACATCAT TATTTCATAAT AGTAAAGGGA TGGAAACAAAC ACAAATGTCC 1920
 ATCAACTTAT GATTAAGAAA AATCTGGTCT ATTCATAGAA TGGAATATTA TTCGACCACA 1980
 AAAAGGAATG ATGTACTGAT CCATGCAATG ATGTGGACAA ACCATGAAAA TAACACTAGA 2040
 TTAAGAAAGC CAGTCAAAA AGGACTTACT GTATGATTCC ATTTACCTGA AATGTTTGGG 2100
 ATAGGCAAAAT CCATAGAAAC AGGAGGTAGA TTCCTGGTTT CCAGGGTCTC CAGGAAGGGA 2160
 AGAATGAAGT ACAAGATTTC TTTTGGAGGT AGTGAAATTG TTGTGGAATG AGATCATGAT 2220
 GATGATAGCA CAACTTTGTG AATATAATAA AATCATTGAA TTGTACAGTT GAATTTATGG 2280
 TATATAAATT ATATGTTAAT AAAAAGGGGG TCCACAAAAC AAACAGCCCC CCATCTGGT 2340
 TGTCAGGGAG ATATTGGATT AAATGGCCTT GGACAACAAC CCCTCTCCCT GGCCACAGAC 2400
 ATTCTTCAGA TTACAAGATA TTCCAGGGGA AACACTGGAA TGAGTCTGAA GCCAGGTGCT 2460
 AAACAGAAAGT ACCATTGAGA AATGTTGTGA TCCTGACAGG TCAAGCAATT TATTTTTCGG 2520
 CTTCATTTTT AAATCTAAAA TTAGAAAGCT GCCATTAAAA ATGGCCCGTC TGTTTCAATT 2580
 GCTCTTCTCA GTGTGAGCCT GTTAACTCAA TGTTTGTAGT TGTTTTTCATG CTGTCTGATA 2640
 AAACATACCT GAGACTGGCA AGAAAAAGAG GTTTAATTGG GCTTAGAGTT CCAGTGATT 2700
 GGGGAGGCCT CAGAATCACA GTAGGAGGCA AAAGTTATTC TTACATGTTG GCTGCAAGAG 2760
 AAGATGAGGA AGAAGCAAAA GAAGAAACCC CTGATAAACCC CATCGGATCT CCTGAGGCTT 2820
 ATTAACATAC ATGAGAAATG CACAAGAAAG ACCGGCCCCC ATGATTCAAT TACCTCTACC 2880
 TGGTCCCTC CAATAACATG TGGAAATTCT GGTAGATACA ATTCAAGTTG AGATTGGGT 2940
 GGGAAACACG CCAAAACCATA TCACCTCAGCA AGGCAGATAA CTTTCTCACT GAGCCTATGC 3000
 AACAGAAAAC CATCTGGGAT GGTGTGAAGG GGCACAGGAA GTGACTGGTA GGATCACTGC 3060
 CAAAGCTGAG CACTCAGGAG AAGGCAATAG AATCCTATTC TCCTAGTAT GCTATAAGAT 3120
 ACTGAAGTAC ACTTCTTCTG TATCTCTTGG GACTTAGAAT TAGCACTACA TTCCTTGTTA 3180
 TACAGAAAAA TTACTAGGA AATTCATAGG ATGACAAAAA CTTTCAGAAC TGAAAAACAG 3240
 GAAATGTAAG CTTTTGTAGT CTTTGGTATT CGAAGTATGC CTAAGAGACA ATGCAAAATC 3300
 CAAGAAAAAG ATGGTGGGGT TTTTGTGTGT TTGTTTGTGT TTTTGTGTTA CAGCTGGAGT 3360
 AGAATACAAA GGGATGGAGT TGAACCAAAAT GAGAGGAAAT TGAATTTCTA AACCTATTCT 3420
 CATTTGGCATT AGAAGAGGCC CTACATGTAT TTCACATGAG CCGGTGACTG CTGACTTGCA 3480
 TTCTTATTTT TTCCCTATAG ATTAAGAAAGG AGGTACAATG GTAGAACTGT AATCCTGTCC 3540
 TTTGTCTATA ATTTTCTAT TCATAAAGGT GAGTGTAGC CCGCTTGTGA AATCTGAAT 3600
 TGAGTAACCT CAAATACTAA CCACAGAGGG AAAGGCAGCA AGAGGAGAGG CATAAATTTA 3660
 GGATCTCACC CTTCATTCCA CAGACACACA CAGCCTCTCT GCCACCTCT CTTCTCTCTA 3720
 GGAACACAGG TAAAGCTTCC AAGCCTCTCC AGCTTAATAA CATGAATTAT TTTTGAAGAT 3780
 AATAATGATA CTGTGTCTTA TATCATGCAT CTCCTGCATT CTGTCTGATT ATATTTTACT 3840
 TATTTGCGCA GAGCAAAAT AAAATACCTA TTTTCATCTGA TTTGTCTTTT ATCTAAATG 3900
 CTTAGTTCCA AGTAAACCAA GGCACCTTTA GGAACACAGA GGGAGAGTGC CTTGCAGCCA 3960
 GAGAGTCTTG AAGGAGATGT CAGGGACGCA TCTTAACAGC TGGTTGGATG TGATCCACAG 4020
 AGGTCTCCTG TTAGCATTTA TTGTAAAGCC ATCCTACCTA GCTCTAGTGT AACAGCAAT 4080
 GAAAGAAAGT TAAAGAGGGT CGATTACTTA TTTACAATAG TCTTTAAAAA CGTAGTTTGT 4140
 TAAGCCTTCT AATTAGGACA TTAATATATT TAATATATGC ACATTGTAGA AAGATTGAAG 4200
 CGTTAAAAAT AAGAGAAAAA CTTTAAATGT CAAATCTCA CAACCCAGAT ATATCATTTT 4260
 TTTAAGAAAA TTGTACTACA AAATACCATT CCATTTATTA AAGTCATTCT GACAGGAATC 4320
 TGATGCTTTT CCAGGAGTTC CAGATCACAT CGAGTTTACC ATGAATTCAC TCAGTGAAGC 4380
 CAACACCAAG TTATGTTTCC ATCTGTTCCA ACAGTTCAGA AAATCAAAAG AGAACACAT 4440
 CTTCTATTCC CTTATCAGCA TCACATCAGC ATTAGGGATG GTCCCTCTAG GAGCCAAAGA 4500
 CAACACTGCA CAACAAATTA GCAGGTAGC TATCAGCATC ATTACGTTGT CCTGTTGCAG 4560
 TTTTCTCTG GTTCCGTCGG CTAGCACGCA GATGGTAATA GATGTGGTGG TCTGATGGGT 4620
 AGCACAGGGG GCTGTGCAGG AATTCCCATA ACTGTGAGAC CACTGACTTA AACAGATCTT 4680
 TTGAGTAAAG TTTTCTGTCT CCGCTTCATG TCTCTCCAG GTTCTTCACT TTGATCAAGT 4740
 CACAGAGAAC ACCAGAGAAA AAGCTGCAAC ATATCATGTG AGTCACAGAG CACTCTGATT 4800
 CAGCTTTAGA TCCCTGAACA GGTCTAGATT TAAACCTGGA ACTTCACAAA AACTAAGAAA 4860
 AGGCCAGTTT TAGGGAAAAA CTTGGACACA AAGATTGAGA CATACAGAGT GGGTTGGCAT 4920
 TTCTATGAC ATAATTATTA TTCTCATTT CTGCGTTACT AAAAGACAGT CAGCACTGTA 4980
 CCTCAGAGCA TAGGTTCTGA TCAGGATAGG CTGGGTTTCC ACTCCAGCTT TGCTCTTCC 5040
 AANTGATGAA TAAAGACAGG ACACAACTGC TCGGAGTCCC AGTGACCTCA TCCACAGAAA 5100
 CTAAGGGTAA GAAAAATCT GACTCAATAC ATGCAATAC ATGCAATGT TTACAACAGT 5160
 GCCTTGCCCA TAAAGTCAAT AATAAATGTT ATTATTATTA TAAAGTAGCT ATAATTATAC 5220
 TAATCATAAT AATGTGAAAA TAATTTAATT TTCATTGAGT CATTAAATGAG ATTCAGAGGA 5280
 ATAAGCACA GTCCAAGTAT ATTTTGGAAA ATGATTGCTA TGGAATATAT TGGTTTAGAG 5340
 CCTTAATAGT GCAAAATGCT TTGCTGGAAG GTAGAAAGTT CTAGATTTAA ACAGGCTTAG 5400
 GTTCAAAACT TGGCACTTCT AATTTATGTC TCTATAAACA GGGTTTTTTT CCCCATTCTC 5460
 TGAGCTTTCT TGTGTTCAAT TGAATTGAAC TAAAGACTTA GAGTTACCCA TGTAAAGTCC 5520
 TTAGCCATGG ACCCTGGCATA CACTCTTCTT ACGTGCAGAG AATGACCATC ATGAGGAAAG 5580
 AGCCACAGAT CAGTCAATGT GTCCATCAAG ATAATAGCAC CAACAGGTAT AACAGGGCTT 5640
 CCTGGCATAA TCTATTTAAA ATATCCAACC TTCAACATAC TCGTATCCCT GATGACTGTT 5700
 AGAAGTAAAT TATGGTCTCT GCCCATAAGG AGCTGAGAGT TTAACCTGGA AGCTAAACCT 5760
 AACCTTTAA ACCAACAGG AGAAAACTA CTGGTAGACA GCGCTGCATC TTTAGTTTCA 5820
 AAGAGAAAG ATTGCAGTAC GTTAGAGCAA GAAGAATTTT CTGGAAGAAG TCAATATAA 5880
 GGTGGATTTT GAAGGGTATT TGAGGTGAAA TACACCAATT ATCAGGGAAT AACATCAAG 5940
 GTCCTCAATG AGACTACCAG CATTTAGGGA CTGATCTAAC AGACTTAGCA TGGGTTTAGT 6000
 ATTTACATTG ATACAGCAAT TGAATGATCT CCTTTTGTGA TGTTTGAAGG TTGATAGGTC 6060
 AGGAAATGTT CATCACCAAG TTCAAAAGCT TCTGACTGAA TTCAACAAAT CCAGTGATGC 6120
 ATATGAGCTG AAGATCCCCA ACAAGCTCTT CGGAGAAAAG ACGTATCAAT TTTTACAGGT 6180
 AATTTCACTT GGCTTACCCA CATTTTCAAT GCATCCTGAT GTCTGTGTCT CTGAGTGGCC 6240
 AAATGGAAGA AAGCAAGGCC GATGAGCCTG GCCGAGCCAG GTGGAGAGCA TTTACTCAGA 6300
 GTGCATTAGC TCCATTTCCA CAACCTCTCC CCAGTGGAGT GTCCAGAGCC CCAACGATAC 6360
 ATCACTGAAG TGTGGATTTA GGGATAATCT TGTGATAAAA GAGGAGGTTG TGAATAGAG 6420
 TGAGTAAGAG TAATAAGTAA TAAGATACCA TCGATAAACT GGCAGTGAAT CAGTCACATA 6480
 CGATACATCT TGGTGGGAAA TGTATGACTA ATGGGATATT ATTGGAATGG GCAGGCTTGG 6540
 GTGAGTTCCCT GAGAATAGTT GAGGAAGTAC CAGGAAATAT TGAATGCACA GGATGAAAGA 6600
 CAAAACAAA GATCAGAAAC ATCATGGTTA AAATTACTGG AGAGAAGTCT GAGAAGCAAT 6660
 GAATCTCCTT CAGGGAAGCC TGCTCTGCAG TTTGCAAAAC ACAGCCTCTT CTGCTCTG 6720
 CTTTGGCCAA GATGATATTG ACCTTCAGTG ACCTCTTCTT TGTGCCAGCC CACATTCCCC 6780
 TTTTGCATTG CCTACATGAC ACCTGTATAA AAATATCCAT GGACAGGAGA TACTGCATCT 6840
 ATTCAGGCTC TGGATTGAGC TTACTGTTGT TACTGTTGT TAAGTTTGGT AATATATAGT 6900
 TACATAAATT ACTCCTAATT CCTACTTCTT CCTTCATATC TCAAGGAAT ATTTAGATGC 6960

	CATCAAGAAA	TTTACCAGA	CCAGTGTGGA	ATCTACTGAT	TTTGCAATG	CTCCAGAAGA	7020
	AAGTCGAAAG	AAGATTAACT	CCTGGGTGGA	AAGTCAAACG	AATGGTAGGA	GAGCCACCCA	7080
	TTATAGAAAC	ACCTTTTGGA	AACCTATGCC	AGTGAGCCTT	GTGCTTGACA	CTGCATGGGG	7140
5	GAACAGGTGT	GGGGATTGAG	ATGGGTTTGC	AGGGAGGGCT	GAAGAGGGCA	CTCCAGATGA	7200
	AGGATTGTCT	CAATTAATA	TGAAGAGAGC	CTAGGGGAGC	CAAGGAGGAA	ATCACAGGAA	7260
	GCCAAATTAGA	TGAAGAACACA	TCTGGAGAAT	TATTTGCTTA	TGGCCCTGCA	TGACAATAGC	7320
	TTTGTGGATC	CCCTGTCTCC	GCTCAGACCT	ATTTTGAGAT	CATATCCTTT	ACTTTAAATC	7380
	AGACTCAAAT	TTTTATGATG	AATATTTAAT	AGAAAACATT	AGAAAGCGTC	TCTCGTCTCC	7440
10	TTTACTAATT	GGGAAACAAG	CAGCTCTCTG	GTAATACACC	CTTTTGTCTC	TGAGCTGGAG	7500
	CTGCCTGGAT	CACATCTGTA	GCCAAATGTG	TCTGCAGGGA	TTATCACAGC	TCTCTTCCCC	7560
	ATCAAGGGCA	AAGAGCTTGA	CAAAGTCTCC	ATTCTACAGA	CATCTTTCTT	ACCTCCCACC	7620
	TCTCATTTACA	GGCCAAACTT	ACAGCAACTC	AACATGAGAG	TGAATAGGAA	GATACCCCGG	7680
	GAAGTAGTGT	CTGACAGCAC	AGGACATGCG	TTTCATATTA	CAGAGCTCAA	GTCACTCATC	7740
15	CTAAATGCA	ATCAGGGCCT	CCTTCTCTG	AATGGGGACC	CCGTAGTTAA	AAAAAATAA	7800
	AAGTAGGAAG	AGGAGGGAGG	AGAGAAAGAA	AGACACATGT	TGGAAGAGTA	GACAAAATCA	7860
	GTTTATCAGT	ATTCCAAATC	AGATGATTGG	AGACATTCAT	ACACAGAGAA	CGTGAACCTC	7920
	TTCTCTATCA	CAAGAAGTGA	TGCTCTCATC	AAGGGTAACT	TTATACGACT	GGAGCCTTGA	7980
	AGAAAGCTGC	ATCTGGTGAA	CCACTGGTCA	GTGAGTCTAA	CAATTCAAAG	ATCAAAGTCA	8040
20	GTGAGTCTCA	AGCAGGGATT	TGGGTCAATA	ATTAACGATC	AGTCACGAAC	ATTTGCAAGG	8100
	CATCTTCCAG	ACAAGCCATT	TGTAGCTTGT	GTAAAAAGCT	CTTTTATTCT	TTCCTTGGCA	8160
	GAAAAAATTA	AAAGCTTATG	TCCTGATGGG	ACTATTGGCA	ATGATACGAC	ACTGGTCTCT	8220
	TGGAAGCGCA	TCTATTTCAA	AGGGCAGTGG	GAGAATAAAT	TTAAAAAGA	AAACACTAAA	8280
	GAGGAAAAAT	TTTGGCCAAA	CAAGGTATTG	TCTATATTTT	ATTTATATAG	TGTAATATGT	8340
25	TAATACATGG	AATGTTAAAC	ATTCTGTATG	GAATGTAACA	TGATAAGTAA	AAAAATAAAA	8400
	TTGTTTCATGT	CTGTATTATT	GTTGTTTATC	TCTTATAACT	TTATTTAGTT	AGGAATACCT	8460
	GAAAAACTAT	TGTTTCTAAC	TCATGGAATT	CCTGGGTTAT	TTCTTAGAAG	AAGAAGGATG	8520
	TGTTGCTATC	TCAATAAATAT	TATCTTTTTC	GTCTTGTGTT	TCACGTGTTA	TTTGTGGGAC	8580
	ACATTGATTT	ATTGCGAAT	ACATACAAAT	CTGTACAGAT	GATGAGGCAA	TACAATTCCT	8640
30	TTAATTTTGC	CTTGTGGGAG	GATGTACAGG	CCAAGTCTCT	GGAAATACCA	TACAAAGGCA	8700
	AAGATCTAAG	CATGATTGTG	CTGCTGCCAA	ATGAAATCGA	TGGTCTGCAG	AAGGTAAAGAA	8760
	CTTGCACTCA	CAACTCTTCC	TTCTACTGCC	GGACATTTTC	CCAAAGATAC	CAAGTTTAAA	8820
	CAAGGTAAAA	GCTTATGACC	GAGTTGCTCC	AAAATGATGA	AAAATCTCAA	ATGAGGAATG	8880
	ATGACTCACC	TTCATATTAT	AAATATTGGA	GCATAGGGCC	TGACACAAAC	TGAAAGCTTA	8940
35	GTTTTTGTTC	GTTTGTGTTT	TTTTATTATT	ATTATTATAA	TACITTAAGC	TTTAGGGTAC	9000
	ATGTGCACAA	TGTGCAGGTT	AGTTACATAT	GTATACATGT	GCCATGCTGG	TGTGCTGCAC	9060
	CCATTAACTG	CTATTATTAG	GTTAGGTATA	TCTCCTAATG	CTATCCCTCC	CCCCCTCCCC	9120
	CACCCCAACG	CAGTCTCTAG	AGTGTGATGT	TACCTTCTCT	TGTCCAAGTG	TTCTCATTTG	9180
	TCAATTCCCA	TCTATGATTT	AATCCATCT	ATGGCTTAGT	TAATGATTAA	TTTATTAGAG	9240
40	TTACATGCAT	TGGATATCAA	TTTGATGATA	TTATTATGCA	GCAATTTAAA	CTTGACTGGG	9300
	AGAAATATAT	ACCAATGTGA	GGAAAGTTTA	CAAATAGGCC	GAGTAGAAAA	GGGAATACAA	9360
	ATTAGGAAT	TTAGGGAATT	ACAAATTAAT	AATTGCAATG	TGTACTAAAT	AATGTATACA	9420
	GAAAAATATG	ATGAGCCTAT	TAAAAATTGA	CACATGTAGT	AGGCTGTTGG	CACAAGAAAT	9480
	AGTGATACAT	ACAGTTCTAT	GTGTACAAAA	TAATGTAATC	ATATTTTACA	TGTGTATCAT	9540
45	ACAGTTGTAT	ACATACATAT	GTACACATAT	ACATATACGT	AAAAACATGA	TTCTGTTTTT	9600
	ACATACATGT	ATATACATAT	ACACATATAA	CCCAATGTAT	TTATATATTC	AGGACTCATA	9660
	TTTTACCTAT	TAGAATAATA	ATGTCTATTA	AAGTGAACCT	TCTGTATTTC	ACATTTATTG	9720
	CCAAAATAAC	GAATCTCCAC	ATAGTCAATT	CATTGTTAAG	GTGTATTAGA	GATCGACAGT	9780
	TAGTCATATC	AGTTTCTTTT	TTCCATTGTT	ATAGCTTGAA	GAGAACTCAA	CTGCTGAGAA	9840
50	ATTGATGGAA	TGGACAAGTT	TGCAGAATAT	GAGAGAGACA	TGTGTGCGAT	TACACTTACC	9900
	TCCGTTCAAA	ATGGAAGAGA	GCTATGACCT	CAAGGACAGC	TTGAGAACCA	TGGGAATGGT	9960
	GAATATCTTC	AATGGGGATG	CAGACCTCTC	AGGCATGACC	TGGAGCCACG	GTCTCTCAGT	10020
	ATCTAAAGTC	CTACACAAGG	CCTTTGTGGA	GGTCACTGAG	GAGGGAGTGG	AAGCTGCAGC	10080
	TGCCACCGCT	GTAGTAGTAG	TCGAATTATC	ATCTCCTTCA	ACTAATGAAG	AGTTCTGTTG	10140
55	TAATCACCCCT	TTCTTATCTT	TCATAAGGCA	AAATAAGACC	AACAGCATCC	TCTTCTATGG	10200
	CAGATTCTCA	TCCCCATAGA	TGCAATTAGT	CTGTCACTCC	ATTTAGAAAA	TGTTCACTTA	10260
	GAGGTGTTCT	GGTAAACTGA	TGTCTGGCAA	CAACAGATTC	TCTTGGCTCA	TATTTCTTTT	10320
	CTATCTCATC	TTGATGATGA	TAGTCATCAT	CAAGAAATTA	ATGATTAAAA	TAGCATGCCT	10380
	TTCTCTCTTT	CTCTTAATGA	GCCACATAT	AAATGTACTT	TTCTTCCAG	AAAAATTTC	10440
60	CTTGAGGAAA	AATGTCCAGT	ATAAGATGAA	TCATTTAATA	CCGTGCTCTC	TAAATTTGAA	10500
	ATATAATTCT	GTTTCTGACC	TGTTTAAAT	GAACCAAAAC	AAATCATACT	TTCTCTTCAA	10560
	ATTAGCAAC	CTAGAAACAC	ACATTTCTTT	GAATTTAGGT	GATACCTAAA	TCTTCTTTAT	10620
	GTTTCTAAAT	TTTGTGATTC	TATAAAACAC	ATCATCAATA	AAATAATGAC	ATAAAATCAT	10680
	TTTTGCTTTA	CCTGTTTTTC	CTCTGGAAG	GGCAAGTGTC	CAGTTACACA	TAGGAAAGAT	10740
65	AATTTAGAGA	TATATTAACT	ATATATAAAG	GAAAAATAAA	AACAGAGTAG	TTCATGATGA	10800
	GCCTGGAGTA	GAAGGCATAT	CCCAGAACAG	GAGGAGCCTT	GTAACCCACA	TAGGAACTTC	10860
	CTATTTTATG	CTAAAGGGAT	AAGAACTCA	TTACAGGCTT	TGATGGTTGT	TTGTCAAAGA	10920
	GGGGCATAAA	ATTATCATAT	CCACATCTAG	AAAATACATC	TCTGGCTACG	CTGATATCAA	10980
	TGGATGCGAG	GAAAGAACAG	TGTGGTTACC	ATATATAAAT	TAGGAAATCA	TTAGAGTATT	11040
70	GGGATGGGAA	ATGGAGAGAA	AGAAAGAGCC	TGGGGGAAAT	ATTTAGGAAA	TAATAGTTAC	11100
	AGAAAGACAT	CTAAGTTGCT	GACCTATCTG	ACTGGATGGA	TGGAAGAATA	TCTTGTTCCT	11160
	GAGAGAAAAA	AAGACTTTGG	GTTTAAATTT	GTACTTGTATG	AATTAAGGTA	CTTTTAATAT	11220
	TCAAAATGGAT	TTGCTTGGCA	GGCACTTGAA	GATATTAGTC	TAAATCTCAG	AAACAGAATA	11280
	TGATCTGAAG	CTCTAAATTT	GTGATATTCA	ATATAAATAC	TTTAGAGTCA	TTGGGATAAA	11340
	TATGGTAGTT	GTAGCTAAAA	GCAAAAAATA	GATACTAGGG	AGAAAGGATA	AAGTTAGAAG	11400
75	AAAGAAGAAAT	CTAGAATTGA	CCTTGAAGTA	TATCAGCATG	TGTAAGATCA	AGGAATTGAT	11460
	CATTTTATT	TTCCAGAAAG	TAGCTTTTCT	TAGGGTTCCA	TATTTACTCC	CATAGATTCT	11520
	TCCC						

Seq ID NO: 465 Protein sequence
Protein Accession #: BAB21525.1

	1	11	21	31	41	51	
85	MNSLSEANTK	FMPDLFQQFR	KSKENNIFYS	PISITSALGM	VLLGAKDNTA	QQISKVLHFD	60
	QVTENTTEKA	ATYHVDKSGN	VHQFQKLLT	EFNKSTDAYE	LKIANKLFG	KTYQFLQEYL	120
	DAIKKPYQTS	VESTDFANAP	EESRKKINSW	VESQTNKIK	NLFPDGTIGN	DTTLVLVNAI	180
	YFKGQWENKF	KKENTKKEKF	WPNKNTYKSV	QMMRQYNSFN	FALLEDEVQAK	VLEIPYRGKD	240

LSMIVLLPNE IDGLQKLEEK LTAEKLMWET SLQNMRETCV DLHLPRFKME ESYDLKDLTR 300
 TMGMVNIFNG DADLSGMTWS HGLSVSKVLH KAFVEVTEEG VERAAATAVV VVELSSPSTN 360
 BEFCNNHPFL PFIRQNKINS ILPYGRFSSP

5

Seq ID NO: 466 DNA sequence
 Nucleic Acid Accession #: NM_001910.1
 Coding sequence: 50..1240

10	1	11	21	31	41	51	
	GGAGAGAAGA	AAGGAGGGGG	CAAGGGAGAA	GCTGCTGGTC	GGACTCACAA	TGAAAACGCT	60
	CCTTCTTTTG	CTGCTGGTGC	TCCTGGAGCT	GGGAGAGGCC	CAAGGATCCC	TTCACAGGGT	120
	GCCCCCTCAGG	AGGCATCCGT	CCCTCAAGAA	GAAGCTGCGG	GCACGGAGCC	AGCTCTCTGA	180
	GTTCTGGAAA	TCCATAAAT	TGGACATGAT	CCAGTTCACC	GAGTCTGCT	CAATGGACCA	240
15	GAGTGCCCAAG	GAACCCCTCA	TCAACTACTT	GGATATGGAA	TACTTCGGCA	CTATCTCCAT	300
	TGGCTCCCA	CCACAGAACT	TCACTGTCT	CTTCGACACT	GGCTCCTCCA	ACCTCTGGGT	360
	CCCCCTCTGTG	TACTGCACTA	GCCCAGCCTG	CAAGACGCAC	AGCAGGTTC	AGCCTTCCCA	420
	GTCCAGCACA	TACAGCCAGC	CAGGTCAATC	TTTCTCCATT	CAGTATGGAA	CCGGGAGCTT	480
	GTCCGGGATC	ATTGGAGCCG	ACCAAGTCTC	TGTGGAAGGA	CTAACCGTGG	TTGGCCAGCA	540
20	GTTTGGAGAA	AGTGTACAG	AGCCAGGCCA	GACCTTTGTG	GATGCAGAGT	TTGATGGAAT	600
	TCTGGGCTCG	GGATGCCCTT	CCTTGGCTGT	GGGAGGAGTG	ACTCCAGTAT	TTGACAAAT	660
	GATGGCTCAG	AACCTGGTGG	ACTTGCCGAT	GTTTCTGTCT	TACATGAGCA	GTAACCCAGA	720
	AGGTGGTGGC	GGGAGCGAGC	TGATTTTGG	AGGCTACGAC	CACCTCCATT	TCTCTGGGAG	780
	CCTGAATTGG	GTCCCACTCA	CCAAGCAAGC	TTACTGGCAG	ATTGCACTGG	ATAACATCCA	840
25	GGTGGGAGGC	ACTGTTATGT	TCTGCTCCGA	GGGCTGCCAG	GCCATTGTGG	ACACAGGGAC	900
	TTCCCTCATC	ACTGGCCCTT	CCGACAAGAT	TAAGCAGCTG	CAAAACGCCA	TTGGGGCAGC	960
	CCCCGTGGAT	GGAGAATATG	CTGTGGAGTG	TGCCAACCTT	AACGTATGCG	CGGATGTAC	1020
	CTTCACCAAT	AACGAGTCC	CCTATACCCT	CAGCCCAACT	GCCTACACCC	TACTGGACTT	1080
	CGTGGATGGA	ATGCAGTTCT	GCAGCAGTGG	CTTCAAGGA	CTTGACATCC	ACCCTCCAGC	1140
30	TGGGCCCCCTC	TGGATCCTGG	GGGATGTCTT	CATTGCAGAG	TTTACTCAG	TCTTTGACCG	1200
	TGGGAATAAC	CGTGTGGGAC	TGGCCCCCAGC	AGTCCCCTAA	GGAGGGGCTG	TGTGTCTGTG	1260
	CCTGCTCTGT	TGACAGACCT	TGAATATGTT	AGGCTGGGGC	ATTCTTTACA	CCTACAAAAA	1320
	GTTATTTTCC	AGAGAATGTA	GCTGTTTCCA	GGGTTGCAAC	TTGAATTAAG	ACCAACAGCA	1380
	ACATGAGAAAT	ACACACACAC	ACACACATAT	ACACACACAC	ACACTTCACA	CATACACACC	1440
35	ACTCCACCA	CCGTCAATGAT	GGAGGAATTA	CGTTATACAT	TCATATTTTG	TATTGATTTT	1500
	TGATTATGAA	AATCAAAAAT	TTTCACATTT	GATTATGAAA	ATCTCCAAAC	ATATGCACAA	1560
	GCAGAGATCA	TGGTATAATA	AATCCCTTTG	CAACTCCACT	CAGCCCTGAC	AACCCATCCA	1620
	CACACGGCCA	GGCCTGTTTA	TCTACACTGC	TGCCCACTCC	TCTCTCCAGC	TCCCATGCT	1680
	GTACCTGGAT	CATTCTGAAG	CAAAATCCGA	GCATTACATC	ATTTTGTCCA	TAAATATTTC	1740
40	TAACATCCTT	AAATATACAA	TCCGAATTCA	AGCATCTCCC	ATTGTCCAC	AAATGTTTGG	1800
	CTGTTTGTG	AAATGGATPV	TTTGTATTAG	GATTCAAGCA	AGGCCCATAT	ATTGCATTGA	1860
	TTTGAAATCT	CTGTAAGTCT	CTTTCCATCT	ACAGAGTTTA	GCACATTGGA	ACGTTGTCTG	1920
	TTGAAATCCC	GAGGTGTCTAT	TTGACATGGT	TCTCTGAACT	TATCTTTTCT	ATAAATGGT	1980
45	AGTTAGATCT	GGAGGTCTGA	TTTTGTGGCA	AAAATACTTC	CTAGGTGGTG	CTGGTACTTT	2040
	CTTGTTCAT	CCTGTCAGGA	GGCAGATAAT	GCTGGTGCTC	CTCTATTGGT	AATGTTAAGA	2100
	CTGCTGGGTG	GGTTGGAGT	TCTTGGCTTT	AATCATTCT	TACAAAGTTC	AGCATTTT	

Seq ID NO: 467 Protein sequence
 Protein Accession #: NP_001901.1

50

1	11	21	31	41	51	
MKTLLELLLV	LLELGEAQGS	LHRVPLRRHP	SLKKKLRRS	QLSEFWKSHN	LDMIQFTESC	60
SMDQSAKEPL	INYLDMEYFG	TISIGSPPQN	FTVIFDTGSS	NLWVPSVYCT	SPACKTHSRP	120
QPSQSSTYSQ	PGQSFSIQYG	TGSLSGIIGA	DQVSVEGLTV	VGQFQGESVT	EPGQTFVDAE	180
FDGILGLGYP	SLAVGGYTPV	FDNMAQNLV	DLPMFVSVM	SNPEGGAGSE	LIFGGYDHS	240
FSGSLNWVVEV	TKQAYWQIAL	DNIQVGGTVM	FCSEGCQAI	DTGTSITLTP	SDKIKQLQNA	300
IGAAPVDGBY	AVECANLNMV	PDVFTINGV	PYTLSPATYT	LLDFVDMQMF	CSSGFQGLDI	360
HPPAGPLWL	GDVFIRQFYS	VFDGRNNRVG	LAPAVP			

60

Seq ID NO: 468 DNA sequence
 Nucleic Acid Accession #: NM_018058.1
 Coding sequence: 319..1575

65

1	11	21	31	41	51	
TACGCGCTGC	GGGACCGGCA	GGGGAACGCC	ATCGGGGTCA	CAGCCTGCGA	CATCGACGGG	60
GACGGCCGGG	AGGAGATCTA	CTTCTCAAC	ACCAATAATG	CCTTCTCGGG	GGTGGCCACG	120
TACACCGACA	AGTTGTTCAA	GTTCCGCAAT	AACCGGTGGG	AAGACATCCT	GAGCGATGAG	180
GTCAACGTGG	CCCGTGGTGT	GGCCAGCCTC	TTTGCAGGAC	GCTCTGTGGC	CTGTGTGGAC	240
AGAAAGGGCT	CTGGACGCTA	CTCTATCTAC	ATTGCCAATT	ACGCCTACGG	TAATGTGGGC	300
CCTGATGCCC	TCATTGAAAT	GGACCCCTGAG	GCCAGTGACC	TCTCCCGGGG	CATTCTGGCG	360
CTCAGAGATG	TGGCTGCTGA	GGCTGGGGTC	AGCAAAATATA	CAGGGGGCCG	AGGCGTCAGC	420
GTGGGCCCCA	TCCTCAGCAG	CAGTGCCTCG	GATATCTTCT	CGCAACAATGA	GAATGGGCCCT	480
AACCTCCTTT	TCCACAACCG	GGGCGATGGC	ACCTTTGTGG	ACGCTGCGGC	CAGTGTCTGGT	540
GTGGACGACC	CCACCCAGCA	TGGGCGAGGT	GTCCGCCCTGG	CTGACTTCAA	CCGTGATGGC	600
AAAGTGGACA	TCGCTATGG	CACCTGGAAT	GGCCCCCACC	GCCTCTATCT	GCAAAATGAGC	660
ACCCATGGGA	AGGTCCGCTT	CCGGGACATC	GCCTCACCCA	AGTTCTCCAT	GCCTCTCCCT	720
GTCCGCACGG	TCATCACGCG	CGACTTTGAC	AATGACCAGG	AGCTGGAGAT	CTTCTTCAAC	780
AACATTGCGT	ACCGCAGCTC	CTCAGCCAAC	CGCTCTTCC	CGCTCATCCG	TAGAGAGCAC	840
GGAGACCCCT	TCATCGAGGA	GCTCAATCCC	GGCGACGCTT	TGGAGCCTGA	GGGCCGGGGC	900
ACAGGGGGTG	TGGTGACCGA	CTTCGACGGA	GACGGGATGC	TGGACCTCAT	CTTGTCCCAT	960
GGAGAGTCCA	TGGCTCAGCC	GCTGTCCGTC	TTCCGGGGCA	ATCAGGGCTT	CAACACAAAC	1020
TGGCTGCGAG	TGGTGCCACG	CACCCGGGTT	GGGGCCTTTG	CCAGGGGAGC	TAAGGTCTGT	1080
CTCTACACCA	AGAAGAGTGG	GGCCCACTG	AGGATCATCG	ACGGGGGCTC	AGGCTACCTG	1140
TGTGAGATGG	AGCCCGTGGC	ACACTTTGGC	CTGGGGAAGG	ATGAAGCCAG	CAGTGTGGAG	1200
GTGACGTGGC	CAGATGGCAA	GATGGTGAGC	CGGAACGTGG	CCAGCGGGGA	GATGAACCTA	1260

GTGCTGGAGA TCCTCTACCC CCGGGATGAG GACACACTTC AGGACCCAGC CCCACTGGAG 1320
 ACACCAATGA ATGCATCCAG TCCCCATTCG TGTGCCCTCG AGACAAGCCC GTATGTGTCA 1380
 ACACCTATGG AAGCTACAGG TGCCCGACCA ACAAGAAGTG CAGTCGGGGC TACGAGCCCA 1440
 ACGAGGATGG CACAGCCTGC GTGGGGACTC TCGGCCAGTC ACCGGGGCCC CGCCCCACCA 1500
 CCCCCACCGC TGCTGCTGCC ACTGCCGCTG CTGCTGCCGC TGCTGGAGCT GCCACTGCTG 1560
 CACCGGTCTC CGTAGATGGA GATCTCAATC TGGGGTCGGT GGTTAAGGAG AGCTGCGAGC 1620
 CCAGCTGCTG AGCAGGGGTG GGCATGAAC CAGCGGATGG AGTCCAGCAG GGGAGTGGGA 1680
 AAGTGGGCTT GTGCTGCTGC CTAGACAGTA GGGATGTAAA GGCCTGGGAG CTAGACCTTC 1740
 CCCAAGCCCA TCCATGCACA TTACTTAGCT AACAAATTAG GAGACTCGTA AGGCCAGGCC 1800
 CTGTGCTGGG CACATAGCTG TGATCACAGC AGACAGGGTC GCTGCCCTGA TGGCGCTTAC 1860
 ATTCCAGTGG GTCTAATGAC CATATCTTAG GACACAGATG TGCCCAAGGA GGTGGTGTCA 1920
 CTGCACAGGA AGTATGAGGA CTTTAGTGTC CTGAGTTCAA ATCCTGATTC AGGAACTCAC 1980
 AAAGCTATGT GACCTTACAC CAGTCACTTA ACTTGTAGC CATCCATTAT CGCATCTGCA 2040
 AAATGGGGAT TAAAGATTAGA ATCTTGGGGT TAGTGTGGAG ATTAGATTAA ATGTATGTAA 2100
 GACACTTGGC ACAAACCTG GCACATAGTA AAGGCTCAAT AAAAACCAAG GCCTCTCACT 2160
 GGGCTTTGTC AACACGTG

Seq ID NO: 469 Protein sequence
 Protein Accession #: NP_060528.1

1 11 21 31 41 51
 MDPEASDLR GILALRDVAA EAGVSKYTG RGVSVGPILS SSASDIFCDN ENGNPFLPHN 60
 RDGDTFVDA ASAGVDDPHQ HGRGVALADF NRDGKVDIVY GNWNGPHRLY LQMSTHGKVR 120
 RFDIASPKFS MPSPVTVIT ADFDNDQELE IFFNNIAYRS SSANRLPRVI RREHGDPLIE 180
 ELNPGDALEP EGRGTGGVVT DFDGDMGLDL ILSHGESMAQ PLSVFRGNQG FNNNWLVRVP 240
 RTRVGAFARG AKVVLTKKS GAHLRIIDGG SGVLCMEPEV AHFGLGKDEA SSVETWPDG 300
 KMSVRNVASG EMNSVLEILY PRDEDTLQDP AFLETMPNAS SSHSCALETS PYVSTPMEAT 360
 GAGPTRSAVG ATSPTRMAQP AWGLSASHRA PAPPPPPPLL PLPLLLPLLE LPLLHRSS

Seq ID NO: 470 DNA sequence
 Nucleic Acid Accession #: AJ279016
 Coding sequence: 1..1962

1 11 21 31 41 51
 ATGTCAGGGA TGTACCGTT CCTGCTGCTG CTCTGGTTTC TGCCCATCAC TGAGGGGTCC 60
 CAGCGGGCTG AACCATGTT CACTGCAGTC ACCAACTCAG TTCTGCCCTC TGACTATGAC 120
 AGTAATCCCA ACCAGCTCAA CTATGGTGTG GCAGTTACTG ATGTGGACCA TGATGGGGAC 180
 TTTGAGATCG TCGTGGCGGG GTACAAATGGA CCCAACCTGG TTCTGAAGTA TGACCGGGCC 240
 CAGAAGCGGC TGGTGAACAT CGCGGTGAT GAGCGCAGCT CACCTACTA CGCGCTGCGG 300
 GACCGGCAGG GGAACGCCAT CGGGGTCA CACTGCGACA TCGACGGGGA CGGCCGGGAG 360
 GAGATCTACT TCCCAACAC CAATAATGCC TTCTCGGGGG TGGCCACGTA CACGACAAG 420
 TTGTTCAAGT TCCGCAATAA CCGGTGGGAA GACATCCTGA GCGATGAGGT CAACGTGGCC 480
 CGTGGTGTGG CCAGCCTCTT TGCCGGACGC TCTGTGGCCT GTGTGGACAG AAAGGGCTCT 540
 GGAGCTACT CTATCTGAT TGCCTTACAT GCCTACGGTA ATGTGGGGCC TGATGGCTTC 600
 ATTGAATAGG ACCCTGAGGC CAGTGACCTC TCCCGGGGCA TTCTGGCGCT CAGAGATGTG 660
 GCTGCTGAGG CTGGGGTCAG CAAATATACA GGGGGCCGAG GCGTCAGCGT GGGCCCCATC 720
 CTCAGCAGCA GTGCCTCGGA TCTCTCTGTC GACAATGAGA ATGGGCCTAA CTTCCTTTTC 780
 CACAACCGGG GCGATGGCAG CTCTGTGGAC GCTGCGGGCA GTGTCTGGT GTGACGACCC 840
 CACCAAGCAT GGCAGGTGTG CGCCCTGGCT GACTTCAACC GTGATGGCAA AGTGGACATC 900
 GTCTATGGCA ACTGGAATGG CCCCCACCGC CTCTATCTGC AAATGAGCAC CCATGGGAAG 960
 GTCCGCTTCC GGGACATCGC CTCACCAAG TTCTCCATGC CCTCCCTGT CCGCACGGTC 1020
 ATCACGCGCG ACTTTGACAA TGACCAAGAG CTGAGATCT TCTTCAACAA CATTGCCTAC 1080
 CGCAGCTCCT CAGCAACCGC CCTCTTCCGC GTCATCCGTA GAGAGCACCG AGACCCCTC 1140
 ATCGAGGAGC CAATCCCGG CGACGCCTTG GAGCCTGAGG GCCGGGGCAC AGGGGGTGTG 1200
 GTGACGAGCT TCGACGGAGA CGGGATGCTG GACCTCATCT TGTCCCATGG AGAGTCCATG 1260
 GCTCAGCCGC TGTCCCTCTT CCGGGGCAAT CAGGGCTTCA ACAACAATG GCTGCGAGTG 1320
 GTGCCACGCA CCCGGTTTGG GGCCTTTGCC AGGGGAGCTA AGGTCGTGCT CTACACCAAG 1380
 AAGATGGGG CCCACCTGAG GATCATCGAC GGGGGCTCAG GCTACCTGTG TGAGATGGAG 1440
 CCGGTGGCAC ACTTTGGCCT GGGGAAGGAT GAAGCCAGCA GTGTGGAGGT GACGTGGCCA 1500
 GATGGCAAGA TGGTGAAGCG GAACGTGGCC AGCGGGGAGA TGAACCTAGT GCTGGAGATC 1560
 CTCTACCCCC GGGATGAGGA CACACTTCAG GACCCAGCCC CACTGGAGTG TGGCCAAGGA 1620
 TTCTCCACAG AGGAAATGCG CATTGTCATG GACACCAATG AATGCATCCA GTTCCCATTC 1680
 GTGTGCCCTC GAGACAAGCC CGTATGTGTC AACACCTATG GAAGCTACAG GTGCCGGACC 1740
 AACAGAAGT GCAGTCGGGG CTACGAGCCC AACGAGGATG GCACAGCTG CGTGGGGACT 1800
 CTCGGCCAGT CACCGGGCCC CCGCCCCACC ACCCCACCG CTGCTGTGTC CACTGCCGCT 1860
 GCTGCTGAGC CTGCTGGAGC TGCCACTGCT GCACCGGTCC TCGTAGATGG AGATCTCAAT 1920
 CTGGGGTCGG TGGTTAAGGA GAGCTGCGAG CCCAGCTGCT GAGCAGGGGT GGGACATGAA 1980
 CCAGCGGATG GAGTCCAGCA GGGGAGTGGG AAAGTGGGCT TGTGCTGCTG CTTAGACAGT 2040
 AGGGATGTAA AGGCCTGGGA GCTAGACCTT CCCCAGCCC ATCCATGCAC ATTACTTAGC 2100
 TAACAATTAG GGAGACTCGT AAGGCCAGGC CCGTGTGCTGG GCACATAGCT GTGATCACAG 2160
 CAGACAGGGT CGCTGCCCTG ATGGCGCTTA CATTCCAGTG GGTCTAATGA CCATATCTTA 2220
 GGACACAGAT GTGCCAGGG AGGTGGTGTG ACTGCACAGG AAGTATGAGG ACTTTAGTGT 2280
 CCTGAGTTCA AATCCTGATT CAGGAACCTA CAAAGCTATG TGACCTTACA CCAGTCACTT 2340
 AACTTGTAG CCATCCATTA TCGCATCTGC AAAATGGGGA TTAAGAAATG AATCTTGGGG 2400
 TTAGTGTGGA GATTAGATTA AATGTATGTA AGACACTTGG CACAAAACCT GGCACATAGT 2460
 AAAGGCTCAA TAAAAACAAG TGCCTCTCAC TGGGCTTTGT CAACACG

Seq ID NO: 471 Protein sequence
 Protein Accession #: CAC08451

1 11 21 31 41 51
 MSRMFLPFLLL LWFLPITEGS QRAEPMFTAV TNSVLPFDYD SNPTQLNYGV AVTDVDHGDG 60
 FEIVVAGYNG PNLVLKYDRA QKRLVNIADV ERSSPYALR DRQNAIGVT ACDIDGDGRE 120
 EIFYFLNTNNA FSGVATYTDK LFKFRNNRWE DILSDEVNVA RGVASLFAGR SVACVDRKGS 180

GRYSIYIANY AYGNVGPDAL IEMDPEASDL SRGILALRDV AAEAGVSKYT GGRGVSVGPI 240
 LSSASDIFC DNENGNFLF HNRDGTFFVD AASAGVDDP HQHGRGVALA DFNDRGKVDI 300
 VYGNWNGPHR LYLQMSHGHK VRFRIASPK FSPSPVVRTV ITADFDNDQE LEIFFNNIAY 360
 RSSSANRLFR VTRREHGDPL IEELNPGDAL EPEGRGTGGV VTDPDGDGML DLILSHGSEM 420
 5 AQPLSVFRGN QGFNNNWLRV VPRTRFGAFA RGAKVVLTK KSGAHLRIID GSGGYLCEME 480
 FVAHFGLGKD EASSVEVTFP DGKMSVRNVA SGEMNSVLEI LYPRDEDTLQ DPAPLECGQG 540
 FSQENGHCMT DINECIQFPF VCPDRKPVCV NTYGSYRCRT NKKCSRGYEP NEDGTACVGT 600
 LGQSPGRPRT TPTAAATAA AAAAAGAATA APVLVDGDLN LGSVVKESCE PSC

Seq ID NO: 472 DNA sequence
 Nucleic Acid Accession #: FGENESH
 Coding sequence: 1..4794

1 11 21 31 41 51
 15 ATGGCGTGTC CGGGAGGACT CCCAGCCCGT TGCTCTGGTT GGATGGGACT GGGTGGGCC 60
 AGCGGCTCCT CCCAGCATC CCCTCCCAT TCCTCTCCA GGTACAATGG ACCCAACTG 120
 GTTCTGAATG ATGACCGGGC CCAGAAGCGG CTGGTGAACA TCGCGGTCGA TGAGCGCAGC 180
 20 TCACCTACT ACGCCCTGCG GGACCGGCAG GGAACGCCA TCGGGGTAC AGCCTGCGAC 240
 ATCGACGGGG ACGGCCGGGA GGAGATCTAC TTCTCAACA CCAATAATGC CTCTCGGGC 300
 CACAGCAGCT CAGCGCAGT CCCTTCTGGG CTCACAGAA ACAGGCCTGT GCTGAAGCCT 360
 CCACCTACAA CCCCTGCAGG CCTCTGGGT CTGCCTCCAC TCAGCGGAAG GGACTTTCC 420
 TCCTCCCTGG GTCCAGGCTC TCCGGACAGC AGGCAGGGAG AGAGGGTGCC GGTCCCTGC 480
 25 TGTGCGGGTG GACTGAGACC TACCATGAA CCAGAACCAT TTCTTCTGAG ACCCAATCA 540
 GGGGTGGCCA CGTACACCGA CAAGTTGTTT AAGTTCCGCA ATAACCGGTG GGAAGACATC 600
 CTGAGCGATG AGGTCAAGT GGCCCGTGGT GTGGCCAGCC TCTTTGCGG ACCTCTGTG 660
 GCCTGTGTGG ACAGAAAGGG CTCTGGACGC TACTCTATCT ACATTGCCAA TTACGCTAC 720
 GGTAAATGTG GCCCTGATGC CCTCATTGAA ATGGACCTG AGGCCAGTGA CCTCTCCCG 780
 30 GGCATTCTGG CGCTCAGAGA TGTGGCTGCT GAGGCTGGGG TCAGCAAATA TACAGAAAGC 840
 TTCTCCACCA CTGCTCTCTC AAGCATTGGT GAGATATCTG GCAGAACCGA GGAGCGGGAA 900
 GGAGGAGAGC CAGAGCAGGT AGATGAGGAG CACAGTGGGG ATGGAAGCAC CAGCCAATG 960
 TGCCGCTGGG GCTGGAAGGA CGGCAGTTC AAGGAAGAAG CAGCAGCTTT GGTGGAGGAA 1020
 CAGAGGGAGG TTGGGGCAGC TGGCGTGCCC AGAGGACGTG TTCGAACAGC TCTGCAGACT 1080
 35 TCCAAAGGCT ATTTGGTGTA CAAGAACCTA TTTGGCCAC CATGTTACTA TTTCTGTGC 1140
 GCGCCTTCTC CAGCCCAACC TTTCCCTGCC CGCAAGCCCC CCCAACCTA CCCTGTAGCC 1200
 CCCTTGTGTA CTCCATTAAT GACACATGGA CGTCTGGCTG GAAACTAGC CCGGAGTGTG 1260
 CCCCACCCCC GAGCCCCAGG AATGGACCCC AAATGTAAGG GCGCCATGC TGAGCCCGGC 1320
 CTGATGGCTG AGGCTTTGGG CGCGTGCCCA GCGCTCAGCA CCACTGTGGT GCCAGGGGG 1380
 40 CTGAGAAGCT GGGAGGAAG CAGGCAGAAG GGGCAGGCCA TGTCCAGATG TGCCTCAGG 1440
 GAGCTGGGAG GTCCCTGAGG CCAAGCCACA CAGCAGCTGC CTGTAGAGA GGTGTATGAC 1500
 CTGGGAGAAC TCTCCATTTT ACAAGAACA GACGGAGATC CAGGAGGAGG AAGGGACTCG 1560
 CCCAAGGTCA CACAGGAGTG CCACTAGTG GCCACCATGC CAGCTCTCGG GGGACTCGAG 1620
 GGCCCCGGGA GGTGGCCCAA GCGAGAGATT GGGAGAGAGA CTGGGCGAGT AGGAAGACCA 1680
 45 CTCTCCCATC CCCTGGTCCC CAACTTCCCC AGCTGCTTGA GGCTCTTGA AGCCGGGACA 1740
 GTGCCGGGAG CTGCCCTGCC TGGGAATCCT GGGAACTGGG TTCTGGACAT GGCCAAGGCC 1800
 CTGGCGTGGA ACCGCTGCGA AAAAGAGGAG GGAAGATTTC ATGGAGACCA TGAGCCGAGA 1860
 TTTAGGCTCA GGAAGCAGC GGAAGCAGAA TTCCCCCAG GCTCTCTGA GGAGCCTCTG 1920
 CTGAGTTTCC CTGAGGCTC CAGAGGCAGC CTTGTCTCCC AGGTGGGCTT GGGCTTTGCT 1980
 50 TCTGCCACTC ACTGTGGGTC GATGTCTTTT CTAGGGGGCC GAGGCGTCAG CGTGGGCCCC 2040
 ATCTCAGCA GAGTGCTCTC GGATATCTTC TCGACAATG AGAATGGGCC TAACCTCTCT 2100
 TTCCAACACC GGGGCAAGTG CACCTTTGTG GACGCTGGG CCAAGTGTGA ACCTCGTTTA 2160
 GCCTTCATCG TTCACTCAA ATATCACCTC TGCAGAGATT TTCTCACTC CCTGTGCCAC 2220
 CTAGCAGAAA CTCTCTCTGC CTCTCTCTGC TGCCCGTGGC ATGCAGCTCT TCTTCAGGCT 2280
 CCACATTGCC ATCATGGTTT GTCTATGAGC TTTACAAGGA CCGGTCACG GTTCTATTCA 2340
 55 TTCTTGAGCG AAGGCTTGGC CTCCAGTGCC CACCGGAGGA CACTCAGCCT CCAGGGTTCT 2400
 CAGGGGGGCC CACCTGCTCT TCTGGCAAGA GCTCCCTGTG TCTTGGGTC TCTGATCCCC 2460
 ATGCGCTATT ACATTGTCTG GTGGTCTGCC ATCCAGAGA GCCTGATGAC CCACAGCTAT 2520
 TTGTCTCTG AAAGATGCAA CGTGGGTGTG GACGACCCCC ACCAGCATGG GCGAGGTGTC 2580
 GGCCTGGCTG ACTTCAACCG TGATGGCAAA GTGACATCG TCTATGGCAA CTGGAATGGC 2640
 60 CCCCACGGCC TCTATCTGCA AATGAGCACC CATGGGAAGG TCCGCTTCCG GGACATCGCC 2700
 TCACCCAAGT TCTCCATGTC CTCCCTGTCT CGCACGGTCA TCACCGCGGA CTTTGACAAT 2760
 GACCAGGAGC TGGAGATCTT CTTCAACAAC ATTGCCTACC GCAGCTCCTC AGCCAACCGC 2820
 CTCTTCCGAT GCTCCATCCT GGCTCGTGGC TCTTCTCCT TGACAGCTGG TGGGAGGAAC 2880
 GGTCAAGGAG AAGGTTTAA GATCAGAAAG GGAGGGTTCC CAGGGCCAGG GGTCAAGGCC 2940
 65 AAGGTCAACA CAGGTCCCTT GATGAAGAAA CAGAAAGGAA GGAAGGACGA GGAAGGGA 3000
 AGAGGCTGTG GGAATGACAG GCAAGGCTGT GCCAAGGAGC CGGCCTCTGC TATTGCAGGG 3060
 AAAGGGAAGG GAAATGTGGC CCAAGGTGTG CCCAGAACCC AAGCGCCACA AGATACAAAG 3120
 CCACACTACC ACAGAAAGGG GCTACAGGGT CCAATCACTA CCAGGAAAGG GGGCTACGGG 3180
 GTCCAATCAC TACCAAGAAA AGGGGCTACG GGTCCAATC ACTACAGGA AAAGGGGCTA 3240
 70 CGGGGTCCAA TCACTACAG GAAAGGGGCT TACGGGGTCC AATCACTACC AGGAAAGGG 3300
 GCTACGGGCT CCAATCACTA CCAGGAAAG GGGCTACAGG GTCCAATCAC TACCAGGAAA 3360
 AGGGGCTACG GGCTCCAATC ACTACAGGA AAAGGGGCTA CAGGGTCCAA TCACTACCA 3420
 AGAAAGGGGC TACCGGCTCC AATCACTACC AGGAAAGGG GCTACGGGGT CCAATCACTA 3480
 CCAGGAAAGG GGGCTACAGG GTCCAATCAC TACCAAGAAA AGGGGCTACG GGGTCCAATC 3540
 75 ACTACAGGA AAAGGGGCTA CGGCTCCCAA TCACTACCA GAAAGGGGCT TACGGGGTCC 3600
 AATCACTACC AGGAAAGGG GCTACAGGGT CCAATCACTA CCAGGAAAG GGGCTACAGG 3660
 GTCCAATCAC TACCAAGAAA AGGGGCTACG GGCTCCAATC ACTACAGGA AAAGGGGCTA 3720
 CGGGGTCCAA TCCACAGAG GAAAGGGGCT TACGGGCTCC AATCACTACC AGGAAAGAG 3780
 GCTATGGGGT CCAATCACTA CCAGGAAAG GGGCTACGGG GTCCAATCAC TACCAAGAAA 3840
 80 AGGGGCTATG GGGTCCAATC ACTACCAAG AAAGGGGCTA CGGGGTCCAA CGTCACTCGT 3900
 AGAGAGCAGC GAGACCCCTT CATCGAGGAG CTCATCCCG GCGACGCTT GAGGCTGAG 3960
 TGGCGGGGCA CAGGGGGTGT GGTGACCGAC TTCAGAGGAG ACGGGATGCT GAGCCTCATC 4020
 TTGTCCCATG GAGAGTCCAT GGCTCAGCGG CTGTCCGTCT TCCGGGGCAA TCAGGGCTTC 4080
 AACCAACACT GGCTGCGAGT GGTGCCACGC ACCCGGTTTG GGGCCTTTGC CAGGGGAGCT 4140
 85 AAGGTCTGTC TCTACACCAA GAAGAGTGGG GCCCACTGGA GGATCATCGA CAGGGGCTCA 4200
 GGCTACCTGT GTGAGATGGA GCCCGTGGCA CACTTTGGCC TGGGAAGGA TGAAGCCAGC 4260
 AGTGTGGAGG TGACGTGGCC AGATGGCAAG ATGGTGAGCC GGAAGCTGGC CAGGGGGAG 4320

WO 02/086443

PCT/US02/12476

ATGAACCTCAG TGCTGGAGAT CCTCTACCCC CGGGATGAGG ACACACTTCA GGACCCAGCC 4380
 CCACTGGAGT GTGGCCAAAGG ATTCTCCACG CAGGAAAATG GCCATTGCAT GGACACCAAT 4440
 GAATGCATCC AGTTCCCATT CGTGTGCCCT CGAGACAAGC CCGTATGTGT CAACACCTAT 4500
 GGAAGCTACA GGTGCCCGAC CAACAAGAA GTCAGTCCGG GCTACGAGCC CAACGAGGAT 4560
 GGCACAGCCT GCGTGGGTAC TGAGCTAGGC TCTAGGCATA CAATGACGTG GAAACCAAGG 4620
 CCAAAAAGG AGCTGCAACT TTCCCAAGGC ATCTGCACCC CCGTCTGGTC CTTTTTCCTG 4680
 CCGGGTTGCC GGCTGCTCCT CAAAAGAGCT CAGCTCCAGG CTGCTCCAG CACCCTTCTC 4740
 CAGAAAGCTC CAGGTATTCC AGAAGCCCAA GTGTATGAAC AAGATCAGGA ATAA

Seq ID NO: 473 Protein sequence
 Protein Accession #: FGENESH predicted

1 11 21 31 41 51
 MACPGGLPAR CSGWMGLGGP SGSSPASPPH SSSRYNGPNL VLKYDRAQKR LVNIAVDERS 60
 SPYYALRDQ GNAIGVTACD IDGDGREETIY FLNTNNAFSG HSSSAQVPSG LHRNRPVLKP 120
 PPTTPAGLLG LPPLSGRDFS SSLGQASPDG RQGERVPVPC CRGGLRPTHPE PEPFLLRPKS 180
 GVATYTDKLF KFRNNRWEDI LSDEVNVARG VASLFAGRSV ACVDRKGSGR YSIYIANYAY 240
 GNVGPDALIE MDPEASDLR GILALRDVAA EAGVSKYTEG FSHTASPSIG EISGRTEERE 300
 GGDPEADEE HSGDGSTSQL CRLGWKDGQF KEEAALVEE QREAGAAGVP RGRVRTALQT 360
 SRSHLADKNL GGPFCYYSVC APSPAHPFA PLVTQLMTHG RLAGKLARSV 420
 PHPRAPGMDP KCKGRHAEFG LMAEALGAWP ALSTTVVPGG LRSWEESRQK GQAMSRCALR 480
 ELGGPWSQAT QHLPALELYD LGEPPILOQT DGDPGRRRDS PKVTQECHLV ATPALGGLE 540
 GPCRVAKREI GRETGAUGRP LSHPLVPNFP SCLRPLEAGT VPGAALPQNP GNVVLDMAKA 600
 LAWNQMEKEE GKINGDHEPR FRLRKAREAE FPPGSSEEP LQPPSGLRGS PVLQVGLGLA 660
 SATHCGSMF LGPPGVSQVP ILSSASDIF CDNENGPFL FHNRGDTFV DAAASAERRL 720
 AFIVHLKYHL CRDFFHSLCH LAETGPSSSC CPWHARLLQA PHCHHGLSMS FTRTGSRFYS 780
 FLTQGLASSA HRRTLISLQGS QGAPPCLLAR APCVLGSLIP TAYYIVLWSA IPESLMTHSY 840
 LSSERVNVGV DDPHQHGRGV ALADFNDRGK VDIVYGNWNG PHRLYLQMS T HGKVRFRDIA 900
 SPKFSMPSPV RTVITADFDN DQELIIFNN IAYRSSANR LFRCSILARG SSSLTAGGRN 960
 GQEGELRIIR GGPPGPGGQA KVTGPLMKK QKGRKDEDA RGCNAGQSL AKEPASAIAG 1020
 KGKGNVAQSV PRTOAPQDTK PHYHKKGLQG PITTRKRGY VQSLPGKQAT GSNHYQEKGL 1080
 RGPITTRKRG YGVQSLPGKG ATGSNHYQEK GLQGPITTRK RGYGLQSLPG KGATGSNHYH 1140
 RKGLRAPITT RKRGVGVQSL PGKATGSNH YQEKGLRGP TTRKRGYGLQ SLPGKATGS 1200
 NHYQEKGLQG PITTRKRGY VQSLPGKQAT GSNHYQEKGL RGPITTRKRG YGLQSLPGKE 1260
 AMGSNHYQEK GLRAPITTRK RGYGVQSLPG KGATGSNVIR REHGDPLIEE LNPDALEPE 1320
 GRGTGTVVD FDDGMLDLI LSHGESMAQP LSVFRGNQGF NNNWLRVVP TRFGAFARGA 1380
 KVVLYTKKSG HRLRIDGGS GYLCEMEFVA HFLGLKDEAS SVEVTWPDGK MVSRRNVASG 1440
 MNSVLEILYP RDEDTLQDPA PLECCQGFSQ QENGHCMOTN ECIQFPFVCP RDKPVCVNTY 1500
 GSYRCRTNKK CSRGYEPNED GTACVGTGLG SRHTMTWKPR PKKELQLSQG ICTPVWSFFL 1560
 PGCRLLLKRA QLQAPSTLL QKAPGIPBAQ VYEQDQE

Seq ID NO: 474 DNA sequence
 Nucleic Acid Accession #: NM_003661.1
 Coding sequence: 1..1152

1 11 21 31 41 51
 ATGAGTGCAC TTTTCTCTGG TGTGGGAGTG AGGGCAGAGG AAGCTGGAGC GAGGGTGCAA 60
 CAAAACGTTT CAAGTGGGAC AGATACTGGA GATCCTCAA GTAAGCCCTT CGGTGACTGG 120
 GCTGCTGGCA CCAATGGACC AGAGAGCAGT ATCTTTATTG AGGATGCCAT TAAGTATTTT 180
 AAGGAAAAAG TGAGCACACA GAATCTGCTA CTCTGCTGTA CTGATAATGA GGCCCTGGAAC 240
 GGATTCGTGG CTGCTGCTGA ACTGCCCAGG AATGAGGCAG ATGAGCTCCG TAAAGCTCTG 300
 GACAACTTGG CAAGACAAAT GATCATGAAA GACAAAAACT GGCACGATAA AGGCCAGCAG 360
 TACAGAAACT GGTTCCTGAA AGAGTTCTCT CGGTGAAAA GTGAGCTTGA GGATAACATA 420
 AGAAGGCTCC GTGCCCTTGC AGATGGGGTT CAGAAGGTCC ACAAAGGCAC CACCATCGCC 480
 AATGTGGTGT CTGGCTCTCT CAGCATTTCC TCTGGCATCC TGACCCCTCGT CGGCATGGGT 540
 CTGGCACCTT TCACAGAGGG AGGCAGCCTT GTACTCTTGG AACCTGGGAT GGAGTTGGGA 600
 ATCACAGCCC CTTTGACCGG GATTACCAGC AGTACCATGG ACTACGGAAG GAAGTGGTGG 660
 ACACAAGCCG AAGCCACGCA CTTGGTCATC AAAAGCCTTG ACAAATTGAA GGAGGTGAGG 720
 GAGTTTTTGG GTGAGAACAT ATCCAACCTT CTTTCCTTAG CTGGCAATAC TTACCAACTC 780
 ACACGAGGCA TTGGGAAGGA CATCCGTGCC CTCAGACGAG CCAGAGCCAA TCTTCAGTCA 840
 GTACCGCATG CCTCAGCCTC ACGCCCCCGG GTCACGTAGC CAATCTCAGC TGAAGCGGT 900
 GAACAGGTGG AGAGGGTTAA TGAACCCAGC ATCCTGGAAG TGAGCAGAGG AGTCAAGCTC 960
 ACGGATGTGG CCCCCTGTAAG CTTCTTTCTT GTGCTGGATG TAGTCTACCT CGTGTACGAA 1020
 TCAAAGCACT TACATGAGGG GGCAAGTCA GAGACAGCTG AGGAGCTGAA GAAGGTGGCT 1080
 CAGGAGCTGG AGGAGAAGCT AACATTCTC AACAATAATT ATAAGATTCT GCAGGCGGAC 1140
 CAAGAACTGT GA

Seq ID NO: 475 Protein sequence
 Protein Accession #: NP_003652.1

1 11 21 31 41 51
 MSALFLGVGV RAEEAGARVO QNVPSGTDGT DPQSKPLGDW AAGTMDPES IFIEDAIKYF 60
 KEKVSTQNL LLLTDNEAWN GFVAAELPR NEADELRKAL DNLARQIMK DKWHDKGQ 120
 YRNWFLKEFP RLKSELEDNI RRLRALADGV QKVHKTITIA NVVSGSLIS SGILTLVGMG 180
 LAPFTEGSL VLEPGMELG ITAALTGITS STMDYGKKW TQAQADLVI KSLDKLKEVR 240
 EPLGENISNF LSLAGNTYQL TRIGKDIRA LRRARANLQS VPHASASRPR VTEPIAESG 300
 EQVERVNEPS ILEMSRGVKL TDVAPVSFFL VLDVYLVYE SKHLHEGAKS ETAEEKLVKA 360
 QELEEKLNIL NNNYKILQAD QEL

Seq ID NO: 476 DNA sequence
 Nucleic Acid Accession #: NM_014452.1
 Coding sequence: 1..1968

1 11 21 31 41 51

	ATGGGGACCT	CTCCGAGCAG	CAGCACCGCC	CTCGCCTCCT	CGACCCGCGAT	CGCCCGCCGA	60
	GCCACAGCCA	CGATGATGCG	GGGCTCCCTT	CTCCTGCTTG	GATTCTCTAG	CACCACCACA	120
5	GCTCAGCCAG	AACAGAAGGC	CTCGAATCTC	ATTGGCACAT	ACCGCCATGT	TGACCGTGCC	180
	ACCGGCCAGG	TGCTAACCTG	TGACAAGTGT	CCAGCAGGAA	CCTATGTCTC	TGAGCATTGT	240
	ACCAACACAA	CGCTGCGCGT	CTGCAGCAGT	TGCCCTGTGG	GGACCTTTAC	CAGGCATGAG	300
	AATGGCATAG	AGAAATGCCA	TGACTGTAGT	CAGCCATGCC	CATGGCCAA	GATTGAGAAA	360
	TTACCTTGTG	CTGCCCTGAC	TGACCGAGAA	TGCACTTGCC	CACCTGGCAT	GTTCCAGTCT	420
10	AACGCTACCT	GTGCCCCCA	TACGGTGTGT	CCTGTGGGTT	GGGGTGTGCG	GAAGAAAGGG	480
	ACAGAGACTG	AGGATGTGCG	GTGTAAGCAG	TGTGCTCGGG	GTACCTTCTC	AGATGTGCTT	540
	TCTAGTGTGA	TGAAATGCAA	AGCATACACA	GACTGTCTGA	GTCAGAACTT	GGTGGTGATC	600
	AAGCCGGGGA	CCAAGGAGAC	AGACAACGTC	TGTGGCACAC	TCCCGTCTCT	CTCCAGCTCC	660
	ACCTCACCTT	CCCCTGGCAC	AGCCATCTTT	CCACGCCCTG	AGCACATGGA	AACCCATGAA	720
15	GTCCCTTCTT	CCACTTATGT	TCCCAAAGGC	ATGAATCAA	CAGAATCCAA	CTCTCTTGCC	780
	TCTGTTAGAG	CAAAAGTACT	GAGTAGCATC	CAGGAAGGGA	CAGTCCCTGA	CAACACAAGC	840
	TCAGCAAGGC	GAAGAGGAGA	CGTGAACAAG	ACCCTCCCAA	ACCTTCAGGT	AGTCAACCAC	900
	CAGCAAGGCC	CCCACACAGC	ACACATCTGT	AAGCTGCTGC	CGTCCATGGA	GGCCACTGGG	960
	GGCGAGAAGT	CCAGCACGCC	CTCAAGGGC	CCCAAGAGGG	GACATCTTAG	ACAGAACCTA	1020
20	CACAAGCATT	TTGACATCAA	TGAGCATTGG	CCCTGGATGA	TTGTGCTTTT	CCTGCTGCTG	1080
	GTGCTTGTGG	TGATTTGTGT	GTGCAGTATC	CGGAAAGGCT	CGAGGACTCT	GAAGAAAGGG	1140
	CCCGGCGAGG	ATCCAGTGCG	CATTGTGGAA	AAGGCAGGGC	TGAAGAAATC	CATGACTCCA	1200
	ACCCAGAACC	GGGAGAAATG	GATCTACTAC	TGCAATGGCC	ATGGTATCGA	TATCCTGAAG	1260
	CTTGTAGACG	CCCAAGTGGG	AAGCAGTGG	AAAGATATCT	ATCAGTTTCT	TTGCAATGCC	1320
25	AGTGAGAGGG	AGGTTGCTGC	TTTCTCCAAT	GGGTACACAG	CCGACCACGA	GGGGGCTTAC	1380
	CGAGCTCTGC	AGCACTGGAC	CATCCGGGGC	CCCGAGGCCA	GCCTCGCCCA	GCTAATTAGC	1440
	GCCTCTGCGC	AGCACCGGAG	AAACGATGTT	GTGGAGAAGA	TTCGTGGGCT	GATGGAGAGC	1500
	ACACCCAGCG	TGGAACCTGA	CAAACTAGCT	CTCCCGATGA	GCCCCAGCCC	GCTTAGCCCC	1560
	AGCCCATCC	CCAGCCGCAA	CGCGAACTT	GAGAATTCCG	CTCTCCTGAC	GGTGGAGCCT	1620
30	TCCCCACAGG	ACAAGAACAA	GGGCTTCTTC	GTGGATGAGT	CGGAGCCCTT	TCTCGCTGT	1680
	GACTCTACAT	CCAGCGGCTG	CTCCGCGCTG	AGCAGGAACG	GTTCCTTTAT	TACCAAGAA	1740
	AAGAAGGACA	CAGTGTTCGC	CGAGGTACGC	CTGGACCCCT	GTGACTTGCA	GCCTATCTTT	1800
	GATGACATGC	TCCACTTTCT	AAATCCTGAG	GAGCTGCGGG	TGATTGAAGA	GATTCCCCAG	1860
	GCTGAGGACA	AACTAGACCG	GCTATTCGAA	ATTATTGGAG	TCAAGAGCCA	GGAGCCAGC	1920
35	CAGACCTCC	TGGACTCTGT	TTATAGCCAT	CTTCTGACC	TGCTGTAG		

Seq ID NO: 477 Protein sequence
Protein Accession #: NP_055267.1

	1	11	21	31	41	51	
40	MGTSPPSSSTA	LASCSRIARR	ATATMIAGSL	LLGLPLSTTT	AQPEQKASNL	IGTYRHVDRA	60
	TGQVLTCDCK	PAGTVVSEHC	TNTSLRVCS	CPVGTPTRE	NGIEKCHDCS	QPCPWPMEIK	120
	LPCAALTDRE	CTCPGPMFQS	NATCAPHTVC	PVGWGVKKKG	TETEDVRKAC	CARGTFSDVP	180
45	SSVMCKKAYT	DCLSNLVVI	KPGTKETDNV	CGTLPSFSSS	TSPSPGTATF	PRPEHMETHE	240
	VPSSTYVPKG	MNSTESNNSA	SVRPKVLSSI	QEGTVPDNTS	SARGKEDVNK	TLPLNLQVNH	300
	QQPHHRHLL	KLLPMEATG	GEKSSTPIKG	PKRGHPRQNL	HKHFDINEHL	PWMIVLFLLL	360
	LVVIVVVC	RKSSRTLKKG	PRQDPSAIVE	KAGLKKSMTP	TQNREKWIYY	CNGHGIDILK	420
	LVAQVGSWG	KDIYQFLCNA	SEREVAAFSN	GYTADHERAY	AALQHWITRG	PEASLAQLIS	480
50	ALRQHRRNDV	VVKIRGLMED	TTQLETDKLA	LPMSPLSP	SPIPSNKL	ENSALLTVEP	540
	SPQDKNKGF	VDESEPLLR	DSTSSGSSAL	SRNGSFITKE	KIDTVLRQVR	LDPCDLQPIF	600
	DMMLHFLNPE	ELRVLEBEP	AEDKLDRLFE	IIGVKSQEAS	QTLDSVYSH	LPDLL	

Seq ID NO: 478 DNA sequence
Nucleic Acid Accession #: XM_044533
Coding sequence: 238..2751

	1	11	21	31	41	51	
60	AGGCTGCCCC	AGCCGAGGCT	GCGGGGCGGG	CGCCGGCGGG	AGGACTGCGG	TGCCCGCGGG	60
	AGGGGCTGAG	TTTGCCAGGG	CCCACTTGAC	CTGTCTTCCC	ACCTCCCGCC	CCCCAGGTCC	120
	GGAGGCGGGG	GCCCCCGGGG	CGACTCGGGG	CGCGACCGCG	GGGCGAGAGT	GCCGCCCGTG	180
	AGTCCGCGCG	AGCCACCTGA	GCCCGAGCCG	CGGGACACCG	TGCTCTCTGC	TCTCCGAATG	240
	CTGCGCACCG	CGATGGGCTG	GAGGAGCTGG	CTGCGCGCCC	CATGGGGCGC	GCTGCGCGCT	300
65	CGGCCACCGC	TGCTGCTGCT	CCTGCTGCTG	CTGCTCCTGC	TGCAGCCGCC	GCCTCCGACC	360
	TGGGCGCTCA	GCCCCCGGAT	CAGCCTGCCT	CTGGGCTCTG	AAGAGCGGCC	ATTCCTCAGA	420
	TTGGAAGCTG	AACACATCTC	CAACTACACA	GCCCTTCTGC	TGAGCAGGGA	TGGCAGGACC	480
	CTGTACGTGG	GTGCTCGAGA	GGCCCTCTTT	GCACTCAGTA	GCAACCTCAG	CTTCCTGCCA	540
	GGCGGGGAGT	ACCAGGAGCT	GCTTTGGGGT	GCAGACGCAG	AGAAGAAACA	GCAGTGACAG	600
70	TTCAAGGGCA	AGGACCCAC	CGCGAGCTGT	CAAACTACA	TCAAGATCCT	CCTGCCGCTC	660
	AGCGGCAGTG	ACCTGTTTAC	CTGTGGCACA	GCAGCCTTCA	GCCCCATGTG	TACCTACATC	720
	AACATGGAGA	ACTTACCCCT	GGCAAGGGAC	GAGAAGGGGA	ATGTCCTCCT	GGAAGATGGC	780
	AAGGGCCGTT	GTCCCTTCGA	CCCGAATTTT	AAGTCCACTG	CCCTGGTGGT	TGATGGCGAG	840
	CTCTACACTG	GAACAGTCAG	CAGCTTCCAA	GGGAATGACC	CGGCCATCTC	GCGGAGCCAA	900
	AGCCTTCGCC	CCACCAAGAC	CGAGAGCTCC	CTCAACTGGC	TGCAAGACCC	AGCTTTTGTG	960
75	GCCTCAGCCT	ACATTCTCTG	GAGCCTGGGC	AGCTTGCAAG	GCGATGATGA	CAAGATCTAC	1020
	TTTTTCTTCA	GCGAGACTGG	CCAGGAATTT	GAGTTCTTTG	AGAACACCAT	TGTGTCCCGC	1080
	ATTGCCCGCA	TCTGCAAGGG	CGATGAGGGT	GGAGAGCGGG	TGCTACAGCA	GCGCTGGACC	1140
	TCCTTCTCTA	AGTCCAGAGT	GCTGTGCTCA	CGGCCGACG	ATGGCTTCCC	CTTCAACGTG	1200
	GTGCAGGATG	TCTTCAAGCT	GAGCCCCAGC	CCCCAGGACT	GGCGTGACAC	CCTTTTCTAT	1260
80	GGGGTCTTCA	GCTTCCAGTG	GCACAGGGGA	ACTACAGAAG	GCTCTGCGGT	CTGTGCTTTC	1320
	ACAATGAAGG	ATGTGCAGAG	AGTCTTCAGC	GGCCTCTACA	AGGAGGTGAA	CCGTGAGACA	1380
	CAGCAGTGGT	ACACCGTGAC	CCACCCGGTG	CCCACACCCC	GGCCTGGAGC	GTGCATCACC	1440
	AACAGTGGCC	GGGAAAGGAA	GATCAACTCA	TCCCTGCAGC	TCCAGAGCCG	CGTGCTGAAC	1500
	TTCTTCAAGG	ACCACCTTCT	GATGGACGGG	CAGGTCGAG	GCGCGCTGCT	GCTGCTGCAG	1560
85	CCCAGGCTCA	GCTACTACGC	CGTGGCTGTA	CACCCGCTGC	CTGGCCTGCA	CCACACCTCA	1620
	GATGTCTCTT	TCCTGGGCAC	TGGTGACGGC	CGGCTCCACA	AGGCAGTGAG	CGTGGGCCCC	1680
	CGGGTGACCA	TCATTGAGGA	GCTGCAGATC	TTCTCATCGG	GACAGCCCGT	GCAGAATCTG	1740

5	CTCCTGGACA	CCCACAGGGG	GCTGCTGTAT	GCGGCTCAC	ACTCGGGCGT	AGTCCAGGTG	1800
	CCCATGGCCA	ACTGCAGCCT	GTACAGGAGC	TGTGGGGACT	GCCTCCTCGC	COGGGACCCC	1860
	TACTGTGCTT	GGAGCGGCTC	CAGCTGCAAG	CACGTACAGC	TCTACCAGCC	TCAGCTGGCC	1920
	ACCAGGCGGT	GGATCCAGGA	CATCGAGGGA	GCCAGCGCCA	AGGACCTTTG	CAGCGCGTCT	1980
	TCGGTTGTGT	CCCCGTCTTT	TGTACCAACA	GGGGAGAAGC	CATGTGAGCA	AGTCCAGTTC	2040
	CAGCCCAACA	CAGTGAACAC	TTTGGCCTGC	CCGCTCCTCT	CCAACCTGGC	GACCCGACTC	2100
	TGGCTACGCA	ACGGGGCCCC	CGTCAATGCC	TCGGCCTCCT	GCCACGTGCT	ACCCACTGGG	2160
	GACCTGCTGC	TGCTGGGCAC	CCAACAGCTG	GGGGAGTTCC	AGTGCTGGTC	ACTAGAGGAG	2220
	GGCTTCCAGC	AGCTGGTAGC	CAGCTACTGC	CCAGAGGTGG	TGGAGGACGG	GGTGGCAGAC	2280
10	CMAACAGATG	AGGGTGGCAG	TGTACCCGTC	ATTATCAGCA	CATCGCTGTG	GAGTGCACCA	2340
	GCTGGTGGCA	AGGCCAGCTG	GGGTGCAGAC	AGGTCCTACT	GGAAGGAGTT	CCTGGTGATG	2400
	TGCACGCTCT	TTGTGCTGGC	CGTGTGCTC	CCAGTTTTAT	TCTTGCTCTA	CCGGCACCCG	2460
	AACAGCATGA	AAGTCTTCTT	GAAGCAGGGG	GAATGTGCCA	GCGTGCACCC	CAAGACCTGC	2520
	CCTGTGGTGC	TGCCCTCTGA	GACCCGCCCA	CTCAAOCGCC	TAGGGCCCCC	TAGCACCCCG	2580
15	CTCGATCACC	GAGGGTACCA	GTCCTGTCTA	GACAGCCCCC	CGGGGTCCCG	AGTCTTCACT	2640
	GAGTCAGAGA	AGAGGCCACT	CAGCATCCAA	GACAGCTTCG	TGGAGGTATC	CCCAGTGTGC	2700
	CCCCGGCCCC	GGGTCCGCTT	TGGCTCGGAG	ATCCGTGACT	CTGTGGTGTG	AGAGCTGACT	2760
	TCAGAGGAGC	GCTGCCCCGG	CTTCAGGGGC	TGTGAATGCT	CGGAGAGGGT	CAACTGGACC	2820
	TCCCTCCGCG	TCTGCTCTTC	GTGGAAACAG	ACCGTGGTGC	CCGGCCCTTG	GGAGCCTTGG	2880
20	GGCCAGCTGG	CCTGTGCTGC	TCCAGTCAAG	TAGCGAAGCT	CCTACCACCC	AGACACCCAA	2940
	ACAGCCGTGG	CCCCAGAGGT	CCTGGCCAAA	TATGGGGGCC	TGCCTAGGTT	GGTGGAACAG	3000
	TGCTCCTTAT	GTAAACTGAG	CCCTTTGTTT	AAAAACAAT	TCCAAATGTG	AAACTAGAA	3060
	GAGAGGGAAG	AGATAGCATG	GCATGCAGCA	CACACGGCTG	CTCCAGTTCA	TGGCCTCCCA	3120
	GGGGTGTCTG	GGATGCTTCC	AAAGTGGTTG	TCTGAGACAG	AGTTGGAAGC	CCTCACCAC	3180
25	TGGCCTCTTC	ACCTTCCACA	TTATCCCGCT	GCCACCGGCT	GCCTGTCTCT	ACTGCAGATT	3240
	CAGGACCAGC	TTGGGCTGCG	TGCGTTCTGC	CTTGCCAGTG	AGCCGAGGAT	GTAGTTGTTG	3300
	CTGCCGTGCT	CCCACCACTT	CAGGACCAGC	AGGGCTAGGT	TGGCACTGCG	GCCTCACCA	3360
	GGTCTGTGGC	TGCGACCCAA	CTCTGGAGCC	TTTCCAGCCT	GTATCAGGCT	GTGSCCAGAC	3420
	GAGAGGACAG	CGCGAGCTCA	GGAGAGATTT	CGTGACAATG	TACGCCCTTC	CCTCAGAAAT	3480
30	CAGGGAAGAG	ACTGTGCGCT	GCCTTCTCTC	GTGTGTGCGT	GAGAACCCGT	GTGCCCCCTC	3540
	CCACCATATC	CACCCCTGCT	CCATCTTTGA	ACTCAAACAC	GAGGAACTAA	CTGCACCCTG	3600
	GTCTCTCTCC	CAGTCCCCAG	TTACCCCTCC	ATCCCTCACC	TTCTCCACT	CTAAGGGATA	3660
	TCAACACTGC	CCAGCACAGG	GGCCCTGAAT	TTATGTGGTT	TTTATACATT	TTTTAATAAG	3720
35	ATGCACITTA	TGTCTTTTTT	TAATAAAGTC	TGAAGAATTA	CTGTTT		

Seq ID NO: 479 Protein sequence
Protein Accession #: XP_044533.3

40	1	11	21	31	41	51	
	MLRTAMGLRS	WLAAPWGALE	PRPPLLLLLL	LLLLLQPPPP	TWALSPRISL	PLGSEERPFL	60
	RFEAEHISNY	TALLLSRDGR	TLYVGAREAL	FALSSNLSPL	PGGEYOELLW	GADAEEKQOC	120
	SFKGKDPQDR	CQNYIKILLP	LSGSHLFTCG	TAAFSPMCTY	INMENFTLAR	DEKGNVLLED	180
45	GKGRCPFPDP	PKSTALVVDG	ELYTGTVSSF	QGNDDPAISRS	QSLRPRTKES	SLNWLQDPAP	240
	VASAYIPESL	GSGLQDDDKI	YFFSETGQBE	FEFFENTIUS	RIARICKGDE	GGERVLLQQRW	300
	TSPLKQQLLC	SRPDDGFPPN	VLQDVFTLSP	SPQDWRDTLP	YGVFTSQWHR	GTTEGSAVCV	360
	FTMKDVQRVP	SGLYKEVNRE	TQQNYTVTHP	VPTPRPGACI	TNSARERKIN	SSLQLPDRVL	420
	NFLKDHFLMD	GQVRSRMLLL	QFQARYQORVA	VHRVPLGHHT	YDVLFLGTGD	GRLHKAHSVVG	480
50	PRVHIEELQ	IPSSGQPVQN	LLLDTHRGLL	YAASHSGVVV	VPMANCSLYR	SCGDCLLARD	540
	PYCAWSGSSC	KHVSLYQPLQ	ATRPNIQDIE	GASAKDLCSA	SSVVSFSPVP	TGEKPCQEVQ	600
	FQNTNVTNLA	CPLLNDGAPVN	ASASCHVLPT	GDLLLVGTQQ	LGEFQCWSLE		660
	EGPQQLVASV	CPEVVEDGVA	DQTEGGSVVP	VIIISTSRVSA	PAGGKASWGA	DRSYWKEFLV	720
	MCTLFVLAVL	LPVLFLLYRH	RNSMKVFLKQ	GECASVHPKT	CPVVLPPETR	PLNGLGPPST	780
55	PLDHRGYSLS	SDSPPGSRVF	TESEKRPLSI	QDSFVEVSPV	CPRPRVRLGS	EIRDSVV	

Seq ID NO: 480 DNA sequence
Nucleic Acid Accession #: NM_004217.1
Coding sequence: 58..1092

60	1	11	21	31	41	51	
	GGCCGGGAGA	GTAGCAGTGC	CTTGGACCCC	AGCTCTCCTC	CCCTTTCTTC	TCTAAGGATG	60
	GGCCAGAAGG	AGAACTCCTA	CCCTGGGCCC	TACGGCCGAC	AGACGGCTCC	ATCTGGCCTG	120
	AGCACCCCTG	CCCAGCGAGT	CCTCCGAAA	GAGCCTGTCA	CCCCATCTGC	ACTTGTCTCT	180
65	ATGAGCCGCT	CCAATGTCCA	GCCACAGACT	GCCCTGGGCC	AGAAGGTGAT	GGAGAATAGC	240
	AGTGGGACAC	CCGACATCTT	AACGCGGCAC	TTCACAATTG	ATGACTTTGA	GATTGGGCGT	300
	CCTCTGGGCA	AAGGCAAGTT	TGGAAACGTG	TACTTGGCTC	GGGAGAAGAA	AAGCCATTTC	360
	ATCGTGGCGC	TCAAGTCTCT	CTTCAAGTCC	CAGATAGAGA	AGGAGGGCGT	GGAGCATCAG	420
70	CTGCGCAGAG	AGATCGAAAT	CCAGGCCAC	CTGCACCATC	CCAACATCCT	CGCTCTCTAC	480
	AACTATTTTT	ATGACCGGAG	GAGGATCTAC	TTGATTCTAG	AGTATGCCCC	CCGCGGGGAG	540
	CTCTACAAGG	AGCTGCAGAA	GAGCTGCACA	TTTGACGAGC	AGCGAACAGC	CACGATCATG	600
	GAGGAGTTGG	CAGATGCTCT	AATGTACTGC	CATGGGAAGA	AGGTGATTCA	CAGAGACATA	660
	AAGCCAGAAA	ATCTGCTCTT	AGGGCTCAAG	GGAGAGCTGA	AGATTGCTGA	CTTCGGCTGG	720
75	TCTGTGCATG	CGCCCTCCCT	GAGGAGGAAG	ACAATGTGTG	GCACCTGGGA	CTACCTGCCC	780
	CCAGAGATGA	TTGAGGGGCG	CATGCACAAT	GAGAAGGTGG	ATCTGTGGTG	CATTGGAGTG	840
	CTTTGCTATG	AGCTGCTGGT	GGGGAACCCA	CCCTTTGAGA	GTGCATCACA	CAACGAGACC	900
	TATCGCCGCA	TGCTCAAGGT	GGACCTAAAG	TTCCCGCTT	CTGTGCCCCAC	GGGAGCCGAG	960
	GACCTCATCT	CCAACTGTCT	CAGGCATAAC	CCCTCGGAAC	GGCTGCCCTT	GGCCCAAGTC	1020
80	TCAGCCCAAC	CTTGGGTCCG	GGCCAACCTC	CGGAGGGTGC	TGCCTCCCTC	TGCCCTTCAA	1080
	TCTGTGCGCT	GATGGTCCCT	GTCATTCACT	CGGGTGCCTG	TGTTTGTATG	TCTGTGTATG	1140
	TATAGGGGAA	AGAAGGGATC	CCTAACTGTT	CCCTTATCTG	TTTTCTACCT	CCTCCTTTGT	1200
85	TTAATAAAGG	CTGAAGCTTT	TTGT				

Seq ID NO: 481 Protein sequence
Protein Accession #: NP_004208

1	11	21	31	41	51
---	----	----	----	----	----

MAQKENSYPW	PYGRQTAPSG	LSTLPQRVLR	KEPVTSPALV	LMSRSNVQPT	AAPGQKVMEN	60
SSGTEDILTR	HFTIDDFEIG	RPLGKGFNG	VYLAREKKSH	FIVALKVLFP	SQIEKEGVEH	120
QLRREIEIQL	HLHHPNLLRL	YNYFYDRRRI	YLILEYAPRG	ELYKELQKSC	TFDEQRTATI	180
MEELADALMY	CHGKVKIHRD	IKPENLLGL	KGELKIADFG	WSVHAPSLRR	KTMCGLDYL	240
PPEMIEGRMH	NEKVDLCIG	VLCYELLVGN	PPFESASHNE	TYRRIVKVDL	KFPASVPTGA	300
QDLISKLLRH	NPSERLFLAQ	VSAHPWVRAN	SRRVLPPSAL	QSV		

Seq ID NO: 482 DNA sequence
Nucleic Acid Accession #: AK055663
Coding sequence: 38..1423

1	11	21	31	41	51	
AGAACGGCTT	CCGCGGGGAG	CTGTGCAGCT	CCTTATCATG	GGGACAATTC	ATCTCTTTTCG	60
AAAACCCACAA	AGATTCCTTTT	TTGGCAAGTT	GTTACGGGAA	TTTAGACTTG	TAGCAGCTGA	120
CCGAAGTCC	TGGAAGATAC	TGCTCTTTGG	TGTAATAAAC	TTGATATGTA	CTGGCTTCCT	180
GCTTATGTGG	TGCAGTTCTA	CTAATAGTAT	AGCTTTAACT	GCCTATACCT	ACCTGACCAT	240
TTTTGATCTT	TTTAGTTTAA	TGACATGTTT	AATAAGTTAC	TGGGTAAACAT	TGAGGAAACC	300
TAGCCCTGTC	TATTCATTGG	GGTTTGAAAG	ATTAGAAATC	CTGGCTGTAT	TTGCCCTCCAC	360
AGTCTTGGCA	CAGTTGGGAG	CTCTCTTTAT	ATTAAAGAA	AGTGCAGAAC	GCTTTTGGGA	420
ACAGCCCGAG	ATACACACGG	GAAGATTATT	AGTTGGTACT	TTTGTGGCTC	TTTGTTCCAA	480
CCTGTTCACG	ATGCTTCTTA	TTCGGAATAA	ACCTTTTGCT	TATGTCTCAG	AAGCTGCTAG	540
TACGAGCTGG	CTTCAAGAGC	ATGTTGCAGA	TCTTAGTCGA	AGCTTGTGTG	GAATTATTCC	600
GGGACTTAGC	AGTATCTTCC	TTCCCGAAT	GAATCCATTT	GTTTGTATTG	ATCTTGCTGG	660
AGCATTAGCT	CTTTGTGCTA	CATATATGCT	CATTGAAATT	AATAATTATT	TTGCCGTAGA	720
CACCTGCTCT	GCTATAGCTA	TTGCCCTGAT	GACATTTGGC	ACTATGTATC	CCATGAGTGT	780
GTACAGTGGG	AAAGTCTTAC	TCCAGACAAC	ACCACCCCAT	GTTATTGGTC	AGTTGGACAA	840
ACTCATGAGA	GAGGTATCTA	CCTTAGATGG	AGTTTATGAA	GTCGGAATAG	AACATTTTTC	900
GACCCTAGGT	TTTGGCTCAT	TGGCTGGATC	AGTGCATGTA	AGAATTGCGA	GAGATGCCAA	960
TGAACAAATG	GTTCTTGCTC	ATGTGACCAA	CAGGCTGTAC	ACTCTAGTGT	CTACTCTAAC	1020
TGTTCAAATT	TTCAAGGATG	ACTGGATTAG	GCCTGCCTTA	TTGTCTGGGC	CTGTTGCAGC	1080
CAATGTCCTA	AACTTTTCAG	ATCATCACGT	AATCCCAATG	CCTCTTTTAA	AGGGTACTGA	1140
TGATTGAAC	CCAGTTACAT	CAACTCCAGC	TAAACCTAGT	AGTCCACCTC	CAGAATTTTC	1200
ATTTAAACAT	CCTGGGAAAA	ATGTGAACCC	AGTTATTCTT	CTAAACACAC	AAACAAGGCC	1260
TTATGGTTTT	GTTCTTCAAT	ATGGACACAC	ACCTTACAGC	AGCATGCTTA	ATCAAGGACT	1320
TGGAGTTCCA	GGAATTGGAG	CAACTCAAGG	ATTGAGGACT	GGTTTTACAA	ATATACCAAG	1380
TAGATATGGA	ACTAATAATA	GAATTGGACA	ACCAAGACCA	TGATAGACTC	TAACITATTT	1440
TTATAAGGAA	TATTGATCTC	TTGGCTTCCA	ATTTATTTAG	TAATCCAACT	TTGCATTGAC	1500
TGTTTAACTA	TTTACTCTAA	ATGTTAGATA	ATAGTAGTCT	TGTTCACTAT	TCATGAAACC	1560
TATGAAACTA	TTTCTTGTGA	AAATGTATTT	GTGACAGTGA	AATCCTCGTA	AATGTTAAAG	1620
GCCTTAAATA	GGCTTCCTTT	AGAAATGTG	TTTCTTTAAA	TTTGGAATTT	GGTATCTTTG	1680
GTTTTGTAGT	TGACTGCAGT	GTGATGTGAC	CTTACCTTTA	TAAGAGCCAC	TTGATGGAGT	1740
AGATCTGTCA	CATTACTAAG	ATACGATATT	TCTTTTITTT	TCCGAGACGG	AGTCTTGCTC	1800
TGCCACTGTG	CCCGGCCAAT	ACATTATTAT	TAACTTAAAG	CTGTACTTTA	TTAAGGCTTC	1860
CTTAGTTTTT	GTTTCTTTT	GTGTTTGGAG	ATGGAGTCTC	ACTCTGTCCG	CCAGGCTGGA	1920
ATGCAGTGGC	ATGATCTCAG	CTCACTGCAA	CCTCTGCCTC	CTGAGTTCAA	ATGATCTCC	1980
TGCCCTCAGC	TCCCGAGTAG	CTGGGATTAC	AGGCACCTGC	CACCACGCCC	AGCTAATTTT	2040
TGTATTTTAA	GTAAGAGACG	GGGATTTTAC	CATGTTGGCC	AGGCTGGTCT	TGAACCTCTG	2100
ACCTCATGAT	CCACCCACCT	TAGCCTCCCA	AAGTGCTGGG	ATTAGGTGTG	AGCCACCGCA	2160
CCTGGCCGAT	ATTTCTTTTA	ATGAAATTTA	TAAATATGCT	TCTTGAATAA	TACACATTTT	2220
GGGAAAGGGA	AAAATGCTCG	TTCAAAAAGT	AAAGGTCTCT	TTTATAGCTT	TTCCAAACTT	2280
AATTGCTAAA	TTTTCTTTTG	AGGTTCTCCT	GAATTATGTC	TTACAAACTA	AAAGCAAAAA	2340
TTTTTAGCAG	AAATTTTGA	ATACATTCTA	TCTAGCACAA	TTTGAATTTT	TAATTATCAA	2400
GATTTTGTGT	AAAGTTTCTC	TCCTTTAAAA	ATTTTAGTAC	ATTTGTAAT		

Seq ID NO: 483 Protein sequence
Protein Accession #: BAB70980.1

1	11	21	31	41	51	
MGTIHLFRKP	QRSFFGKLLR	EPRLVAADRR	SWKILLFVGI	NLICTGFLLM	WCSSTNSIAL	60
TATYTLTIFD	LFSLMTCLIS	YVVTLRKPSP	VYSFGFERLE	VLAVFASTVL	AQLGALFILK	120
ESAERPLEQP	BIHTGRLLVG	TFVALCFNLP	TMLSIRNKPF	AYVSEAASTS	WLQEHVADLS	180
RSLCGIIPGL	SSIFLPRMNP	FVLIDLAGAF	ALCITYMLIE	INNYFAVDTA	SAIAIALMTF	240
GTMPYMSVYS	GKVLQITPP	HVIGQLDKLI	REVSTLDGVL	EVNRNEFWTL	GFGSLAGSVH	300
VRIRRDANEQ	MVLAVHTNRL	YTLVSTLTQV	IFKDDWIRPA	LLSGPVAANV	LNFSDDHVIP	360
MFLLKGTDDL	NPVTSTPAKP	SSPPPEFSFN	TPGKNVNPVI	LLNTQTTPYG	FGLNHGHTPY	420
SSMLNQGLGV	PGIGATQGLR	TGFTNIPSRV	GTNNRIGQPR	P		

Seq ID NO: 484 DNA sequence
Nucleic Acid Accession #: FGENESH predicted
Coding sequence: 1..900

1	11	21	31	41	51	
ATGCCGCCGC	GGGAGCTGAG	CGAGGCCGAG	CGGCCCCGCG	TCCGGGCCCC	GACCCCTCCC	60
CGCGGGCGCG	GTAGCGCGCC	CCAGAGCTG	GGCATCAAGT	GCGTGTGGT	GGGCGACGGC	120
GCCGTGGGCA	AGAGCAGCTT	CATCGTCAGC	TACACCTGCA	ATGGGTACCC	CGCGCGCTAC	180
CGGCCCACTG	CGCTGGACAC	CTTCTCTGCT	ACGTACGTTT	AATCGCCCGT	CGCGCGCGGT	240
GGCTGCGCGG	GGGCTGTGCA	CCGGGGAGCT	GGGGCGGGCG	TCTCGGCGGG	AGGGCGCAGA	300
GGACCCCGGG	GAGGAGACTG	GAGCAGGCC	CGAGGTGGCG	CTGTTGCGGC	CCAGGACGCT	360
CTTCTTAATC	CAGGCTCTCC	CGGCCCGCGC	CCTGCACTGC	AAGTCTGGT	GGATGGAGCT	420
CCGGTGCAGA	TTAGCTCTG	GGACACAGCG	GGACAGGAGG	ATTTGACCG	ACTTCGTTCC	480
CTTTGCTACC	CGGATACCGA	TGTCTTCTCG	GCGTGCTTCA	GCGTGGTGCA	GCCAGCTCC	540
TTTCAAAACA	TCACAGAGAA	ATGGCTGCCC	GAGATCCGCA	CGCACAAACC	CCAGGCGCCT	600
GTGCTGCTGG	TGGGCACCCA	GGCGACCTG	AGGGACGATG	TCAACGTACT	AATTCAGCTG	660

GACCAAGGGG GCGGGGAGGG CCCCCTGCCC CAACCCAGG CTGAGGGTCT GGCCGAGAAG 720
 ATCCGAGCCT GCTGCTACCT TGAGTGCTCA GCCTTGACGC AGAAGAACTT GAAGGAAQDA 780
 TTTGACTCGG CTATTCTCAG TGCCATTGAG CACAAAGCCC GGCTGGAGAA GAAACTGAAT 840
 GCCAAAGGTG TCGGCACCCCT CTCCCGCTGC CGCTGGAAGA AGTTCTTCTG CTTCGTTTGA

Seq ID NO: 485 Protein sequence
 Protein Accession #: FGENESH predicted

1 11 21 31 41 51
 MPPRELSEAE PPPLRAPTPP PRRRSAPPEL GIKCVLVGDG AVGKSSLIVS YTCNGYPARY 60
 RPTALDTFSC TYVQSPVRPR GCGGAVHRGA GAGVSAGRRR GPRGGSWSRP RGGAGAAQDA 120
 LPNSGSPRPA FAVQVLVDGA PVRIELWDTA GQEDFDRLRS LCYPDTDVFL ACPFVVQPSS 180
 FQNITEKWL P EIRTHNPQAP VLLVGTQADL RDDVNVLIQL DQGGREGVPV QPQAQGLAEK 240
 IRACCYLECS ALTQKNLKEV FDSAILSABE HKARLEKKLN AKGVRTLSRC RWKKFECFV

Seq ID NO: 486 DNA sequence
 Nucleic Acid Accession #: XM_063832.2
 Coding sequence: 1..711

1 11 21 31 41 51
 ATGCCGCGGC GGGAGCTGAG CGAGGCGGAG CGGCCCCCGC TCCGGGCCCC GACCCCTCCC 60
 CCGCGGCGGC GTAGCGCGCC CCCAGAGCTG GGCATCAAAGT GCGTGCTGGT GGGCGACGGC 120
 GCCGTGGGCA AGAGCAGCCT CATCGTCAGC TACACCTGCA ATGGGTACCC CGCGCGCTAC 180
 CGGCCCACTG CGCTGGACAC CTCTCTGTG CAAGTCTCTG TGGATGGAGC TCCGGTGGCG 240
 ATTGAGCTCT GGGACACAGC GGGACAGSAG GATTTTGACC GACTTCGTTC CCTTTGCTAC 300
 CCGGATACCG ATGTCTTCCT GCGTGCTTTC AGCGTGGTGC AGCCCAAGCTC CTTTCAAAAC 360
 ATCAGAGAGA AATGGCTGCC CGAGATCCGC ACGCACAAAC CCCAGGCGCC TGTGCTGCTG 420
 GTGGGCAACC AGGCCGACCT GAGGGACGAT GTCAACGTAC TAATTGAGCT GGACCAAGGG 480
 GGCCGGGAGG GCCCGGTGCC CCAACCCAG GCTCAGGGTC TGGCCGAGAA GATCCGAGC 540
 TGCTGCTACC TTGAGTGCTC AGCCTTGACG CAGAAGAACT TGAAGGAAGT ATTTGACTCG 600
 GCTATTCTCA GTGCCATTGA GCACAAAGCC CGGCTGGAGA AGAAACTGAA TGCCAAAGGT 660
 GTGGCGACCC TCTCCGCTG CGCTGGAAG AAGTCTTCT GCTTCGTTTG A

Seq ID NO: 487 Protein sequence
 Protein Accession #: XP_063832.1

1 11 21 31 41 51
 MPPRELSEAE PPPLRAPTPP PRRRSAPPEL GIKCVLVGDG AVGKSSLIVS YTCNGYPARY 60
 RPTALDTFSV QVLVDGAPVR IELWDTAGQE DFDRLSLCY PTDVFLACP SVVQPSFQFN 120
 ITEKWLPEIR THNPQAPVLL VGTQADLRDD VNVLIQLDQG GREGVPVPQ QGLAEKIRA 180
 CCYLECSALT QKNLKEVFDS AILSAIEHKA RLEKKLNAGK VRTLSRCRWK KFFCFV

Seq ID NO: 488 DNA sequence
 Nucleic Acid Accession #: NM_014398.1
 Coding sequence: 64..1314

1 11 21 31 41 51
 GGCACCGATT CGGGGCTGCG CCGGACTTCG CCGCACGCTG CAGAACCTCG CCCAGCGCCC 60
 ACCATGCCCC GGCAGCTCAG CGCGCGCGCC GCGCTCTTCG CGTCCCTGGC CGTAATTTTG 120
 CACGATGGCA GTCAAATGAG AGCAAAAGCA TTTCCAGAAA CCAGAGATTA TTCTCAACCT 180
 ACTGCAGCAG CAACAGTACA GGACATAAAA AAACCTGTCC AGCAACGAGC TAAGCAAGCA 240
 CCTCACCAAA CTTTAGCAGC AGAGATTCAT GATGGTCATA TCACCTTTCA AACAGCGGCC 300
 ACAGTAAAAA TTCCAACAAC TACCCAGCA ACTACAAAAA AACTGCAAC CACCAGCCCA 360
 ATTACTACA CCGTGGTTCAC AACCCAGGCC ACACCCAACA ACTCACACAC AGCTCCTCCA 420
 GTTACTGAAG TTACAGTCCG CCCTAGCTTA GCCCCTTATT CACTGCCACC CACCATCACC 480
 CCACGAGCTC ATACAGCTGG AACCAAGTCA TCAACCGTCA GCCACACAAC TGGGAACACC 540
 ACTCAACCCA GTAACCAAGC CACCCCTTCA GCAACTTTAT CGATAGCACT GCACAAAAGC 600
 ACAACCGGTC AGAAGCCTGA TCAACCCACC CATGCCCCAG GAACAACGGC AGCTGCCACC 660
 AATACCAACC GCACAGCTGC ACCTGCCTCC ACGGTTCTCG GGCCCAACCT TGCACCTCAG 720
 CCATCGTCAG TCAAGACTGG AATTTATCAG GTTCTAAACG GAAGCAGACT CTGTATAAAA 780
 GCAGAGATGG GGATACAGCT GATTGTTCAA GACAAGGAGT CGGTTTTTTC ACCTCGGAGA 840
 TACTTCAACA TCGACCCCAA CGCAACGCAA GCCTCTGGGA ACTGTGGCAC CCGAAAATCC 900
 AACCTTCTGT TGAATTTTCA GGGCGGATTT GTGAATCTCA CATTACCAA GGATGAAGAA 960
 TCATATTATA TCAGTGAAGT GGGAGCCTAT TTGACCGTCT CAGATCCAGA GACAGTTTAC 1020
 CAAGGAATCA AACATGCGGT GGTGATGTTT CAGACAGCAG TCGGGCATTG CTTCAAGTGC 1080
 GTGAGTGAAC AGAGCCTCCA GTTGTGAGCC CACCTGCAGG TGAACAACAC CGATGTCCAA 1140
 CTTCAAGCCT TTGATTTTGA AGATGACCAC TTTGGAAAATG TGGATGAGTG CTCGTCTGAC 1200
 TACACAATTG TGCTTCTCTG GATTTGGGGCC ATCGTGGTTG GTCTCTGCCT TATGGGTATG 1260
 GGTGTCTATA AAATCGCCT AAGGTGTCAA TCATCTGGAT ACCAGAGAAT CTAATTGTTG 1320
 CCCGGGGGGA ATGAAAATAA TGGAAATTAG AGAACTCTTT CATCCCTTCC AGGATGGATG 1380
 TTGGGAAATT CCCTCAGAGT GTGGGTCTTT CAAACAATGT AAACCAACAT CTTCTATTCA 1440
 AATGAAGTGA GTCATGTGTG ATTTAAGTTC AGGCAGCACA TCAATTCTTA AATACTTTT 1500
 GTTTATTTTA TGAAGATAT AGTGAGCTGT TTATTTTCTA GTTTCCTTTA GAATATTTTA 1560
 GCCATCAAAA GTCAATATT GTGATATGTT GAATTAACAT AATATATGTA AAGTAGAATA 1620
 AGCCTTCAAA TTATAAACCA AGGTCATATT GTAACATAA CTACTGTGTG TGCATTGAAG 1680
 ATTTTATTTT ACCCTTGATC TTAACAAGC CTTTGCTTTG TTATCAAATG GACTTTCAGT 1740
 GCTTTTACTA TCTGTGTTTT ATGTTTTCAT GTAACATACA TATTCCTGGT GTAGCACTTA 1800
 ACTCCTTTTC CACTTTAAAT TTGTTTTTGT TTTTGGAGAC GGAGTTTCAC TCTGTTCACC 1860
 CAGGCTGGAG TACAGTGGCA CGATCTCGGC TTATGGCAAC CTCGCGCTCC CGGGTTCAAG 1920
 TGATTTCTCT GCTTCAGCTT CCGGAGTAGC TGGGATTACA GGCACACACT ACCACGCTG 1980
 GCTAATTTT GTATTTTAT TATAGACGGG TTTCAACATG TTGGCCAGAC TGGTCTTGAA 2040
 CTCTTGACCT CAGGTGATCC ACCCACTCA GCCTCCCAA GTGCTGGGAT TACAGGCATG 2100
 AGCCATTGCG CCCGGCCTTA AATGTTTTT TTAATCATCA AAAGAACAA CATATCTCAG 2160

GTTGTCTAAG TGTTTTTATG TAAACCAAC AAAAAGAACA AATCAGCTTA TATTTTTTAT 2220
 CTTGATGACT CCTGCTCCAG AATTGCTAGA CTAAGAATTA GGTGGCTACA GATGGTAGAA 2280
 CTAACAATA AGCAAGAGAC AATAATAATG GCCCTTAATT ATTAACAAAG TGCCAGAGTC 2340
 TAGGCTAAGC ACTTTATCTA TATCTCATTT CATCTCACA ACTTATAAGT GAATGAGTAA 2400
 ACTGAGACTT AAGGGAACCT AATCACTTAA ATGTACACCTG GCTAACTGAT GGCAGAGCCA 2460
 GAGCTTGAAT TCATGTTGGT CTGACATCAA GGTCTTTGGT CTTCTCCCTA CACCAAGTTA 2520
 CCTACAAGAA CAATGACACC ACACCTCTGCC TGAAGGCTCA CACCTCATAC CAGCATACGC 2580
 TCACCTTACA GGGAAATGGG TTTATCCAGG ATCATGAGAC ATTAGGGTAG ATGAAAGGAG 2640
 AGCTTTGCAG ATAACAAAT AGCCTATCCT TAATAAATCC TCCACTCTCT GGAAGGAGAC 2700
 TGAGGGGCTT TGTAAACAT TAGTCAGTTG CTCATTTTAA TGGGATTGCT TAGCTGGGCT 2760
 GTAAAGATGA AGGCATCAAA TAAACTCAAA GTATTTTAA ATTTTTTGA TAATAGAGAA 2820
 ACTTCGTAA CCAACTGTTT TTTCTGAGT GTATAGCCCC ATCTTGTGGT AACTTGCTGC 2880
 TTCTGCATT CATATCCATA TTTCTATG TTCACTTAT TCTGTAGAGC AGCCTGCCAA 2940
 GAATTTTATT TCTGCTGTTT TTTTGTCTGC TAAAGAAAGG AACTAAGTCA GGATGTTAAC 3000
 AGAAAAGTCC ACATAACCTT AGAATTCTTA GTCAAGGAAT AATTCAAGTC AGCCTAGAGA 3060
 CCATGTTGAC TTTCTCATG TTTTCTCTTA TGACTCAGTA AGTTGGCAAG GTCCTGACTT 3120
 TAGTCTTAAT AAAACATTGA ATTGTAGTAA AGGTTTTTGC AATAAAAACT TACTTTGG

Seq ID NO: 489 Protein sequence

Protein Accession #: NP_055213.1

1 11 21 31 41 51
 MPRQLSAAAA LFASLAVILH DGSQMRKAF PETRDYSQPT AAATVQDIKK PVQPAKQAP 60
 HQTLAARFMD GHITFQTAAT VKIPTTTTAT TKNTATTSPI TYTLVTTQAT PNNSTAPPV 120
 TEVTVGPFLA PYSLPPTITP PAHTAGTSSS TVSHTTGNTT QPSNQTTLPA TLSIALHKST 180
 TGQKPDQPTH APGTTAAAHN TTRTAAPAST VPGPTLAPQP SSVKTIYQV LNSRLCLKA 240
 EMGIQLIVQD KESVFPSPRY FNIDPNATQA SGNGCTRKSN LLLNFQGGFV NLFTKDEES 300
 YYISEVGAYL TVSDPETVYQ GIKHAVVMFQ TAVGHSFKCV SEQSLQLSAH LQVKTTDVQL 360
 QAFDFEDDHF GNVDECSSDY TIVLPVIGAI VVGLCLMGMG VYKIRLRCQS SGYQRI

Seq ID NO: 490 DNA sequence

Nucleic Acid Accession #: NM_005409.3

Coding sequence: 94..378

1 11 21 31 41 51
 TTCCTTTCAT GTTCAGCAAT TCTACTCCTT CCAAGAAGAG CAGCAAAGCT GAAGTAGCAG 60
 CAACAGCACC AGCAGCAACA GCAAAAAACA AACATGAGTG TGAAGGGCAT GGCTATAGCC 120
 TTGGCTGTGA TATGTGTGTC TACAGTTGTT CAAGGCTTCC CCATGTTCAA AAGAGGACGC 180
 TGTCTTTGCA TAGGCCCTGG GGTAAAAGCA GTGAAAGTGG CAGATATTGA GAAAGCCTCC 240
 ATAATGTACC CAACTAACAA CTGTGACAAA ATAGAAGTGA TTATTACCTT GAAAGAAAAA 300
 AAAGGACAAC GATGCCATAA TCCCAATCG AAGCAAGCAA GGCTTATAAT CAAAAAAGTT 360
 GAAAGAAAGA ATTTTAAAAA ATATCAAAAC ATATGAAGTC CTGGAAGAGG GCATCTGAAA 420
 AACCTAGAAC AAGTTTAACT GTGACTACTG AAATGACAAG AATTCTACAG TAGGAACTG 480
 AGACTTTTCT ATGGTTTGTG GACTTTCAAC TTTGTACAG TTATGTGAAG GATGAAAGGT 540
 GGGTGAAGAG ACCAAAAACA GAAATACAGT CTTCTGAAT GAATGACAAT CAGAAATCCA 600
 CTGCCAAAGG GATGCCAGCA ATTAATGGA TTTCTAGGAA AAGCTACCTT AAGAAAGGCT 660
 GGTACCATC GAGTTTACA AAGTGCTTTC ACGTTCTTAC TTGTGTATT ATACATTCAT 720
 GCATTTCTAG GCTAGAGAAC CTTCTAGATT TGATGCTTAC AACTATTCTG TTGTGACTAT 780
 GAGAACATTT CTGTCTCTAG AAGTTATCTG TCTGTATTGA TCTTTATGCT ATATTACTAT 840
 CTGTGGTTAC AGTGGAGACA TTGACATTAT TACTGGAGTC AAGCCCTTAT AAGTCAAAAG 900
 CATCTATGTG TCGTAAAGCA TTCTCAAAC ATTTTTCAT CAAATATACAC ACTTCTTTCC 960
 CCAATATCA TGTAGACAT CAATATGTAG GAAACATTC TTATGCATCA TTTGGTTTGT 1020
 TTTATAACCA ATTCATTAAA TGTAAATCAT AAAATGTACT ATGAAAAAAA TTATACGCTA 1080
 TGGGATAGTG GCACAGTGTC ACATATTCTA TAACCAAATT AGCAGCACCG GTCTTAATTT 1140
 GATGTTTTTC AACTTTTATT CATCTGAGATG TTTTGAAGCA ATTAGGATAT GTGTGTTTAC 1200
 TGTACTTTTT GTTTTGAATC GTTTGTATAA ATGATAGCAA TATCTTGGAC ACATTGAAA 1260
 TACAAATGT TTTTGTCTAC CAAAGAAAAA TGTGAAAAA TAAGCAATG TATACCTAGC 1320
 AATCACTTTT ACTTTTGTGA ATTCTGTCTC TTAGAAAAAT ACATAATCTA ATCAATTTCT 1380
 TTGTTTATGC CTATATACTG TAAATTTTAG GTATACTCAA GACTAGTTTA AAGAAATCAA 1440
 GTCATTTTTT TCTCTAATAA ACTACCACAA CCTTCTTTT TTAACAAAAA AAA

Seq ID NO: 491 Protein sequence

Protein Accession #: NP_005400.1

1 11 21 31 41 51
 MSVKGMAIAL AVILCATVVQ GPFMFKRGRC LCIGPGVKAV KVADIEKASI MYPSNNCDKI 60
 EVIITLKENK GQRCLNPKSK QARLIHKVE RKNF

Seq ID NO: 492 DNA sequence

Nucleic Acid Accession #: NM_000577.1

Coding sequence: 41..520

1 11 21 31 41 51
 GGCACGAGGG GAAGACCTCC TGTCTATCA GGCCCTCCCC ATGGCTTTAG AGACGATCTG 60
 CCGACCTCTT GGGAGAAAAA CCAGCAAGAT GCAAGCCTTC AGAATCTGGG ATGTTAAACA 120
 GAAGACCTTC TATCTAGGGA ACAACCAACT AGTTGCCGGA TACTTGCAAG GACCAATGT 180
 CAATTTAGAA GAAAGATAG ATGTGGTACC CATTGAGCCT CATGCTCTGT TCTTGGGAAT 240
 CCATGGAGGG AAGATGTGCC TGTCTGTGT CAAGTCTGGT GATGAGACCA GACTCCAGCT 300
 GGAGGCAGTT AACATCACTG ACCTGAGCGA GAACAGAAAG CAGGACAAGC GCTTCGCCTT 360
 CATCCGCTCA GCAGTGGGCC CCACCACCAG TTTTGTGCTT GCGCGCTGCC CCGGTTGGTT 420
 CCTCTGCACA GACGAGGAG CGTGACGCTC ACCAATATGC CTGACGAAAG 480
 CGTCATGCTC ACCAAATTCT ACTTCCAGGA GGACGAGTAG TACTGCCAGC GCCTGCCTGT 540
 TCCCATTTCT GCATGGCAAG GACTGCAGGG ACTGCCAGTC CCCCTGCCCC AGGGCTCCCC 600

GCTATGGGG CACTGAGGAC CAGCCATTGA GGGGTGGACC CTCAGAAGGC GTCACAACAA 660
 CCTGGTCACA GGA CTCTGCC TCCTCTTCAA CTGACCAGCC TCCATGCTGC CTCCAGAATG 720
 GTCTTTCTAA TGTGTGAATC AGAGCACAGC AGCCCCCTGCA CAAAGCCCTT CCATGTGCC 780
 TCTGCATTCA GGATCAAAAC CCGACCACCT GCCCAACCTG CTCTCTCTT GCCACTGCCT 840
 CTTCTCTCCCT CATTCACCAT TCCCATGCCC TGGATCCATC AGGCCACTTG ATGACCCCA 900
 ACCAAGTGGC TCCACACACC TGTTTTACAA AAAAGAAAAG ACCAGTCCAT GAGGGAGGTT 960
 TTTAAGGGTT TGTGGAAAAT GAAAATTAGG ATTTCATGAT TTTTCTTTT CAGTCCCGT 1020
 GAAGGAGAGC CCTTCATTG GAGATTATGT TCTTTCGGG AGAGGCTGAG GACTTAAAT 1080
 ATTCTGCTAT TTGTGAAATG ATGGTGAAAG TAAGTGSTAG CTTTCCCTT CTTTCTCTC 1140
 TTTTCTGTG ATGTCCCAAC TTGTAATAAT TAAAGTTAT GGTACTATGT TAGCCCCATA 1200
 ATTTTTTTTT TCCTTTTAAA ACACTTCCAT AATCTGGACT CCTCTGTCCA GGCAGTCTG 1260
 CCCAGCTCC AAGCTCCATC TCCACTCCAG ATTTTTCACA GCTGCTGCA GTACTTTACC 1320
 TCCTATCAGA AGTTCTCAG CTCCAAGGC TCTGAGCAA TGTGGCTCT GGGGTTCTT 1380
 TCTTCTCTG CTGAAGGAAT AAATTGCTCC TTGACATTGT AGAGCTTCTG GCACCTGGAG 1440
 ACTTGTATGA AAGATGGCTG TGCCTCTGCC TGTCTCCCC ACCAGGCTGG GAGCTCTGCA 1500
 GAGCAGGAAA CATTGCTCGT ATATGTCTCA GGTCCCTGCA GGGCCAAGCA CAGTACCTCG 1560
 CTCTTGCGAG GTACTCAGCG AATGAATGCT GTATATGTTG GGTGCAAGT TCCCTACTTC 1620
 CTGTGACTTC AGCTCTGTTT TACAATAAAA TCTTGAATAA GCCTAAAAA AAAAAAAA 1680
 AAAAAAAA AAAAAAAA AAAAAAAA AAAAAA

Seq ID NO: 493 Protein sequence
 Protein Accession #: NP_000568.1

1 11 21 31 41 51
 MALETICRPS GRKSSSKMQAF RIWDVNQKTF YLRNNQLVAG YLQGPVNLE EKIDVVPPIEP 60
 HALFLGIHGG KMCLSCVKSQ DETRLQLEAV NITDLSENRK QDKRFAPIRS DSGPTTSFES 120
 AACPGWFLCT AMEADQPVSL TMPDEGVMV TKFYFQEDE

Seq ID NO: 494 DNA sequence
 Nucleic Acid Accession #: NM_002081.1
 Coding sequence: 222..1898

1 11 21 31 41 51
 GGCTGCCCGA GCGAGCGTTC GGACCTCGCA CCCCGCGCGC CCCGCGCGCC CGCGCGCGCC 60
 GGCTTTTGTG GTCTCGGCTT CCTCGGCGCG CGCGCGCTCT GGACCGCGAG CCGCGCGCGC 120
 CGGAGACCTG GCTCTGCCCT TCGCGGCGCG GAACTGCGCA GGACCCGCGC AGGATCCGAG 180
 AGAGGCGCGG GCGGGTGGCC GGGGGCGCGG CGGCTCCGCG CATGGAGCTC CGGCGCGGAG 240
 GCTGGTGGCT GCTATGTGCG GCCGCGCGCG TGGTCCGCTG CGCCCGCGGG GACCCGCGCA 300
 GCAAGAGCGG GAGCTGCGCG GAGGTCCGCG AGATCTACGG AGCCAAGGGC TTCAGCCTGA 360
 GCGACGTGCC CAGGCGGAG ATCTCGGGTG AGCACCTGCG GATCTGTCCC CAGGGCTACA 420
 CCTGCTGCAC CAGCGAGATG GAGGAGAAC TGGCCAACCG CAGCCATGCC GAGCTGGAGA 480
 CCGGCTCCG GGACAGCAGC CGGCTCTGCG AGGCCATGCT TGGCACCAG CTGCGCAGCT 540
 TCGATGACCA CTTCAGCAC CTGCTGAACG ACTCGGAGCG GACGCTCGAG GCCACCTTCC 600
 CCGGCGCTT CCGAGAGCTG TACACGCGAG ACAGGAGGGC CTTCCGGGAC CTGTACTCAG 660
 AGCTGCGCCT GTACTACGCG GGTGCCAAC TGCACTTGGG GAGAGCGCTG GCCGAGTTCT 720
 GGGCCGCGCT GCTCGAGCGC CTCTCAAGC AGCTGCACCC CAGCTGCTG CTGCTGATG 780
 ACTACCTGGA CTGCTGGGCG AAGCAGGCGG AGGCGCTGCG GCCCTTCGGG GAGGCCCGGA 840
 GAGAGCTGCG CTTGCGGGCC ACCCGTGCTT TCGTGGCTGC TCGCTCCTTT GTGCGAGGCG 900
 TGGGCGTGGC CAGCGACGTG GTCCGGAAG TGGCTCAGGT CCCCCTGGGC CCGGAGTGCT 960
 CGAGAGCTGT CATGAAGCTG GTCTACTGTG CTCACTGCCT GGGAGTCCCC GGGCGCAGGC 1020
 CCTGCCCTGA CTATTGCCGA AATGTGCTCA AGGGCTGCCT TGCCAACAG CCGCAGCTGG 1080
 ACGCCGAGTG GAGGAACCTC CTGGACTCCA TGGTGTCTAT CACCGACAAG TTCTGGGGTA 1140
 CATCGGCTGT GGAGAGTGTC ATCGGAGCGG TGCACACGTG GCTGGCGGAG GCCATCAACG 1200
 CCCTCCAGGA CAACAGGGAC ACCTCAACGG CCAAGGTCAT CCAGGGCTGC GGGAAACCCA 1260
 AGGTCAACCC CAGGCGCCCT GGGCTGAGG AGAAGCGCGG CCGGGCGAAG CTGCGCCCGC 1320
 GGGAGAGGCC CACTTCAAGC ACCTGGGAGA AGCTGGTCTC TGAAGCCAAG GCCCAGCTCC 1380
 GCGACGTCCA GGACTTCTGG ATCAGCCTCC CAGGGACACT GTGCACTGAG AAGATGGCCC 1440
 TGAGCACTGC CAGTGATGAC CGCTGCTGGA ACGGGATGGC CAGAGGCGCG TACCTCCCCG 1500
 AGGTCAATGG TGACGGCTG GCCAACCAGA TCAACAACCC CGAGGTGGAG GTGGACATCA 1560
 CCAAGCCGGA CATGACCATC CGGCAGCAGA TCAATGCAGT GAAGATCATG ACCAACCAGC 1620
 TGGCAGCGC CTACAACGGC AACGACGTGG ACTTCCAGGA CGCCAGTGAC GACGGCAGCG 1680
 GCTCGGCGAG CGGTGATGCG TGTCTGGATG ACCTCTCGCG CCGGAAGGTC AGCAGGAAGA 1740
 GCTCCAGCTC CCGGACGCCC TTGACCCATG CCTTCCAGG CTTGTACAG CAGGAAGGAC 1800
 AGAAGACCTC GGCTGCCAGC TGCCCCCAGC CCCGACCTT CCTCTGCCC CTCTCTCTCT 1860
 TCCTGGCCCT TACAGTAGCC AGGCCCGCGT GCGGTAACCT GCCCAAGGC CCCAGGGACA 1920
 GAGGCCAAGG ACTGACTTTG CCAAAAATAC AACACAGACG ATATTTAATT CACTCAGCC 1980
 TGGAGAGGCC TGGGTGGGA CAGGGAGGGC CGGCGGCTCT GAGCAGGGGC AGGCGCAGAG 2040
 GTCCAGCCC CAGGCTGCG CTGCGCTGCC TTTCTGCCTT TTAATTTTGT ATGAGGTCTT 2100
 CAGGTCACTT GGGAGCCAGT GTGCCAAAA GCCATGTATT TCAGGACCT CAGGGGCACC 2160
 TCGGCTGCC TAGCCCTCCC CCCAGCTCCC TGACCCGCG CAGAAGCAGC CCTTCGAGGC 2220
 CTACAGAGGA GGCCTCAAAG CAACCCGCTG GAGCCCAAG CAGGCTGTG CCTTCTCTCC 2280
 CGCTCTCTCC CACTGGGACT CCCAGCAGAG CCCACCAAGC AGCCCTGGCC CACCCCCAGC 2340
 CCTCCAGAGA AGCCCCGAC GGGCTGTCTG GGTGTCCGCC ATCCAGGTC TGGCAGAGCC 2400
 TCTGAGATGA TGCATGATG CCTCCCTTCA GCGCAGGCTG CAGAGCCCG CCCACCTCTC 2460
 CTGCGCCCTT GAGGGCCCCC AGOGTCTGCA GGGTGAAGCC TGAGACAGCA CCACTGTCTGA 2520
 GGAATCTGAG GACTGTCTTC CCACAGACCC TGCACTGAGG GGCCTTCCAT GCGCAGATGA 2580
 GGGGCCACTG ACCCACTGCG GCTTCTGCTG GAGGAGGGGA AGCTGGGCCC AAAGGCCAGC 2640
 GGAGCAGCG TGGCTCTGCG CAATGTGGGC TGCCCCCTCG ACACAGGGCT CACAGGGCAG 2700
 GCCTTGCTGG GGTCCAGGGC TGTGGAGGA CCCCGAGGGC TGAGGAGCAG CCAGGACCCG 2760
 CAGGCTCCCA TCCTCAACCA GATCAGGAAC CAGGGCTCTC CTGTTCACGG TGACACAGGT 2820
 CAGGGCTCAG AGTGACCTCC GGCTGTACCC TGCTCAGAG GATGCTGGTG GCTGGTGAGA 2880
 CCCGCACTG CACACGGGAA TGCCCTAGGTC CCTTCCGAC CCAGCCAGCT GCACTGCAGG 2940
 GCACGGGGAG CCGATAGTT AGGGCTTTT CCAAAATGCG ATCCATTAC TGACACTTCC 3000
 TGTCTTGTG CATGGAGAGC TGTTCGCTCC TCCAGATGG CTTCCGAGGC CCGCAGGGCC 3060
 CACTTGGAG CCTGGTGACC TCCTGTCACT CACTGAGGCC ATCAGGGCCC TGCCCCAGGC 3120

WO 02/086443

PCT/US02/12476

CTGGACGGGC CCTCCTTCCC TCCTGTGCCC CAGCTGCCAG GTGGCCCTGG GGAGGGGTGG 3180
 TGTGGTGTGG GGAAGGGGTC CTGCAGGGGG AGGAGGACTT GGAGGGTCTG GGGGCAGCTG 3240
 TCCTGAACCG ACTGACCCCTG AGGAGGCCGC TTAGTGCTGC TTTGCTTTTC ATCACCGTCC 3300
 CGCACAGTGG ACGGAGGTCC CCGGTTGCTG GTCAAGTCCC CATGGCTTGT TCTCTGGAAC 3360
 CTGACTTTAG ATGTTTGTGG ATCAGGAGCC CCCAACACAG GCAAGTCCAC CCCATAATAA 3420
 CCTGCCAGT GCCAGGGTGG GCTGGGACT CTGGCACAGT GATGCCGGGC GCCAGGACAG 3480
 CAGCACTCCC GCTGCACACA GACGGCCTAG GGGTGGCGCT CAGACCCAC CCTACGCTCA 3540
 TCTCTGGAAG GGGCAGCCCT GAGTGGTCAC TGGTCAGGGC AGTGGCCAAG CCTGCTGTGT 3600
 CCTTCTCCA CAAGGTCCCC CCACGCTCA GTGTCAGCGG GTGACGTGTG TTCTTTTGTAG 3660
 TCCTTGTATG AATAAAGGC TGGAAACCTA AA

Seq ID NO: 495 Protein sequence
 Protein Accession #: NP_002072.1

1 11 21 31 41 51
 MELRARGMWL LCAAAALVAC ARGDPAKSKR SCGEVRQIYG AKGFSLSDPV QAEISGEHLR 60
 ICPQGYTCTT SEMENLANR SHALETALR DSSRVLQAML ATQLRSFDDH FQHLNDNSR 120
 TLQATPPGAP GELYTONARA FRDLYSELRL YVRGANLHLE BTLAEFWARL LERLFKQLHP 180
 QLLLPDDYLD CLGKQAEALR PFGEAPRELRL LRATRAFVAA RSPVQGLGVA SDVVRKVAQV 240
 PLGPECSRVA MKLVYCAHCL GVPGARPCPD YCRNVLKGL ANQADLDAEW RNLLDSMVL 300
 TDKFWGTSGV ESVGSVHTW LAEAINALQD NRDTLTAKVI QGCGNPKVNP QGPGPEEKRR 360
 RGKLAPRERP PSGTLEKLV EAKAQLRDVQ DFWSLPGTL CSEKMALSTA SDDRCWNGMA 420
 RGRYLPEVMG DGLANQINNP EVEVDITKPD MTIRQQIMQL KIMTNRLRSA YNGNDVDFQD 480
 ASDDGSGSGS

Seq ID NO: 496 DNA sequence
 Nucleic Acid Accession #: NM_001650.2
 Coding sequence: 40.1011

1 11 21 31 41 51
 GGGGCAGGCA ATGAGAGCTG CACTCTGGCT GGGGAAGGCA TGAGTGACAG ACCCACAGCA 60
 AGGCGGTGGG GTAAGTGTGG ACCTTTGTGT ACCAGAGAGA ACATCATGGT GGCTTTCAAA 120
 GGGGTCTGGA CTCAGCTTT CTGGAAGCA GTCAAGCGG AATTTCTGGC CATGCTTATT 180
 TTTGTTCTCC TCAGCTGGG ATCCACCATC AACTGGGGTG GAACAGAAAA GCCTTTACCG 240
 GTGACATGG TCTCATCTC CCTTTGCTTT GGAATCAGCA TTGCAACCAT GGTGCGATGC 300
 TTTGGCCATA ESAGCGGTGG CCACATCAAC CCTGCAGTGA CTGTGGCCAT GGTGTGCACC 360
 AGGAAGATCA GCATCGCCAA GTCTGTCTTC TACATCGCAG CCCAGTGCCT GGGGGCCATC 420
 ATTGGAGCAG GAATCCTCTA TCTGGTCACA CCTCCAGTG TGGTGGGAGG CCTGGGAGTC 480
 ACCATGGTTC ATGGAATCT TACCGCTGGT CATGGTCTCC TGGTTGAGTT GATAATCACA 540
 TTTCAATTGG TGTTTACTAT CTTTGCCAGC TGTGATTCCA AACGCAGTGA TGTCACTGGC 600
 TCAATAGCTT TAGCAATTGG ATTTTCTGTT GCAATTGGAC ATTTATTGTC AATCAATTAT 660
 ACTGTGTCCA GCATGAATCC CGCCGATCC TTTGGACCTG CAGTTATCAT GGGAAATTTG 720
 GAAAACCATT GGATATATTG GGTGGGCC ATCATAGGAG CTGTCTCTGC TGGTGGCCTT 780
 TATGAGTATG TCTCTGTGCC AGATGTTGAA TTCAAACGTC GTTTTAAAGA AGCCTTCAGC 840
 AAAGCTGCCC AGCAACAAAA AGGAAGCTAC ATGGAGGTGG AGGACAACAG GAGTCAGGTA 900
 GAGACGGATG ACCTGATTCT AAAACCTGGA GTGGTGCATG TGATTGACGT TGACCGGGGA 960
 GAGGAGAAAG AGGGGAAAGA CCAATCTGGA GAGGTATTGT CTTCAAGTATG ACTAGAAGAT 1020
 CGCACTGAAA CAGACAAGA CTCCTTAGAA CTGTCTCTAG ATTTCTCTCC ACCCATTAAG 1080
 GAAACAGATT TGTATATAAT TAGAAATGTG CAGGTTTGTG GTTTCATGTC ATATTACTCA 1140
 GTCTAAACAA TAAATATTTC ATAATTACA AAGGAGGAAC GGAAGAAACC TATTGTGAAT 1200
 TCCAAATCTA AAAAAAGAAA TATTTTAAAG ATGTTCTTAA GCAATATAT ACCTATTTTA 1260
 TCTAGTTACC TTTCATTAA AACCNAATTT AACCGTGTGT CAAGATTGGG TTAAGCTCTG 1320
 CCTGACAGAA CTCAAAGACA CGTCTATCAG CTTATTCTCT CTCTACTGGA ATATTGGTAT 1380
 AGTCAATTCT TATTTGAATA TTTATTCTAT TAAACTGAGT TTAACAATGG C

Seq ID NO: 497 Protein sequence
 Protein Accession #: NP_001641.1

1 11 21 31 41 51
 MSDRPTARRW GKCGPLCTRE NIMVAFKGVW TQAFWKAVTA EFLAMLIFVL LSLGSTINWG 60
 GTEKPLPVDV VLISLCFGLS IATMVQCFGH ISGGHINPAV TVAMVCTRKI SIAKSVFYIA 120
 AQCLGAIIGA GILYLVTPPS VVGLGVMTMV HGNLTAGHGL LVELIITFQL VFTIFASCD 180
 KRDTVTSIA LAIGFSVAIG HLPAINYGA SMNPARSFGP AVIMGNWENH WIYWVGPIIG 240
 AVLAGGLYEY VPCPDVEFKR RFKEAFSKAA QQTKGSYMEV EDNRSQVETD DLILKPGVVH 300
 VIDVDRGEEK KGKQSGEVL SSV

Seq ID NO: 498 DNA sequence
 Nucleic Acid Accession #: AB020684.1
 Coding sequence: 1..1744

1 11 21 31 41 51
 CCCCCTTGTC ATTAATACAT TAAAAAGATT CAATCTTTAC CCTGAGGTAA TTTTGGCCAG 60
 TTGGTACCGG ATTTATACCA AAATAATGGA CTTGATTGGT ATTCAAACCA AGATATGTTG 120
 GACGGTTACC AGAGGAGAAG GACTCAGTCC TATTGAAGC TGTGAAGGAT TGGGAGATCC 180
 TGCTTGCTTT TATGTTGCTG TAATTTTAT TTTAAATGGA CTAATGATGG CATTATTCTT 240
 CATATATGCG ACATATTTAA GTGGCAGCCG ATTAGGAGGC CTGGTTACAG TGTGTGCTT 300
 CTTTTCATCA CATGAGAGT GTACCCGTGT AATGTGGACA CCACCTCTCC GTGAAAGCTT 360
 CTCATATCCA TTTCTTGTTC TTCAGATGTT GCTAGTGACT CATATTCTCA GGGCTACAAA 420
 ACTTTATAGA GGAAGCTTGA TTGCACTCTG CATTTCCAAT GTATTTTCA TGCTTCCTTG 480
 GCAGTTTGCT CAGTTTGATC TTCTTACTCA GATTGCATCA TTATTGTCAG TATATGTTGT 540
 CGGGTACATT GATATATGTA AATTACGGA GATCATTAT ATACACATGA TTTCTCTTGC 600
 ACTTTGTTTT GTTTTGATGT TTGGGAACCT AATGTTATTA ACTTCTTATT ATGCTTCTTC 660
 TTTGTAATT ATTTGGGGTA TTCTGGCAAT GAAACCACAT TTCTGAAAA TAAATGTATC 720

5
10
15
20
25
30
35
40
45
50
55
60
65

TGAACCTAGT TTATGGGTTA TTCAAGGATG TTTTGGTTA TTTGGAAGTG TCATACTTAA 780
 ATACTTGACA TCTAAATTTT TTGGTATTGC AGATGACGCT CATATTGGCA ACTTACTAAC 840
 ATCAAATTC TTTAGTTATA AGGATTTTGA TACTTTATTG TATACCTGTG CAGCGGAGTT 900
 TGACTTTATG GAAAGAGAGA CTCCACTGAG ATACACAAAG ACATTTATTG TCCAGTTGT 960
 TCTTGTAGTG TTTGTTGCTA TTGTTAGAAA GATTATTAGT GATATGTGGG GTGTCTTAGC 1020
 TAAACAACAG ACACATGTAA GAAAACACCA GTTTGATCAT GGAGAGCTGG TTTACCATGC 1080
 ATTGCAATTG TTAGCATATA CAGCCCTTGG TATTTTAATT ATGAGACTAA AACTCTTCTT 1140
 GACACCACAC ATGTGTGTTA TGGCATCACT GATCTGCTCA AGACAGCTAT TTGGATGGCT 1200
 CTTTGGCAAA GTACATCTCG GTGCTATTGT GTTGTCTATA TTAGCAGCAA TGTCAATACA 1260
 AGGTTTCAGCA AATCTGCAAA CCCAGTGGAA TATTGTAGGG GAGTTCAGCA ATTTGCCCCA 1320
 AGAAGAACTT ATAGAATGGA TCAAAATATG TACTAAACCA GATGCAGTGT TTGCGGGTGC 1380
 CATGCCACAG ATGGCAAGTG TTAAGCTCTC TGCACCTCGG CCCATTGTGA ATCATCCACA 1440
 TTATGAAGAC GCAGGCTTGA GAGCCAGAAC AAAAATAGTA TACTCAATGT ATAGTCGGAA 1500
 AGCAGCCGAA GAAGTGAAGC GAGAACTGAT AAAGTTAAAA GTGAACATTG ACATTCTAGA 1560
 AGAGTCATGG TGTGTAAAGAA GATCCAAGCC TGGTTGCAGT ATGCCTGAAA TTTGGGATGT 1620
 AGAAGATCCT GCCAATCTAG GAAAACCTCC CTTATGTAAC CTCTTGGTGA AGGATTCCAA 1680
 ACCTCACTTC ACCACTGTAT TCCAGAACAG TGTTCACRAA GTCCTAGAAG TTGTAAGAAG 1740
 ATGACTGCTA CATGACCTGC TGCTACGGA GAACACTATC TGTAAATGGT TTAATGTTTT 1800
 CTAAAGTCAT GTAGTCTTCA TATCCCAAAA ACTTTTATAG GTAACCTGTT TCAAAATAGAA 1860
 AACGTTTTAT TTGGTCAATT TGAATGTCAT TCTAATTATA AAAATGACTT ACACCTTTAT 1920
 CAATTGGTAT GCGATTTCAAT GCACCCCTTA AAATTGCTA TGCAATGAG TATATGCTTG 1980
 TACTTGACTT TAATATTGTG GCTAAAGTGA GCAAAGCTAC CTGTATAAAG AAAACACAGT 2040
 GGGTTGTGAC AAGGATGACA TGAATAATCA GGACAATTCT GACAATGTAG GGGCTGATTT 2100
 TATAGTGTAA GAAGTATTA TGGCCCTTGC TTCTTTTTC TGCCCTCTGC TCTTGTCTTT 2160
 TGGACATTTT AGTGATTGTA AGTCTTCCG TCAATGTCAG CCCTGTCTAT AACTTGAGTT 2220
 ACAGTAGATT GCGCAGACAT GGAGTGTGTT CTATATAAAA CTATCTGTTT GTTTTACTTC 2280
 CTTGTGCGCT TTTTGTCTC TGTCTCTTG TTAATGAAGC TTTTCTGCCC CATTATTAAT 2340
 CCAAACTCTT GGACCTTGTG GTTAGGAAAT TCCCTTAACT TCCAGCCATA TGGCATTATC 2400
 GTGTCTCTCT CTCTCTCTCT CTCTCTCTCT CTCTCTCTCT CTCTCTCTCT TTTTCTGTCA 2460
 AATAAGTACT GTTACTACTT TTAGTTGCTT ATCAAGTACT TATCTTGGT TTTAAAAAAA 2520
 ATTAATGGTA TCTGATTTT TCTCATTTT AGCATTATTC AAATGTTTAT ATTTTAATAC 2580
 CTTTAAACCA CTTTAAAGTT TTTTCAATGT TAATTATAGT TTTAAGAAAA ACTATTTTGA 2640
 ACAACCCCAA ATATAGTGCA TCTAGAAACT AATGTATATT TGATTAGACA TCATTTTATAG 2700
 TGGAAACAGTA GACTGTAGTA CATGTAATTT TTTCTTTTAC TATTAAGATA CAATAAAAAA 2760
 TGACTAATTT TGCTGTCAAA AATGTAAAGA ATAATGATAA ATGGAGTTTT TTATATTTTA 2820
 CTTTAAAGAT TGCCTGTCTT TAATAAGACA AAGCCTTAAG CCTTATGTTA TAATTTTGGT 2880
 TCTAAAAACC ATCATTTCAG TATAAGGAAT AAGTATATTT CGTCTCTCTC TTTAGTTTTT 2940
 TTCTTCTAT TATTTTAT TTTGAAAAAT TTCTACACCT TCTTTGAATT CCTTGTATGA 3000
 ATTTTGTGTT CTTAGAAGTT AATTTGTGTG AAATGAGATT CTTCAAAACG ATGAAACCTC 3060
 ATAGCTCTGA GAAAGGTTTT TAGGGTTTTA AATCTTAAGC AAAGCGTGAC TATGGCTGAC 3120
 AGACTACACA TTTAATTATA CAGCTTCTCT TTCTTAAACCA CAGGCAGATT AACCTCATTG 3180
 TGGATTGTCC TTCAGACCTT AGTCTCAGG CATGTTTTCT GGTGCCCACT CCTGGAAGCC 3240
 GCTGTTCCCT TTCTACCTTC TTACCAGAGC CCAAGGGCAG GCCTGGTCCC GGGGAAGCAG 3300
 CAGCTTCTG ACATAAGTCA GCTGCAAGG CTGAGGAGTG TGCCCTCAGA GAAGCACCGC 3360
 CCCCCAGTCT TGTGCCAGCG CCTAGAGCCG CAGCTCCAGG GGATGCTCCT TCCTGGAGG 3420
 CAGCCACGGA GAGGAGCTCT GGCAGCGTTC TTCAGATTG TGGCCACTGT TTCTCATTG 3480
 CTGTTGAGCT GTTTTATTT CTAGGCTTT TGCTAGTTTT AGAAAAATAGG GAAGCAGCCC 3540
 TTGATTGTG GATTAAAGC AACATTGAG CGATGATGCA CAACAGTCCA GGAATAATGG 3600
 CGGTGGACAC TTGAGGCTGA GATGGGAGT TGACATGAGC AGGAGAGGG AGGTGCGGCG 3660
 TGCTTATCTG TGATTGTGTC TCACCTGAGT GTGGCTGATT GTGTACATCC AGCAGTTACA 3720
 ATTTTAAAAA ATTTTATTT TACATTTATT TTATATTTT CTACCCCCCA GTAATTTCT 3780
 TCCAAAGAAG TTCACATGTA ATAAGTAGAA ATCTGTATA GGAATAAAGC ATTAATAATA 3840
 CTATTATAAG TGCTTCATT CTGGGAACC ATTAAGTA ATATAAATTA GCTTTTCCA 3900
 GAAGGATCCT TTTGTAGCAG TGTATTATGAA TGTAACCCCC AGCAAAATAT GGCTATATAT 3960
 TAGGGGAGCC AGTTTGGAGC AGAGGCCCTGA AGGTCCCTGC TATGCAGCCG TGGCCACAGC 4020
 TGCAGGCCCA AGCATGTGG AGCATCCACA CCTTTGATGG CAATGCAGAT TGGTAGCAGG 4080
 TTCCATAGGC GTACAAAAAC GTATTAAAGC TCAGTGTGTT GCATATTGTT AGCATTTACA 4140
 AATATTTTGG CTTTAGTATG AGGAAGGTAA GGATGGGCAA AGAAGCGATC AAAATAGCTA 4200
 TTGCTACAAC ATTTTCGAAA ACAAGTTGG GGCTGTATTT CTTTAAAAAG ATAAGCCTCT 4260
 AAAAAATGCTT GGCAAAAAAA ATATAGTGTT AAAATAGGCC AGTGATATTA ATGAGAAAAT 4320
 GAAAGTATGT ATCAGGAATA AAGTGATATT GCATAGGAGT ATGTATTTT TATGAATTTT 4380
 ATGCCAGTTG TTTACATGTA CTATATATGT TAAATTAATA AAAATCATGA GAAATG

Seq ID NO: 499 Protein sequence
 Protein Accession #: BAA74900.1

70
75
80

1 11 21 31 41 51
 | | | | |
 PLVINTLKRF NLYPEVILAS WYRIYTKIMD LIQIQTKICW TVTRGEGLSP IESCEGLGDP 60
 ACFFYVAVIF LNLMLMALFF IYGYLSGSR LGQLVTVLCF PFNHGECTRV MNTPLRESF 120
 SYFFLVQLML LVTHILRATK LYRGLIALC ISNVFFMLPW QFAQFVLLTQ IASLPAVVV 180
 GYIDICKLRK IYIHMISLA LCPVLMFGNS MLLTSYIASS LVIIWGILAM KPHFLKINVS 240
 ELSLWVIQGC FWFPGTVILK YLTSKIFGIA DDAHIGNLLT SKFPSYKDFD TLLYTCAAEF 300
 DFMEKETPLR YTKTLLPVV LVVFVAIVRK IISDMWGVLA KQTHVRKHQ FDHGLVYHA 360
 LQLLAYTALG ILIMRLKFL TPHMCMVASL ICSRQLFGWL FCKVHPGAIV FAILAAMSIQ 420
 GSANLQTOWN IVGEFSNLPQ EELIEWIKYS TKPDAVPAGA MPTMASVKLS ALRPIVNHPH 480
 YEDAGLRART KIVYSMSYRK AAEVVKRELI KLVNYYILE ESWCVRRSKP GCSMPEIWDV 540
 EDPANAGTFP LCNLLVKDSK PHFTTVFQNS VYKVLVVKE

Seq ID NO: 500 DNA sequence
 Nucleic Acid Accession #: NM_001276.1
 Coding sequence: 127..1278

85

1 11 21 31 41 51
 | | | | |
 AGTGGAGTGG GACAGGTATA TAAAGGAAGT ACAGGGCCTG GGAAGAGGCG CCTGTCTAGG 60
 TAGCTGGCAC CAGGAGCCGT GGGCAAGGGA AGAGGCCACA CCTGCGCCTG CTCTGCTGCA 120

5 GGCAGAAATGG GTGTGAAGGC GTCTCAAACA GGCTTTGTGG TCCTGGTGCT GCTCCAGTGC 180
 TGCTCTGCAT ACAAACTGGT CTGCTACTAC ACCAGCTGGT CCCAGTACCG GGAAGGCGAT 240
 GGGAGCTGCT TCCCAGATGC CCTTGACCGC TTCCTCTGTA CCCACATCAT CTACAGCTTT 300
 10 GCCAATATAA GCAACGATCA CATCGACACC TGGGAGTGA ATGATGTGAC GCTCTACGGC 360
 ATGCTCAACA CACTCAAGAA CAGGAACCCC AACCTGAAGA CTCTCTGTGC TGTGCGAGGA 420
 TGGAACTTTG GGTCTCAAAG ATTTTCCAAG ATAGCCTCCA ACACCCAGAG TCGCCGGACT 480
 TTCATCAAGT CAGTACCGCC ATTCCTGCGC ACCCATGGCT TTGATGGGCT GGACCTTGCC 540
 TGGCTCTACC CTGGACGGAG AGACAAACAG CATTTTACCA CCCTAATCAA GGAAATGAAG 600
 GCGAATTTA TAAAGGAAGC CCAGCCAGGG AAAAAGCAGC TCCTGCTCAG CGCAGCACTG 660
 15 TCTGCGGGGA AGGTCAACAT TGACAGCAGC TATGACATTG CCAAGATATC CCAACACCTG 720
 GATTTTCATTA GCATCATGAC CTACGATTTT CATGGAGCCT GGCCTGGGAC CACAGGCCAT 780
 CACAGTCCCC TGTTCGAGG TACGAGGAT GCAAGTCTCTG ACAGATTGAG CAACACTGAC 840
 TATGCTGTGG GGTACATGTT GAGGCTGGGG GCTCCTGCCA GTAAGCTGGT GATGGGCATC 900
 CCCACCTTGG GGAGGAGCTT CACTCTGGCT TCTTCTGAGA CTGGTGTGG AGCCCCAATC 960
 20 TCAGGACCGG GAATTCAGG CCGGTTCAAC AAGGAGGAGG GGACCTTTCG CTACTATGAG 1020
 ATCTGTGACT TCCTCCGGGG AGCCACAGTC CATAGAACC TCGCCAGCA GGTCCCTAT 1080
 GCCACCAAGG GCAACCGATG GGTAGGATAC GACGACCAGG AAAGCGTCAA AAGCAAGGTG 1140
 CAGTACCTGA AGGATAGGCA GCTGGCAGGC GCCATGGTAT GGGCCCTGGA CCTGGATGAC 1200
 TTCCAGGGCT CCTTCTGCGG CCAGGATCTG CGCTTCCCTC TCACCAATGC CATCAAGGAT 1260
 25 GCACTCGCTG CAACGTAGCC CTCTGTCTG CACACAGCAC GGGGGCCAA GATGCCCCGT 1320
 CCCCTCTGCT TCCTCAGCGG CCGGAGCCTT GATCACCTGC CCTGCTGAGT CCCAGGCTGA 1380
 GCCTCAGTCT CCCTCCCTTG GGGCCTATGC AGAGGTCCAC AACACACAGA TTTGAGCTCA 1440
 GGCCTGGTGG CACAGAGAGT AGGGATGGGG CTGTGGGGAT AGTGAGGCAT CGCAATGTAA 1500
 GACTCGGGAT TAGTACACAC TTGTTGATGA TTAATGGAAA TGTTTACAGA TCCCAAGCC 1560
 30 TGGCAAGGGA ATTTCTCAA CTCCTGCCCC CCTAGCCCTC CTTATCAAAG GACACCATTT 1620
 TGGCAAGCTC TATKISQHLDF ISIMTYDFHG AWRGTTGHHS PLFRGQEDAS PDRFSNTDYA 1680
 TACCCCTGTC AAAGCCAGCT TGAACCTTC ACTTAGGAAC GTAATCGTGT CCCCTATCCT 1740
 ACTTCCCTTT CCTAATTCAC CAGCTGCTCA ATAAAGTACA AGAGTTTAACT AGTGTGTTGG 1800
 CGCTTGTGCT TGGTCTATCT TTGAGCGCCC ACTAGACCCA CTGGACTCAC CTCCCCCATC 1860
 35 TCTTCTGGGT TCCTTCTCT GAGCCTTGGG ACCCCTGAGC TTGCAGAGAT GAAGGCCGCC 1920
 ATGTT

Seq ID NO: 501 Protein sequence
 Protein Accession #: NP_001267.1

35 1 11 21 31 41 51
 | | | | |
 40 MGVKASQTGF VVLVLLQCCS AYKLVCYVTS WSQYREGDGS CFPDLDRLPL CTHIIYSPAN 60
 ISNDHIDTWE WNDVLYGML NTLKRNPNL KTLISVGGWN FGSQRFKIA SNTQSRRTPI 120
 KSVPPFLRTH GFDGLDLAWL YPGRRDQHF TLLIKEMKAE FIKEAQPGKK QLLLSAALSA 180
 45 GKVTIDSSVD IAKISQHLDF ISIMTYDFHG AWRGTTGHHS PLFRGQEDAS PDRFSNTDYA 240
 VGYMLRLGAP ASKLVMIPT FGRSFTLASS ETGVGAPISG PGIPGRFKE AGTLAYYEIC 300
 DFLRGATVHR TLGQVVPYAT KGNQWVGYDD QESVSKSVQY LKDRQLAGAM VWALDLDLDFQ 360
 GSFCGQDLRF PLTNAIKDAL AAT

Seq ID NO: 502 DNA sequence
 Nucleic Acid Accession #: NM_006474.1
 Coding sequence: 181..669

50 1 11 21 31 41 51
 | | | | |
 55 GCTGCCTAGG GTCTGGAAG CTGCGGCACC CTCCTCTCC GGGGCTCCTG CTCCCACCCC 60
 TCGGCGCCCC CCACCGTCCG GCTCCTCCAG GCTGGGCTG TGGCCGCGGT GCTTTTAATT 120
 TTCCCCCAGC TCAGAATCTT GCTGCTCGGC CCCAGGAGA GCAACAACTC AACGGGAACG 180
 60 ATGTGGAAGG TGTCAGCTCT GCTCTTCGTT TTGGGAAGCG CGTCGCTCTG GGTCTGGCA 240
 GAAGGAGCCA GCAACAGGCA GCACAGGAT GACACTGAGA CTACAGGTTT GGAAGGCGGC 300
 GTTGCCATGC CAGGTGCCGA AGATGATGTG GTGACTCCAG GAACCAAGCA AGACCGCTAT 360
 AAGTCTGGCT TGACCACTCT GGTGGCAACA AGTGTCAACA GTGTAACAGG CATTGCTATC 420
 65 GAGGATCTGC CACTTCAGA AAGCACAGTC CACGCGCAAG AACAAAGTCC AAGCGCCACA 480
 GCCTCAAAGC TGGCCACCAG TCACTCCACG GAGAAAGTGG ATGGAGACAC ACAGACAACA 540
 GTTGAGAAAG ATGGTTGTG AACAGTGACC CTGGTTGGAA TCATAGTTGG GGTCTTACTA 600
 GGCATCGGTT TCATTTGTGG AATCATCGTT GTGGTTATGC GAAAAATGTC GGAAGGATAC 660
 TCGCCCTAAA GAGCTGAAG GTTACGCCCT GCTTGCCAAC GTGCTTTAAA AAAAGACCGT 720
 70 TTCTGACTCT GTGGCCCTGT CCTGAGCTC GTGGGAGAA GATGACCTG GGAACATTG 780
 CGGGCCCAAT CAGATCCAC GGTGACTTTC CGTTTGCCA ATTAACCGAG GAAAGACCTT 840
 TCACAGATT TGGTCTTAA ACTTT

Seq ID NO: 503 Protein sequence
 Protein Accession #: NP_006465.1

70 1 11 21 31 41 51
 | | | | |
 75 MWKVSALLFV LGSASLWVLA EGASTGQPED DTETTGLEGG VAMPGAEDDV VTPGTSEDY 60
 KSLGTLVAT SVNSVTGIRI EDLPTSESTV HAQEQSPSAT ASNVATSHST EKVGDGTQTT 120
 VEKDLSTVT LVGIIVGVLL AIGFIGIIV VVMRKMSGRY SP

Seq ID NO: 504 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 62..895

80 1 11 21 31 41 51
 | | | | |
 85 CACTGCTCTG AGAATTTGTG AGCAGCCCTT AACAGGCTGT TACTTCACTA CAACTGACGA 60
 TATGATCATC TTAATTTACT TATTTCTCTT GCTATGGGAA GACACTCAAG GATGGGGATT 120
 CAGGATGGA ATTTTTCATA ATCCATATG GCTTGAACGA GCAGCCGGTG TGTACCACAG 180
 AGAAGCACGG TCTGGCAAT ACAAGCTCAC CTACGCAGAA GCTAAGGCGG TGTGTGAATT 240
 TGAAGGCGGC CATCTCGCAA CTTACAAGCA GCTAGAGGCA GCCAGAAAAA TTGGATTTC 300

5	TGCTGTGCT	GCTGGATGGA	TGGCTAAGGG	CAGAGTTGGA	TACCCCATTTG	TGAAGCCAGG	360
	GCCCAACTGT	GGATTTGGAA	AAACTGGCAT	TATTGATTAT	GGAATCCGTC	TCAATAGGAG	420
	TGAAAGATGG	GATGCCTATT	GCTACAACCC	ACACGCAAG	GAGTGTGGTG	GCGTCTTTAC	480
	AGATCCAAAG	CAAAATTTTA	AATCTCCAGG	CTTCCCAAT	GAGTACGAAG	ATAACCAAAAT	540
	CTGCTACTGG	CACATTAGAC	TCAAGTATGG	TCAGCGTATT	CACCTGAGTT	TTTAGATT	600
	TGACCTTGAA	GATGACCCAG	GTTGCTTGGC	TGATTATGTT	GAAATATATG	ACAGTTACGA	660
	TGATGTCCAT	GGCTTTTGGG	GAAGATACTG	TGGAGATGAG	CTTCCAGATG	ACATCATCAG	720
	TACAGGAAT	GTCATGACCT	TGAAGTTTCT	AAGTGATGCT	TCAGTGACAG	CTGGAGGTTT	780
10	CCAAATCAAA	TATGTTGCAA	TGGATCCTGT	ATCCAAATCC	AGTCAAGGAA	AAAATACAAAG	840
	TACTACTTCT	ACTGGAAATA	AAAACCTTTT	AGCTGGAAGA	TTTAGCCACT	TATAAAAAAA	900
	AAAAAAAGGA	TGATCAAAAC	ACACAGTGT	TATGTTGGAA	TCTTTTGGAA	CTCCTTTGAT	960
	CTCACTGTTA	TTATTAACAT	TTATTTATTA	TTTTTCTAAA	TGTGAAAGCA	ATACATAAAT	1020
	TAGGGAAT	TGGAAATAT	AGGAACTTT	AAACGAGAAA	ATGAAACCTC	TCATAATCCC	1080
	ACTGCATAGA	TATGTTGCAA	TGTAACATTT	TCATATTTTT	TTCITTCAGT	CATTTTCTA	1140
15	TTTGTGGTAT	ATGATATAT	GTACCTATAT	GTATTGTCAT	TGAAATTTT	GGAATCCTGC	1200
	TCATGTACA	GTTTGTATT	ATACCTTTTA	AATCTTGAAC	TTTATAAACA	TTTTCTGAAA	1260
	TCATTGATTA	TTCTACAAA	ACATGATTTT	AAACAGCTGT	AAAATATCT	ATGATATGAA	1320
	TGTTTATGC	ATTATTTAAG	CCTGTCTCTA	TTGTTGGAAT	TTGAGGTCAT	TTTCATAAAT	1380
20	ATTGTTGCAA	TAAATATCCT	TGAACACACA	AAAAAAA	AA		

Seq ID NO: 505 Protein sequence
Protein Accession #: Eos sequence

25	1	11	21	31	41	51	
	MILLIYLFLL	LWEDTQGWGF	KDGIFHNSIW	LERAAAGVYHR	EARSQKYKLT	YAEAKAVCEP	60
	EGGHLATYKQ	LEAARKIGFH	VCAAGWMKAG	RVGYPIVKPG	PNCGFGKTGI	IDYGIRLNRS	120
	ERWDAYCYNP	HAKECGGVFT	DPKQIFKSPG	FPNEYEDNQI	CYWHIRLKYG	QRIHLSFLDF	180
30	DLEDDPGCLA	DYVEIYDSYD	DVHGFVGRYC	GDELDDIIS	TGNVMTLKFL	SDASVTAGGF	240
	QIKYVAMDFV	SKSSQGNKTS	TTSTGNKNFL	AGRFPSHL			

Seq ID NO: 506 DNA sequence
Nucleic Acid Accession #: NM_007115.1
Coding sequence: 69..902

35	1	11	21	31	41	51	
	GAATTCGCAC	TGCTCTGAGA	ATTTGTGAGC	AGCCCCCTAAC	AGGCTGTTC	TTCACTACAA	60
	CTGACGATAT	GATCATCTTA	ATTACTTAT	TTCTCTTGCT	ATGGGAAGAC	ACTCAAGGAT	120
40	GGGGATTCAA	GGATGGAATT	TTTCATAACT	CCATATGGCT	TGAACGAGCA	GCCGGTGTGT	180
	ACCACAGAGA	AGCAGCGTCT	GGCAAAATACA	AGCTCACCTA	CGCAGAAAGT	AAGGCGGTGT	240
	GTGAATTTGA	AGGCGGCCAT	CTCGCAACTT	ACAAGCAGCT	AGAGGCAGCC	AGAAAAATTG	300
	GATTTTCATGT	CTGTGCTGCT	GGATGGATGG	CTAAGGCGAG	AGTTGGATAC	CCCATTGTGA	360
	AGCCAGGGCC	CAACTGATGA	TTTGGAAAAA	CTGGCATTAT	TGATTATGGA	ATCCGCTCTCA	420
45	ATAGGAGTGA	AAGATGGGAT	GCCTATTGCT	ACAACCCACA	CGCAAAAGAG	TGTGGTGGCG	480
	TCTTTACAGA	TCCAAGCGA	ATTTTAAAT	CTCCAGGCTT	CCCAAAATGAG	TACGAAGATA	540
	ACCAATCTG	CTACTGGCAC	ATTAGACTCA	AGTATGGTCA	GCGTATTAC	CTGAGTTTTT	600
	TAGATTTTGA	CCTTGAAGAT	GACCCAGGTT	GCTTGGCTGA	TTATGTTGAA	ATATATGACA	660
50	GTTACGATGA	TGTCATGGC	TTTGTGGGAA	GATACTGTGG	AGATGAGCTT	CCAGATGACA	720
	TCATCAGTAT	AGGAAATGTC	ATGACCTTGA	AGTTTCTAAG	TGATGCTTCA	GTGACAGCTG	780
	GAGGTTTCCA	AATCAATAT	GTTGCAATGG	ATCCTGTATC	CAAAATCCAGT	CAAGGAAAAA	840
	ATACAGTATC	TACTTCTACT	GGAATAAAAA	ACTTTTATAGC	TGGAAGATTT	AGCCACTTAT	900
	AAAAAAATAA	AAGATGTATC	AAAAACACACA	GTGTTTATGT	TGGAATCTTT	TGGAACCTCCT	960
55	TTGATCTCAC	TGTTATTATT	AACATTATT	TATTATTTTT	CTAAATGTGA	AAGAAATACA	1020
	TAAATTTAGG	AAAATTTGGA	AATATAGGAA	ACTTTAAAGC	AGAAAAATGAA	ACCTCTCATA	1080
	ATCCCACTGC	ATAGAAATGA	CAAGCGTTAA	CATTTCATTA	TTTTTTCTT	TCAGTCATT	1140
	TTGTATTGTT	GGTATATGTA	TATATGTACC	TATATGTATT	TGCATTTGAA	ATTTTGAAT	1200
	CCTGCTCTAT	GTACAGTTT	GTATTATCT	TTTAAATCT	TGAACCTTAT	GAACATTTTC	1260
60	TGAAATCATT	GATTATTTCTA	CAAAAACATG	ATTTTAAACA	GCTGTAAAT	ATTCTATGAT	1320
	ATGAATGTTT	TATGATTTAT	TTAAGCCTGT	CTCTATTGTT	GGAATTTTCAG	GTCAATTTTCA	1380
	TAAATATTGT	TGCAATAAAT	ATCCTTCGGA	ATTC			

Seq ID NO: 507 Protein sequence
Protein Accession #: NP_009046.1

65	1	11	21	31	41	51	
	MILLIYLFLL	LWEDTQGWGF	KDGIFHNSIW	LERAAAGVYHR	EARSQKYKLT	YAEAKAVCEP	60
	EGGHLATYKQ	LEAARKIGFH	VCAAGWMKAG	RVGYPIVKPG	PNXXFGKTGI	IDYGIRLNRS	120
70	ERWDAYCYNP	HAKECGGVFT	DPKRIKSPG	FPNEYEDNQI	CYWHIRLKYG	QRIHLSFLDF	180
	DLEDDPGCLA	DYVEIYDSYD	DVHGFVGRYC	GDELDDIIS	TGNVMTLKFL	SDASVTAGGF	240
	QIKYVAMDFV	SKSSQGNKTS	TTSTGNKNFL	AGRFPSHL			

Seq ID NO: 508 DNA sequence
Nucleic Acid Accession #: NM_001044.1
Coding sequence: 129..1991

80	1	11	21	31	41	51	
	ACCGCTCCGG	AGCGGGAGGG	GAGGCTTCGC	GGAACGCTCT	CGGCGCCAGG	ACTCGGTGTC	60
	AAAGCCAGG	CCCGGGCGGC	CAGACCAAGA	GGGAAGAAGC	ACAGAAATCC	TCAACTCCCA	120
	GTGTGCCAT	TAGTAAGAGC	AAATGCTCCG	TGGGACTCAT	GTCTTCCGTG	GTGGCCCCGG	180
	CTAAGGAGCC	CAATGCCGTG	GGCCCGAAGG	AGGTGGAGCT	CATCCTTGTG	AAGGAGCAGA	240
85	ACGGAGTGCA	GTCACACAGC	TCCACCTCTA	CCAACCCCGG	CGAGAGCCCC	GTGGAGGCC	300
	AGGATCGGGA	GACCTGGGGC	AAGAAGATCG	ACTTTCCTCT	GTCGCTCATT	GGCTTTGCTG	360
	TGGACCTGGC	CAACGTCTGG	CGGTTCCCT	ACCTGTGCTA	CAAAAAATGGT	GGCGGTGCTT	420

5	TCCCTGGTCCC	CTACTGTGTC	TTTATGGTCA	TTGCTGGGAT	GCCACTTTTC	TACATGGAGC	480
	TGGCCCTCGG	CCAGTTCAAC	AGGGAAGGGG	CCGCTGGTGT	CTGGAAGATC	TGCCCCATAC	540
	TGAAAGGTGT	GGGCTTCACG	GTTCATCTCA	TCTCACTGTA	TGTGGGCTTC	TTCTACAACG	600
	TCATCATCGC	CTGGGCGCTG	CACATCTCTT	TCTCTCTCTT	CACCACGGAG	CTCCCTGGGA	660
	TCCACTGCAA	CAACTCTCTG	AACAGCCCCA	ACTGCTCGGA	TGCCCATCCT	GGTGACTCCA	720
	GTGGAGACAG	CTCGGCGCTC	AACGACACTT	TTGGGACCAC	ACCTGCTGCC	GAGTACTTTG	780
	AACGTGGCGT	GCTGCACCTC	CACCAGAGCC	ATGGCATCGA	CGACTGTGGG	CCTCCGCGGT	840
	GGCAGCTCAC	AGCCTGCTG	GTGCTGGTCA	TCGTGCTGCT	CTACTTCAGC	CTCTGGAAGG	900
10	GGGTGAAGAC	CTCAGGGAAG	GTGGTATGGA	TCACAGCCAC	CATGCCATAC	GTGGTCTCTA	960
	CTGCCCTGCT	CCTGCGTGGG	GTCAACCTCC	CTGGAGCCAT	AGACGGCATC	AGAGCATACC	1020
	TGAGCGTTGA	CTTCTACCGG	CTCTGCGAGG	CGTCTGTTTG	GATTGACGCG	GCCACCCAGG	1080
	TGTGCTTCTC	CCTGGGCGTG	GGGTTGCGGG	TGCTGATCGC	CTTCTCCAGC	TACAACAAGT	1140
	TCACCAACAA	CTGCTACAGG	GACGCGATTG	TCACCACCTC	CATCAACTCC	CTGACGAGCT	1200
	TCTCTCTCCG	CTTGGTCTGC	TTCTCTCTCC	TGGGGTACAT	GGCACAGAAG	CACAGTGTGC	1260
15	CCATCGGGGA	CGTGCCCAAG	GACGGGCCAG	GGCTGATCTT	CATCATCTAC	CCGGAAGCCA	1320
	TGCGCACGGT	CCCTCTGTCC	TACGCTGGG	CCGTGGTCTT	CTTCATCATG	CTGCTCACCC	1380
	TGGGTATCGA	CAGCGCCATG	GGTGGTATGG	AGTCAGTGAT	CACCGGGCTC	ATCGATGAGT	1440
	TCAGCCTGCT	GCACAGACAC	CGTGAGCTCT	TCACGCTCTT	CATCGTCTCT	GCGACCTTCC	1500
20	TCCTGTCCCT	CTTGTGCTGC	ACCAACGGTG	GCATCTACGT	CTTCACGCTC	CTGGACCATC	1560
	TTGCAGCCGG	CACGTCCATC	CTCTTTGGAG	TGCTCATCGA	AGCCATCGGA	GTGGCTTGGT	1620
	TTCTATGGTG	TAGGCTGGTC	AGCGACGACA	TCCAGCAGAT	GACCGGGCAG	CGGCCACAGG	1680
	TGTACTGGCG	GCTGTGCTGG	AAGCTGGTCA	GCCCTGCTTT	TCTCTGTGTC	TGGTCTGTGG	1740
	TCAGCATTGT	GACCTTCAGA	CCCCCCCAC	ACGGAGCCTA	CATCTTCCCC	GACTGGGCCA	1800
25	ACGCGCTGGG	CTGGGTCTATC	GCCACATCCT	CCATGGCCAT	GGTGCCCATC	TATGCGGCTC	1860
	ACAAGTTCTG	CAGCTGCGCT	GGGTCTCTTC	GAGAGAAACT	GGCTACGCCC	ATTGCAACCG	1920
	AGAAGGACCG	TGAGCTGTGG	GACAGAGGGG	AGGTGCGCCA	GTTACGCTCT	CGCCACTGGT	1980
	TCAGGTGTGA	GAGGAGCAG	AGACGAAGAC	CCCAGGAAGT	CATCTGCAA	TGGGAGAGAC	2040
	ACGAACAAAC	CAAGGAATC	TAAGTTTCGA	GAGAAAGGAG	GGCAACTTCT	ACTCTCAAC	2100
30	CTCTACTGAA	AACACAAACA	ACAAAGCAGA	AGACTCTCT	CTTCTGACTG	TTTACACCTT	2160
	TCGGTGCCGG	GAGCGCACCT	CGCGGTGTCT	TGTGTGTGCT	TAATAACGAC	GTAGATCTGT	2220
	GCAGCGAGCG	CACCCCGGTT	GTGTCTCTCT	CAGGGCAGAA	AAACGCTCTA	CTTCATGCTG	2280
	TCTGTGTGAG	GCTCCCTCCC	TCCCTGTCTC	CTGCTCCCGG	CTCTGAGGCT	GCCCCAGGGG	2340
	CACGTGTGTT	TCAGGCGGGG	ATCACGATCC	TTGTAGACGC	ACCTGCTGAG	AATCCCGCTG	2400
35	CTCACAGTAG	CTTCTAGAGC	CATTACTTTT	GCCCATATTA	AAAAGCCAAG	TGCTCTGCTT	2460
	GGTTTAGCTG	TGCAGAAAGT	GAAATGGAGG	AAACACAA	TTCTGCAAA	GTCTTTTCCC	2520
	GATGCGTGGC	TCCGAGCAGA	GGCGTAAAT	TGAGCGTTCA	GTTGACACAT	TGCACACACA	2580
	GTCTGTTTCA	AGGCATTGGA	GGATGGGGGT	CCTGGTATGT	CTCACCAGGA	AATTCTGTTT	2640
	ATGTTCTTGC	AGCAGAGAGA	AATAAACTC	CTTGAAACCA	GCTCAGGCTA	CTGCCACTCA	2700
40	GGCAGCCTGT	GGGTCTTGT	GGGTAGGGA	ACGGCTGAG	AGGAGCGTGT	CCTATCCCCG	2760
	GACGATGCA	GGGCCCCCAG	AGGAGCGTGT	CCTATCCCCG	GACGATGCA	GGGCCCCCAG	2820
	AGGAGCATGT	CTATCCCTCT	GACGATGCA	GGGCCCCCAG	AGGAGCGTGT	ACTACCCAG	2880
	AACGATGCA	GGGCCCCCAG	AGGAGCGTGT	ACTACCCAG	GACGATGCA	GGGCCCCCAG	2940
	TGGAGCGTGT	ACTACCCAG	GACGATGCA	GGGCCCCCAG	AGGAGCGTGT	CCTATCCCCG	3000
45	GACCGGACGC	ATGCGGGGCC	CCCACAGGAG	CGTGTACTAC	CCCAGGACGC	ATGCGGGGCC	3060
	CCCACAGGAG	CGTGTACTAC	CCCAGGATGC	ATGCGGGGCC	CCCACAGGAG	CGTGTACTAC	3120
	CCCAGGACGC	ATGCGGGGCC	CCCAGGATGC	CAGCGCTGAG	ACCAACACTC	TGCTTGGCTG	3180
	TGAGCGGTGA	CCTCCAGGAA	GGGACCCAC	TGGAATTTTA	TTTCTCTCAG	GTGCGTGCCA	3240
	CATCAATAAC	AACAGTTTTT	ATGTTTTCGA	ATGGCTTTTT	AAAATCATAT	TTACTGTGTA	3300
50	ATCAAAACAA	ATTCAAGAA	GCAGTATCCG	CGAGCCTGCT	TGCTGATATT	GCAGTTTTTG	3360
	TTTACAGAA	TAATTAGCAA	TACTGAGTGA	AGGATGTTGG	CCAAAGCTG	CTTTCATAGG	3420
	CACACTGCCC	TCTGCCACTG	ACAGGAAAGT	GGATGCCATA	GTTTGAATTC	ATGCTTCAAG	3480
	TCGGTGGGCC	TGCTTACGTT	CTGCCCCAGG	GCAGGGGCCG	TGCAGGGCCA	GTGATGGCTG	3540
	TCCCTGTCNA	GTGAGCGTGG	GCTCCAGGGA	CTGGAGTGTG	ATGCTCGGTG	GGAGCCGTGA	3600
55	GCCTGTGAAC	TGCCAGGCGG	CTGCAGTTAG	CACAGAGGAT	GGCTTCCCCA	TTGCCTTCTG	3660
	GGGAGGGAGA	CAGAGGACGG	CTTCCCCATC	GCCTTCTGGC	CGCTGCAGTC	AGCACAGAGA	3720
	GCCTTCTCCC	CATTGCTTTC	TGGGAGGGGA	CACAGAGGAC	AGTTTCCCCA	TGCTTCTG	3780
	GTGTGTGAAG	ACAGCACAGA	GAGCGGCTTC	CCCATCGCCT	TCTGGGGAGG	GGCTCCGTGT	3840
	VTFRPFHYGA	YIFPDWANAL	TGCTGTGTGA	CCAATCTCTA	TTGAGCATCG	TGTGGGTCCC	3900
60	TAAGCACAAT	AAAAGACATC	CACAATGGAA	AAAAAAAAG	GAATTC		

Seq ID NO: 509 Protein sequence
Protein Accession #: NP_001035.1

65	1	11	21	31	41	51	
	MSKSKCSVGL	MSSVVAPAKE	FNAVGPKEVE	LILVKEQNGV	QLTSSTLTNP	RQSPVEAQDR	60
	ETWKKIDFL	LSVIGFAVDL	ANVWRFPYLC	YKNGGAFILV	PYLLFMVIAG	MPLFYMELAL	120
	GQFNREGAAG	VWKICPILKG	VGFTVILISL	YVGFYFNVII	AWALHYLFSS	FTTELFWIHC	180
70	NNSWNFPNCS	DAHPSDSSGD	SSGLNDTFGT	TPAAEYFERG	VHLHQSHGI	DDLGPFRWQL	240
	TACLVLVIVL	LYFSLWKGVK	TSGLVWNITA	TNPYVVLTLA	LLRGVTLPGA	IDGIRAYLSV	300
	DFYRLCEASV	WIDAATQVCF	SLGVGFGVLI	AFSSYNKFTN	NCYRDAIVTT	SINSLTSFSS	360
	GFVVFSLGY	MAQKHSVPIG	DVAKDGPGLI	FIYPEAIAT	LPLSSAAVAV	PFIMLLTLGI	420
	DSAMGMESV	ITGLIDEFQL	LHRHRELFTL	FIVLATFLLS	LFCVTNGGIY	VFTLLDHFAA	480
75	GTSLFVGLI	EAIGVAWFYQ	VGQFSDDIQQ	MTGQRPSLYW	RLCWKLVSFC	FLLFVVVSI	540
	VTFRPFHYGA	YIFPDWANAL	GWVIATSSMA	MVPIYAAKYF	CSLPGSFREK	LAYAIAPERD	600
	RELVDREGEV	QFTLRHNLKV					

Seq ID NO: 510 DNA sequence
Nucleic Acid Accession #: NM_001216.1
Coding sequence: 43..1422

85	1	11	21	31	41	51	
	GCCCCGTACAC	ACCGTGTGCT	GGGACACCCC	ACAGTCAGCC	GCATGGCTCC	CCTGTGCCCC	60
	AGCCCCCTGGC	TCCCTCTGTT	GATCCCGGCC	CCTGCTCCAG	GCCTCACTGT	GCAACTGCTG	120
	CTGTCACTGC	TGCTTCTGAT	GCCTGTCCAT	CCCCAGAGGT	TGCCCCGGAT	GCAGGAGGAT	180
	TCCCCCTTGG	GAGGAGGCTC	TTCTGGGGAA	GATGACCCAC	TGGCGGAGGA	GGATCTGCCC	240

AGTGAAGAGG ATTCAACCCAG AGAGGAGGAT CCACCCGGAG AGGAGGATCT ACCTGGAGAG 300
 GAGGATCTAC CTGGAGAGGA GGATCTACCT GAAGTTAAGC CTAATTCAGA AGAAGAGGGC 360
 TCCTGGAAGT TAGAGGATCT ACCTACTGTT GAGGCTCCTG GAGATCCTCA AGAACCCAG 420
 AATAATGCCC ACAGGGACAA AGAAGGGGAT GACCAGAGTC ATTGGCGCTA TGGAGGCGAC 480
 CGGCCCTGCG CCCGGGTGTC CCCAGCCTGC GCGGGCGGCT TCCAGTCCCC GGTGGATATC 540
 CGCCCCCAGC TCGCCGCTT CTGCCCGGCC CTGCCCGCCC TGGAACTCCT GGGCTTCCAG 600
 CTCCCGCGCG TCCAGAACT GCGCTGCGC AACAAATGGC ACAGTGTGCA ACTGACCCCTG 660
 CCTCTGGGCG TAGAGATGGC TCTGGGTCCC GGGCGGGAGT ACCGGGCTCT GCAGCTGCAT 720
 CTGCACTGGG GGGCTGCAGG TCGTCCGGGC TCGGAGCACA CTGTGGAAGG CCACCGTTTC 780
 CTTGCCGAGA TCCAGTGGT TCACCTCAGC ACCGCTTTG CCAGAGTTGA CGAGGCTTGG 840
 GGGCGCCCGG GAGGCTGGC CGTGTGGCC GCCTTTCTGG AGGAGGGCCC GGAAGAAAAC 900
 AGTGCCTATG AGCAGTTGCT GTCTCGCTG GAAGAAATCG CTGAGGAAGG CTCAGAGACT 960
 CAGGTCCCAG GACTGGACAT ATCTGCACTC CTGCCCTCTG ACTTCAGCG CTACTTCCAA 1020
 TATGAGGGGT CTCTGACTAC ACCGCCCTGT GCCCAGGGTG TCATCTGGAC TGTGTTTAAAC 1080
 CAGACAGTGA TGCTGAGTGC TAAGCAGCTC CACACCTCT CTGACACCTT GTGGGGACCT 1140
 GGTGACTCTC GGCTACAGT GAACCTCCGA GCGACGCAGC CTTTGAATGG GCGAGTGATT 1200
 GAGGCTCCTC TCCCTGCTGG AGTGGACAGC AGTCTCGGG CTGTGAGGCC AGTCCAGCTG 1260
 AATTCTCTGC TGGCTGCTGG TGACATCCTA GCCCTGGTTT TTGGCTCTCT TTTTGTCTGC 1320
 ACCAGCGTCG CTTTCTTGT GCAGATGAGA AGGCAGACA GAAGGGGAAC CAAAGGGGGT 1380
 GTGAGCTACC GCCCAGCAGA GGTAGCCGAG ACTGGAGCCT AGAGGCTGGA TCTTGGAGAA 1440
 TGTGAAGAG CAGCCAGAGG CATCTGAGG GAGCGCGGTA ACTGTCTGT CCTGCTCATT 1500
 ATGCCACTTC CTTTAACTG CCAAGAAATT TTTTAAATA AATATTTATA AT

Seq ID NO: 511 Protein sequence
 Protein Accession #: NP_001207.1

1 11 21 31 41 51
 MAPLCPSFWL PLLIPAPAPG LTVQLLSLL LLMPVHPQRL PRMQEDSPGL GSSGSEDPL 60
 GEEDLPSEED SPREDPPGE EDLPGEEDLP GEEDLPVVKP KSEEGSLKL EDLPTVEAPG 120
 DPQEPQNNAH RKEGDDQSH WRYGGDPFPP RVSPACAGRF QSPVDIRPQL AAPCPALRPL 180
 ELLGFQLPPL PELRLRNNGH SVQLTLPPGL EMALGPGRBY RALQLHLHWG AAGRPGSEHT 240
 VEGHRFPFAEI HVVHLSTAFR RVDEALGRPG GLAVLAFLF EGPEENSAYE QLSRLLEEIA 300
 EEGSETQVPG LDISALLPSD PSRYFYQYGS LTPPPCAQGV IWTVFNTQVM LSAKQLHTLS 360
 DTLWGPDSR LQLNFRATQP LNRGVIEASF PAGVDSPPRA AEPVQLNSCL AAGDILALVF 420
 GLFAVTSVA FLVQMRQRHR RGTGGSYSR PAEVAETGA

Seq ID NO: 512 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1..3978

1 11 21 31 41 51
 ATGTGGGGT AAGGACCCTA CCTTATCTCA GATCTGGACC AGCGAGGCGG GCGGAGATCC 60
 TTTGAGAAA GATATGACCC CAGCCTGAAG ACCATGATCC CAGTGCGACC CTGTGCAAGG 120
 TTAGCACCCA ACCCGGTGGA TGATGCCGGG CTACTCTCCT TCGCCACATT TTCTGCTC 180
 ACGCGGTGA TGGTGAAGG CTACCGGCAA AGGCTGACCG TAGACACCTT GCCCCATTG 240
 TCACATATG ACTCATCTGA CACCAATGCC AAAAGATTTC GAGTCTTTG GATGAAGAG 300
 GTAGCAAGGG TGGTCTCTGA GAAGGCTCT CTGAGCCACG TGGTGTGGA ATTCCAGAGG 360
 ACACGCGTGT TGATGGACAT CGTGGCCAAC ATCCTGTGCA TCATCATGGC AGCCATAGGG 420
 CCGACAGTTC TCATTACCA AATCCTCCAG CAGACTGAGA GGACCTCTGG GAAAGTCTGG 480
 GTTGGCATG GACTGTGAT AGCCCTTTT GCCACCGAGT TTACCAAAGT CTCTTTTGG 540
 GCCCTGCTCT GAGCCATCAA CTACCGCACG GCCATCCGGT TGAAGGTGGC GCTCTCCACC 600
 TTGTTTCTG AAAACCTAGT GTCCTTCAAG ACATTGACCC ACATCTCTGT TGGCGAGGTG 660
 CTCATATATG TGTCAGTGA TAGCTATCTT TGTGTTGAAG CTGCTTTGTT TTGCTCTTGG 720
 CCAGCCACCA TCCCGATCTT AATGGTCTTT TGTGCGCGT AGCCTTTTCT CATCTGCGG 780
 CCCACAGCTC TCATCGGGAT ATCAGTGTAT GTCATATTCA TACCCGTCCA GATGTTTATG 840
 GCCAAGCTCA ATTCACTTTT CCGAAGGTCA GCAATTTTGG TGACAGACAA GCGAGTTCAG 900
 ACAATGAATG AGTTTCTGAC CTGATCAGG CTGATCAAAA TGTATGCCCT GGAGAAATCT 960
 TTTACCAACA CTATCCAAGA TATAAGAAG AGGGAAGAA AATTACTGGA AAAAGCTGGA 1020
 TTTGTCAAAA GTGGAAACTC TGCCCTGGCC CCCATCGTGT CCACCATAGC CATCGTCTG 1080
 ACATTATCTT GCCACATCTT CCTGAGACGC AAATCACC CGCCGCTGGC ATTTAGTGTG 1140
 ATTGCCATGT TTAATGTAAT GAAGTTTCTC ATTGCAATCT TGCCCTTCTC CATCAAAGCA 1200
 ATGCGTGAAG CGAATGTCTC TCTAAGGAGA ATGAAGAAA TTCTCATAGA TAAAGCCCC 1260
 CCATCTTACA TCACCAACCC AGAAGACCCA GATACTGTCT TGCTTTAGC AATGCCACC 1320
 TTGACATGGG AGCATGAAGC CAGCAGGAAA AGTACCCCAA AGAAATTGCA GAACCAGAAA 1380
 AGGCATTATG GCAAGAAACA GAGGTGAGG GCATACAGTG AGAGGAGTCC ACCAGCCAAG 1440
 GGAGCCACTG GCCCAGAGGA GCAAAGTGAC AGCCTCAAAT CGGTTCTGCA CAGCATAAGC 1500
 TTTGTGGTGA GAAAGTTATG TCGTTATCCC GAAGCCGAGC TCCTGGCTTG GAGGTGGCCA 1560
 GCAGTGTGTT TGGGAGAAT CATCAGAGGA TACAGGCCTC ATGGATTTTC TGCTAAAGAC 1620
 AAGGATGAAT CTAGAAGGCT TCTTACTTGG CCCCAGAAG TGGATAGGAC TCAAAGGCA 1680
 GCCAAATACC TGGGGAAGAT CTGCGGAATA TGTGGGAATG TGGGAAGTGG AAAGAGCTCC 1740
 CTCCTTGCGC CTCTCTAGG ACAGATGAGC CTGCAGAAAG GGGTGGTGGC AGTCAATGGA 1800
 ACTTTGGCCT ACCTTTTACA GCAGGCATGG ATCTTTCATG GAAATGTGAG AGAAAAATA 1860
 CTCTTTGGAG AAAAGTATGA TCACCAAAGG TATCAGCACA CAGTCCGCTG CTGTGGCTC 1920
 CAGAAGGACC TGAGCAACCT CCCCTATGGA GACCTGACTG AGATTGGGGA GCGGGGCTC 1980
 AACCTCTCTG GGGGGCAGAG GCAGAGGATT AGCCTGGCCC GCGCTGTCTA CTCGACCGT 2040
 CAGCTCTACC TGCTGAGCA GACCTGTGCG GCGCTGAGCG CCCAGTGGG GAAGCAGCTC 2100
 TTTGAGGAGT GCATTAGAA GACGCTCAGG GGAAGACAG TCGTCTGCTG GACCCACCAG 2160
 CTACAGTTCT TAGAGTCTTG TGATGAAGTT ATTTTATTAG AAGATGAGA GATTGTGAA 2220
 AAGGGAACCC ACAAGGAGTT AATGGAGGAG AGAGGGCGCT ATGCAAACT GATTCAAC 2280
 CTGCGAGAGT TGCAGTTCAA GGATCCTGAA CACCTTTACA ATGCAGCAAT GGTGGAAGCC 2340
 TTCAAGGAGA GCCCTGCTGA GAGAGAGGAA GATGCTGGTA TAATCGGGA CTCTCTTCT 2400
 CTCTTCACTG TGTCTCTCTT CCTCTGATG ATTGGCAGCG CTGCTTCTAG CAATCTGTTG 2460
 CTGGGTCTCT GGTGAGACAA GGGCTACGG ATGACCTGTG GGGCCAGGG CAACAGGACC 2520
 ATGTGTGAGG TCGGCGCGGT GCTGGCAGAC ATCGGTGAGC ATGTGTACCA GTGGGTGTAC 2580
 ACTGCAAGCA TGGTGTCTAT GCTGGTGTG GCGTCACCA AAGGCTTCGT CTTCAACCAAG 2640

5
 10
 15
 20
 25

ACCCACTGA TGGCATCCTC CTCTCTGCAT GACACGGTGT TTGATAAGAT CTAAAGAGC 2700
 CCAATGAGTT TCTTTGACAC GACTCCCACT GGCAGGCTAA TGAACCGTTT TTCCAAGGAT 2760
 ATGGACGAGC TGGATGTGAG GCTGCCGTTT CACGACAGAG ACTTCTGCA GCAGTTTTTT 2820
 ATGGTGGTGT TTATTTCTGT GATCTTGGCT GCTGTGTTTC CTGCTGTCTT TTTAGTCGTG 2880
 GCCAGCCTTG CTGTAGGCTT CTTCATCTCT TTACGCATT TCCACAGAGG AGTCCAGGAG 2940
 CTCAGAAGG TGGAGAAATG CAGCCGGTCA CCTTGGTTCA CCCACATCAC CTCCTCCATG 3000
 CAGGGCCTGG GCATCATTC ACGCTATGGC AAGAAGGAGA GCTGCATCAC CTATACTTCA 3060
 TCCAAAGGCC TGTCAATTGC ATACATCATC CAGCTGAGCG GACTGCTCCA AGTGTGTGTG 3120
 CGAACGGGAA CAGAGACGCA AGCCAAATTC ACCTCCGTGG AGCTGCTCAG GGAATACATT 3180
 TCGACCTGTG TTCCTGAATG CACTCATCCC CTCAAAGTGG GGACCTGTCC CAAGGACTGG 3240
 CCCAGCTGTG GGGAGATCAC CTTCAAGAGC TATCAGATGA GATACAGAGA CAACACCCCC 3300
 CTTGTTCCTG ACAGCCTGAA CTTGAACATA CAAAGTGGGC AGACAGTCCG GATTGTGTGA 3360
 AGAACAGGTT CCGGAAAGTC ATCGTTAGGA ATGGCTTGTG TTCGTCTGGT GGAGCCAGCC 3420
 AGTGGCACAA TCTTTATTGA TGAGGTGGAT ATCTGCATT TCAAGCTTGA AGACCTCAGA 3480
 ACCAAGCTCA CTGTGATCCC ACAGGATCCT GTCCGTGTTG TAGGTACAGT AAGGTACAAC 3540
 TTGGATCCCT TTGAGAGTCA CACCGATGAG ATGCTCTGGC AGGTTCTGGA GAGAACATTG 3600
 ATGAGAGACA CAATAATGAA ACTCCAGAA AAATTACAGG CAGAAGTCAC AGAAAATGGA 3660
 GAAAACCTCT CAGTAGGGGA ACGTCAGCTG CTTTGTGTGG CCGAGCTCT TCTCCGTAAT 3720
 TCAAAGATCA TTCTCCTTGA TGAAGCCACC GCCTCTATGG ACTCCAAGAC TGACACCCCTG 3780
 GTTCAGAAAC CCATCAAAGA TGCCTCAAG GGCTGCACTG TGCTGACCAT CGCCACCCGC 3840
 GTCAACACAG TCTCAACTG CGATCACGTC CTGGTTATGG AAAATGGGAA GGTGATTGAG 3900
 TTTGACAAGC CTGAAGTCTT TGCAGAGAAG CCAGATTCTG CATTTGGCAT GTTACTAGCA 3960
 GCAGAAGTCA GATTGTAG

Seq ID NO: 513 Protein sequence
Protein Accession #: Eos sequence

30
 35
 40
 45
 50

1 11 21 31 41 51
 MVGEGPYLIS DLDQGRRRS FAERYDPSLK TMIPVRPCAR LAPNFVDDAG LLSFATFSWL 60
 TPVMVKGYRQ RLTVDTLPL STYDSSDNTA KRFRVLWDEE VARVGPEKAS LSHVVVKFQR 120
 TRVLMDIVAN ILCIIMAAG PTVLIHQILQ QTERTSGKVM VGIGLCIALF ATEFTKVFFW 180
 ALAWAINYRT AIRLKVAST LVFENLVSPK TLTHISVGEV LNILSSDSYS LFEALFCPL 240
 PATIPILMVF CAAYAPFILG PTALIGISV VIFIPVQPMF AKLNSAFRRS AILVTDKRVQ 300
 TMNEFLTICR LKMYAWKES FTNTIQDIRR RERKLEKAG FVQSGNSALA PIVSTIAIVL 360
 TLSCHILLRR KLTAPVAFSV IAFENVMPKS IALLPFSIKA MAEANVSLRR MKKILIDKSP 420
 PSYITQPEPD DTVLLANAT LTWEHEASRK STPKKLQNK RHLCKKQSE AYSESPPAK 480
 GATGPEEQSD SLKSVLHSIS FVVRKLCRYP EAQLLAWRP AVFVGRIIRG YRPHGFSAD 540
 KDESRRLLTW PQEVDRTQRA AKYLKILGI CGNVSGSKSS LLAALLGQM LQKGVVAVNG 600
 TLAYVQQAW IFHGNVRENI LFGKEYDHQR YQHTVRVCG LKQDLNLPYG DLTEIGERGL 660
 NLSGGQRQAR SLARAVSDR LQYLLDDPLS AVDAHVGHV FEECIKKTLR GKTVVLVTHQ 720
 LQFLBSCEEV ILLEDEGECE KGTHELMEE RGRYAKLIHN LRGLQFKDPE HLYNAAMVEA 780
 FKESPAEREE DAGIIGVLLS LFTVFLFLM IGSAAFSNWM LGLWLDKGSR MTCGPQGNRT 840
 MCEVGAVLAD IGQHVYQWVY TASMVFLVP GVTKEFVPTK TTLMASSSLH DTVFDKILKS 900
 PMSFPTDPTL GRLMNRFSDK MDELVDRLPF HAENFLQFP MVVFILVILA AVFPVLLV 960
 ASLAVGFFPL LRIFHRGQES LKVENVSRS PWFTHITSSM QQLGIHAYG KKECITYTS 1020
 SKGLSLSYII QLSGLLQVCV RTGTETQAKP TSVELLREYI STCVPECTHP LKVGTCPKDW 1080
 PSCGETFPD YQMRYRDNTP LVLDLNLNI QSGQTVGIVG RTGSGKSSLG MALFRLVEPA 1140
 SGTIFIDEVD ICILSLEDLR TKLTVIPQDP VLPVGTVRYN LDPFESHTDE MLWQVLERTF 1200
 MRDTIMKLEP KLQAEVTENG ENFSVGERQL LCVARALLRN SKIILLDEAT ASMDSKTDTL 1260
 VQNTIKDAFK GCTVLTIAHR LNTVLNCDHV LVMENGVKIE FDKPEVLAEK PDSAFAMLLA 1320
 AEVRL

Seq ID NO: 514 DNA sequence
Nucleic Acid Accession #: Z31560
Coding sequence: 1-966

60
 65
 70
 75

1 11 21 31 41 51
 CACAGCGCCC GCATGTACAA CATGATGGAG ACGGAGCTGA AGCCGCGCGG CCGCGAGCAA 60
 ACTTCGGGGG GCGGCGGGG CAACTCCACC GCGGCGGGG CCGGCGGCAA CCAGAAAAAC 120
 AGCCCGGACC GCGTCAAGCG GCCCATGAAT GCCTTCATGG TGTGGTCCCG CCGGCGAGCG 180
 CGCAAGATGG CCGAGAGAA CCCCAGATG CACAACTCGG AGATCAGCAA CGCCTGGGC 240
 GCGAGTGGG AACTTTTGTG GGAGACGGAG AAGCGGCGGT TCATCGACGA GGCTAAGCGG 300
 CTGCGAGCGC TGCACATGAA GGAGCACCGG GATTATAAAT ACCGCGCCCG GCGGAAAACC 360
 AAGACGCTCA TGAAGAAGGA TAAGTACACG CTGCCCGGGG GGCTGCTGGC CCGGCGCGGC 420
 AATAGCATGG CGAGCGGGGT CCGGGTGGGC GCGGCGCTGG GCGGCGGGCT GAACGAGCGC 480
 ATGGACAGTT ACGCGACAT GAACGGCTGG AGCAACGGCA GCTACAGCAT GATGCAGGAC 540
 CAGCTGGGCT ACCCGAGCA CCGGGGCTC AATGCGCAG GCGCAGCGCA GATGCAGCCC 600
 ATGCACCGCT ACGAGTGGG CGCCCTGCAG TACAACCTCA TGACAGCTC GCAGACCTAC 660
 ATGAACGGCT CGCCACCTA CAGCATGTCC TACTCGCAG AGGGCACCCC TGGCATGGCT 720
 CTTGGCTCCA TGGGTTCGGT GGTCAAGTCC GAGGCCAGCT CCAGCCCCC TGTGGTTACC 780
 TCTTCTCTCC ACTCTCGGGC GCGGCGGACC TCCGGGACAT GATCAGCATG 840
 TATCTCCCG GCGCGAGGT GCGGGAACCC GCGGCGGACC GCAGACTTCA CATGTCCCAG 900
 CACTACCAGA GCGGCGGGT GCGGCGCACG GCCATTAAAG GCACACTGCC CCTCTCACAC 960
 ATGTGAGGGC CGGACAGCGA ACTGGAGGGG GGAGAAATTT TCAAAGAAAA ACGAGGGAAA 1020
 TGGGAGGGGT GCAAAGAGG AGAGTAAGAA ACAGCATGGA GAAAACCCGG TACGCTCAAA 1080
 AAAAA

Seq ID NO: 515 Protein sequence
Protein Accession #: CAA83435

80
 85

1 11 21 31 41 51
 HSARMYNNME TELKPPGPQQ TSGGGGNGST AAAAGGNQKN SPDRVKRPMN AFMVWSRGQR 60
 RKMAQENPKM HNSEISKRLG AEWKLLSETE KRPFIDEAKR LRALHMKHP DYKYRPRRKT 120
 KTLMKDKYK LPGGLLAPGG NSMASGVGVG AGLGAGVNQR MDSYAHMNGW SNGSYMMQD 180

QLGYPPQHPGL NAHGAAQMOP MHRVDVSLQ YNSMTSSQTY MNGSPITYSMS YSQOQTGMA 240
 LGSMGSPVKS EASSSPFVVT SSSHSRAPCQ AGDLRDMISM YLPGAEPPEP AAPSLHMSQ 300
 HYQSGPVPPT AINGTLPLSH M

5 Seq ID NO: 516 DNA sequence
 Nucleic Acid Accession #: U91618
 Coding sequence: 29..541

10 1 11 21 31 41 51
 CGGACTTGGC TTGTTAGAAG GCTGAAAGAT GATGGCAGGA ATGAAAATCC AGCTTGTATG 60
 CATGCTACTC CTGGCTTTCA GCTCCTGGAG TCTGTGCTCA GATTGAGAAG AGGAAATGAA 120
 AGCATTAGAA GCAGATTCTT TGACCAATAT GCATACATCA AAGATTAGTA AAGCACATGT 180
 TCCCTCTTGG AAGATGACTC TGCTAAATGT TTGCAGTCTT GTAAATAATT TGAACAGCCC 240
 15 AGCTGAGGAA ACAGGAGAAG TTCATGAAGA GGAGCTTGTG GCAAGAAAGGA AACTTCTCTAC 300
 TGCTTTAGAT GGCCTTAGCT TGGAGCAAT GTTGACAATA TACCAGCTCC ACAAATCTGT 360
 TCACAGCAGG GCTTTTCAAC ACTGGGAGTT AATCCAGGAA GATATTCTTG ATACTGGAAA 420
 TGACAAAAT GGAAAGGAAG AAGTCATAAA GAGAAAAATT CCTTATATTC TGAACCGGCA 480
 20 GCTGTATGAG AATAAACCCA GAAGACCCTA CATACTCAA AGAGATTCTT ACTATTACTG 540
 AGAGAATAGG TCA'TTTATTT ACATGTGATT GTGATTCTAC ATCCCTTAAT TAAATATCAA 600
 ATTATATTTT TGTGAAAATG TGACAAACAC ACTTATCTGT CTCTTCTACA ATTGTGGTTT 660
 ATTGAATGTG TTTTCTGCA CTAATAGAAA TTAGACTAAG TGTTTTCAAA TAAATCTAAA 720
 TCTTCAAAAA AAAAAAATAA AATGGGGGCC GCAATT

25 Seq ID NO: 517 Protein sequence
 Protein Accession #: AAB50564

30 1 11 21 31 41 51
 MMAGMKIQLV CMLLAFSSW SLCSDEEEM KALEADFLTN MHTSKISKAH VPSWKMTLLN 60
 VCSLVNMLNS PAETGEVHE EELVARRKLP TALDGFSLA MLTIYQLHKI CHSRAFQHWB 120
 LIQEDILDG NDKNGKEEVI KRKIPYILKR QLYENKPRRP YILKRDYVY

35 Seq ID NO: 518 DNA sequence
 Nucleic Acid Accession #: NM_006536.2
 Coding sequence: 109..2940

40 1 11 21 31 41 51
 ACCTAAACAC TTGCAAGTTC AGGAAGAAAC CATCTGCATC CATATTGAAA ACCTGACACA 60
 ATGTATGCAG CAGGCTCAGT GTGAGTGAAC TGGAGGCTTC TCTACAACAT GACCCAAAGG 120
 AGCATTGCGAG GTCCTATTGT CAACCTGAAG TTGTGACTC TCCTGGTTCG CTTAAGTTCA 180
 GAACTCCCAT TCCTGGGAGC TGGAGTACAG CTTCAAGACA ATGGGTATAA TGGATTGCTC 240
 45 ATTGCAATTA ATCCTCAGGT ACCTGAGAAT CAGAACCTCA TCTCAAACAT TAAGGAAATG 300
 ATAACTGAAG CTTATTTTAA CCTATTTAAT GCTACCAAGA GAAGAGTATT TTTCAGAAAT 360
 ATAAAGATT TAATACCTGC CACATGGAAA GCTAATAATA ACAGCAAAAT AAAACAAGAA 420
 TCATATGAAA AGGCATAATG CATAGTGACT GACTGGTATG GGGCAGATGG AGATGATCCA 480
 TACACCCTAC AATACAGAGG GTGTGGAAA GAGGGAAT ACATTCATT CACACCTAAT 540
 50 TTCCTACTGA ATGATAACTT AACAGCTGGC TACGGATCAC GAGGCCGAGT GTTTGTCCAT 600
 GAATGGGGCC ACCTCCGTGT GGGTGTGTTC GATGAGTATA ACAATGACAA ACCTTCTTAC 660
 ATAAATGGGC AAAATCAAAT TAAAGTGACA AGGTGTTCAT CTGACATCAC AGGCATTTTT 720
 GTGTGTGAAA AAGGTCTCTG CCCCCAAGAA AACTGTATTA TTAGTAAGCT TTTTAAAGAA 780
 GGATGCACCT TTATCTACAA TAGCACCCAA AATGCAACTG CATCAATAAT GTTCATGCAA 840
 55 AGTTTATCTT CTGTGGTGA ATTTTGTAAAT GCAAGTACCC ACAACCAAGA AGCACCACAC 900
 CTACAGAACC AGATGTGCAG CCTCAGAAGT GCATGGGATG TAATCACAGA CTCTGCTGAC 960
 TTTCAACCA CACTTCCCAT GAATGGGACT GAGCTTCCAC CTCCTCCAC ATCTCTGCTT 1020
 GTACAGGCTG GTGACAAAT GGTCTGTGTA GTGCTGGATG TGTCAGCAAA GATGGCAGAG 1080
 GCTGACAGAG TCCCTCAACT ACAACAAGCC GCAGAAATTT ATTTGATGCA GATTGTTGAA 1140
 60 ATTACATCTT TCGTGGGCAT TGCCAGTTTC GACAGCAAAG GAGAGATCAG AGCCAGCTA 1200
 CACCAATTA ACAGCAATGA TGATCGAAAG TTGCTGGTTT CATATCTGCC CACCAGTGA 1260
 TCAGCTAAAA CAGACATCAG CATTTGTTCA GGGCTTAAGA AAGGATTGGA GGTGGTTGAA 1320
 AAACCTGAAT GAAAGCTTA TGGCTCTGTG ATGATATTAG TGACCAGCGG AGATGATAAG 1380
 CTCTTGGCA ATTGCTTACC CACTGTGCTC AGCAGTGGTT CAACAATTCA CTCATTGCC 1440
 65 CTGGGTTCAT CTGCAGCCCC AAATCTGGAG GAATTATCAC GTCTTACAGG AGGTTTAAAG 1500
 TTCTTTGTT CAGATATATC AAATCCCAAT AGCATGATTG ATGCTTTCAG TAGAATTTCC 1560
 TCTGGAACCT GAGACATTTT CCAGCAACAT ATTCAGCTTG AAAGTACAGG TGAATATGTC 1620
 AAACCTCACC ATCAATTGAA AAACACAGTG ACTGTGGATA ATACTGTGGG CAACGACACT 1680
 ATGTTTCTAG TTACGTGGCA GGCCAGTGGT CCTCCTGAGA TTATATTATT TGATCCTGAT 1740
 70 GGACGAAAAT ACTACACAAA TAATTTATC ACCAATCTAA CTTTTCGGAG AGCTAGTCTT 1800
 TGGATTCCAG GAACAGCTAA GCCTGGGCAC TGGACTTACA CCCTGAACAA TACCCATCAT 1860
 TCTCTGCAAG CCTGAAAGT GACAGTGACC TCTCGGCCT CCAACTCAGC TGTGCCCCCA 1920
 GCCACTGTGG AAGCCTTTGT GGAAAGAGAC AGCCTCCATT TTCTCATCC TGTGATGATT 1980
 75 TATGCCAATG TGAACAGAGG ATTTTATCCC ATTCTTAATG CCACTGTCACT TGCCACAGTT 2040
 GAGCCAGAGA CTGGAGATCC TGTACGCTG AGACTCCTTG ATGATGGAGC AGGTGCTGAT 2100
 GTTATAAAAA ATGATGGAAT TTACTCGAGG TATTTTCTT CTTTGTCTG AAATGGTGA 2160
 TATAGCTTGA AAGTGCATGT CAATCACTCT CCCAGCATAA GCACCCAGC CCACTCTATT 2220
 CCAGGAGTCT ATGCTATGTA TGTACCAGGT TACACAGCAA ACGGTAATAT TCAGATGAAT 2280
 GCTCCAAGGA ATCAGTAGG CAGAAATGAG GAGGAGCGAA AGTGGGGCTT TAGCCGAGTC 2340
 80 AGCTCAGGAG GCTCCTTTTC AGTGCTGGGA GTTCCAGCTG GCCCCACCC TGATGTGTTT 2400
 CCACCATGCA AAATTATTGA CTTGGAAGCT GTAAAGTAG AAGAGGAATT GACCCATCT 2460
 TGGACAGCAC CTGGAGAAGA CTTTGATCAG GGCCAGGCTA CAAGCTATGA AATAAGAATG 2520
 AGTAAAGATC TACAGATAT CCAAGATGAC TTTAACAATG CTATTTTAGT AAATACATCA 2580
 AAGCGAATC CTCAGATAGC TGGCATCAGG GAGATATTTA CGTTCTCACC CCAGATTTC 2640
 85 AGCAATGGAG CTGACATCAT GCCAAATGGA GAAACACATG AAAGCCACAG AATTTATGTT 2700
 GCAATGAGAG CAATGATAG GAACTCCTTA CAGTCTGCTG TATCTAACAT TGCCAGGCG 2760
 CCTCTGTTTA TTCCCCCAA TTCTGATCCT GTACCTGCCA GAGATTATCT TATATTGAAA 2820
 GGAGTTTTAA CAGCAATGGG TTTGATAGGA ATCATTTGCC TTATTATAGT TGTGACACAT 2880

CATACCTTTAA GCAGGAAAAA GAGAGCAGAC AAGAAAGAGA ATGGAACAAA ATTATTATATA 2940
 ATAAATATCC AAAGTGTCTT CCTCTTAGA TATAAGACCC ATGGCCTTCG ACTACAAAAA 3000
 CATACTAACA AAGTCAAATT AACATCAAAA CTGTATTAAA ATGCATTGAG TTTTGTGACA 3060
 ATACAGATAA GATTTTTACA TGGTAGATCA ACAATTCITT TTGGGGGTAG ATTAGAAAAA 3120
 CCTTACACTT TGGCTATGAA CAAATAATAA AAATATTCTT TAAAGTAAT GTCTTTAAAG 3180
 GCAAAGGGAA GGGTAAAGTC GGACCAAGTGT CAAGGAAAGT TTGTTTATT GAGGTGGA 3240
 AATAGCCCCA AGCAGAGAAA AGGAGGGTAG GTCTGCATTA TAACTGTCTG TGTGAAGCAA 3300
 TCATTAGATT ACTTTGATTA ATTTTCTCTT TCTCCTTATC TGTGCAGTAC AGGTTGCTTG 3360
 TTTACATGAA GATCATGCTA TATTTATAT ATGTAGCCCC TAATGCAAG CTCTTACCT 3420
 CTGTCTATT TGTATATAT ATTTCAAGAT ACATCTCCCT GCTAATGCTC AGAGATCTTT 3480
 TTTCACTGTA AGAGGTAACC TTTAACAATA TGGGTATTAC CTTTGTCTCT TCATACCGGT 3540
 TTTATGACAA AGGTCTATTG AATTATTATG TGTGTAAAGT TCTACTCCCA TCAAAGCAGC 3600
 TTTCTAAGTT TATTGCCCTG GGTATTATG GAATGATAGT TATAGCCCN TATAATGCCT 3660
 TACCTAGGAA A

Seq ID NO: 519 Protein sequence
 Protein Accession #: NP_006527.1

1 11 21 31 41 51
 MTQRSIAGPI CNLKFVTLV ALSSELPLFL AGVOLQDNGY NGLLIAINPQ VPENQNLIISN 60
 IKEMITEASF YLFNATKRRV PFRNIKILIP ATWKANMNSK IKQESYEKAN VIIVTDWYGAH 120
 GDDPYTLQYR GCGKEGKYIH FTPNFLNDN LTAGYGRGR VFWHEWAHLR WGVFDEYNND 180
 KPFIYINGQNI IKVTRCSSDI TGIFVCEKGP CPQENCIISK LPKEGCTFIY NSTQNATASI 240
 MFMQSLSSVV EFCNASTHNQ EAPNLQNMOC SLRSAWDVIT DSADPHHSFP MNGTELPPPP 300
 TFSLVQAGDK VVCLVLDVSS KMAEADRLLO LQQAEEFYLM QIVEIHTFVG IASFDSKGEI 360
 RAQLHQINSN DDRKLLVSYL PTTVSAKTDI SICSGLKGKF EVVEKLNGKA YGSMILVTS 420
 GDDKLLGNCL PTVLSSSGSTI HSIALGSSAA PNLEELSRIT GGLKFPVPDI SNSNSMIDAP 480
 SRISSTGTDI PQQHILQEST GENVKPHQL KNTVTVDNTV GNDTMFLVTW QASGPPEIL 540
 FPDGGRKYIT NNFTINLFR TASLWIPGTA KPGHWYTLN NTHSLQALK VTVTSRANS 600
 AVPPATVEAF VERDSLHFPF VMIIYANVKV GPYPILNATV TATVEPETGD FVTLRLDDG 660
 AGADVINKDG IYSRYFFSFA ANGRYSKLVH VNHSPSISTP AHSIPGSHAM YVPGYTANGN 720
 IQMNAFRKSV GRNEEERKWO PSRVSSGGSP SVLGVFAGPH PDVFPCKII DLEAVKVEE 780
 LTLSTWAPGE DFDGQATSY EIRMSKSLQN IQDDFNAIL VNTSKRNPQ AGIREIFTFS 840
 PQISTNGPEH QPNGETHESH RIYVAIRAMD RNSLQSAVSN IAQAPLPIPP NSDPVPARDY 900
 LILKGLVTAM GLIGIICLII VVTHHTLSRK KRADKKENG T KLL

Seq ID NO: 520 DNA sequence
 Nucleic Acid Accession #: NM_000228.1
 Coding sequence: 82..3600

1 11 21 31 41 51
 GCTTTCAGGC GATCTGGAGA AAGAACGGCA GAACACACAG CAAGGAAAGG TCCTTTCTGG 60
 GGATCACCCC ATGGCTGAA CTGAGAGCCA TTCTTCCTCT TGTGTTTTCG CTGCGCTGGC 120
 CTCCTGCATG CCCAACAGC CTGCTCCCGT GGGGCTCTGT ATCCACCTGT TGGGGACCTG 180
 CTCTGTGGGA GGACCCGGTT TCTCCGAGCT TCATCTACCT GTGGACTGAC CAAGCCTGAG 240
 ACCCTACGCA CCGAGTATGG CGAGTGGCAG ATGAAATGCT GCAAGTGTGA CTCACGCGAG 300
 CCTCACAACT ACTACAGTCA CCGAGTAGAG AATGTGGCTT CATCTCCGG CCCCATGCGC 360
 TGGTGGCAGT CCCAGAAATGA TGTGAACCTT GTCTCTCTGC AGCTGGACCT GGACAGGAGA 420
 TTCCAGCTTC AAGAAGTCAT GATGGAGTTC CAGGGGCCCA TGCCCGCCGG CATGCTGATT 480
 GAGCGCTCCT CAGACTCTGG TAAGACCTGG CGAGTGTACC AGTACCTGGC TGCCGACTGC 540
 ACCCTCACCT TCCCTCGGGT CCGCCAGGGT CGGCTCAGA GCTGGCAGGA TGTTCGGTGC 600
 CAGTCCCTGC CTCAGAGGCC TAATGCACGC CTAATGGGG GGAAGGTCCA ACTTAACCTT 660
 ATGGATTTAG TGTCTGGGAT TCCAGCAACT CAAAGTCAA AAATTCAAGA GGTGGGGGAG 720
 ATCACAAATC TAGAGATCAA TTTACACAG CTGGCCCTGT TGCCCCAAAG GGGCTACCC 780
 CCTCCAGCGC CTAATATGTC TGTGTCCAG CTCTGTCTGC AGGGGAGCTG CTCTGTCTAC 840
 GGCCATGCTG ATCGCTGCGC ACCCAAGCCT GGGGCTCTG CAGGCCCTTC CACCGCTGGC 900
 CAGSTCCACG ATGTCTGTGT CTGCCAGCAC AACACTGCCG GCCCAAATTG TGAGCGCTGT 960
 GCACCCCTCT ACAACAACCG GCCCTGGAGA CCGGCGGAG GCCAGGACGC CCATGAATGC 1020
 CAAAGGTGCG ACTGCAATGG GCACTCAGAG ACATGTCACT TTGACCCCG TGTGTTTGGC 1080
 GCCAGCCAGG GGGCATATGG AGGTGTGTGT GACAATTGCC GGGACACAC CGAAGGCAAG 1140
 AACTGTGAGC GGTGTACGCT GCACTATTTC CGGAACCGGC GCCCGGGAGC TTCCATTGAG 1200
 GAGACCTGCA TCTCTGCGA GTGTGATCCG GATGGGGCAG TGCCAGGGGC TCCCTGTGAC 1260
 CCAAGTACCG GGCAGTGTGT GTGCAAGGAG CATGTGCAGG GAGAGCGCTG TGACCTATGC 1320
 AAGCCGGGCT TCATGGACT CACCTACGCC AACCCGAGG GCTGCCACCG CTGTGACTGC 1380
 AACATCTGG GGTCCCGGAG GGACATGCCG TGTGACGAGG AGAGTGGGGC CTGCCTTTGT 1440
 CTGCCCAAGC TGGTGGGTCC CAAATGTGAC CAGTGTGCTC CCTACCACTG GAAGCTGGCC 1500
 AGTGGCCAGG GCTGTGAACC GTGTGCCTGC GACCCGCACA ACTCCCTCA GCCCAGATG 1560
 GAACCACTT ACAGGGCAGT GCCCTGTGG GAAGGCTTTG GTGGCTGTAT GTGCAGCGCT 1620
 GCAGCCATCC GCCAGTGTCC AGACCGGACC TATGGAGACG TGGCCACAGG ATGCCGAGCC 1680
 TGTGATCTGT ATTTCCGGGG AACAGAGGGC CCGGGCTGCG ACAAGGCATC AGGCCGCTGC 1740
 CTCTGCGGCC CTGGCTTGAC CGGGCCCGGC TGTGACCACT GCCAGCGAGG CTACTGCAAT 1800
 CGCTACCGCG TGTGCTGGC CTGCCACCT TGTCTCCAGA CCTATGATGC GGACCTCCGG 1860
 GAGCAGGCC TGGCTTTTGG TAGACTCCGC AATGCCACCG CCAGCCTGTG GTGAGGGCCT 1920
 GGGCTGGAGG ACCGTGGCCT GGCCTCCCGC ATCCTAGATG CAAAGAGTAA GATTGAGCAG 1980
 ATCCGAGCAG TTCTCAGCAG CCCCGCAGTC ACAGAGCAGG AGGTGGCTCA GGTGGCCAGT 2040
 GCCATCTCT CTCTCAGCG AACTCTCCAG GGCCTGCAGC TGGATCTGCC CCTGGAGGAG 2100
 GAGACGTTAT CCCTTCCGAG AGACCTGGAG AGTCTTGACA GAAGCTTCAA TGGTCTCCTT 2160
 ACTATGTTT AGAGGAAGAG GGAGCAGTTT GAAAAAATAA GCAGTGTCTG TCCTTCAGGA 2220
 GCCTTCCGGA TGTGAGCAC AGCCTACGAG CAGTCAGCCC AGGCTGTCTA GCAGGTCTCC 2280
 GCAGCTCGC GCCTTTTGGG CCAGCTCAGG GACAGCCGGA GAGAGGCGAG GAGGCTGGTG 2340
 CGGAGGGCG GAGGAGGAG AGGCACCGGC AGCCCAAGC TTGTGGCCCT GAGCTGGAG 2400
 ATGCTTCTGT TGCCCTGACT GACACCCACC TTCAACAAGC TCTGTGGCAA CTCCAGGCAG 2460
 ATGGCTTGA CCCCAATATC ATGCCCTGGT GAGCTATGTC CCAAGACAA TGGCAGAGC 2520
 TGTGGCTCCC GCTGCAGGGG TGTCTTCCC AGGGCCGGTG GGGCTTCTT GATGGCGGGG 2580
 CAGGTGGCTG AGCAGCTGCG GGGCTTCAAT GCCCAGCTCC AGCCGACCAG GCAGATGATT 2640

AGGGCAGCCG AGGAATCTGC CTCACAGATT CAATCCAGTG CCCAGCGCTT GGAGACCCAG 2700
 GTGAGCGCCA GCCGCTCCCA GATGGAGGAA GATGTCAGAC GCACACGGCT CCTAATCCAG 2760
 CAGGTCGGGG ACTTCTTAAC AGACCCCGAC ACTGATGCAG CCACTATCCA GGAGGTGAGC 2820
 GAGGCGGTGC TGGCCCTGTG GCTGCCACCA GACTCAGCTA CTGTTCTGCA GAAGATGAAT 2880
 GAGATCCAGG CCATTGACAG CAGGCTCCCC AACGTGGACT TGGTGCTGTC CCAGACCAAG 2940
 CAGGACATTG CCGGTGCCCC CCGGTTGCAG GCTGAGGCTG AGGAAGCCAG GAGCCGAGCC 3000
 CATGCAGTGG AGGGCCAGGT GGAAGATGTG GTTGGGAACC TGCGGCAGGG GACAGTGGCA 3060
 CTCGAGGAAG CTCAGGACAC CATGCAAGGC ACCAGCCGCT CCCCTCGGCT TATCCAGGAC 3120
 AGGGTTGCTG AGGTTTCAGCA GGTACTGCGG CCAGCAGAAA AGCTGGTGAC AAGCATGACC 3180
 AAGCAGCTGG GTGACTTCTG GACACGGATG GAGGAGCTCC GCCACCAAGC CCGGCAGCAG 3240
 GGGGCAGAGG CAGTCCAGGC CCAGCAGCTT GCGGAAGGTG CCAGCGAGCA GGCATTGAGT 3300
 GCCCAAGAGG GATTTAGAG AATAAAACAA AAGTATGCTG AGTTGAAGGA CCGGTTGGGT 3360
 CAGAGTTCCA TGCTGGGTGA GCAGGGTGCC CGGATCCAGA GTGTGAAGAC AGAGGCGAGAG 3420
 GAGCTGTTTG TGGAGACCAT GGAGATGATG GACAGGATGA AAGACATGGA GTTGGAGCTG 3480
 TCGCGGGGCA GCCAGCCCAT CATGCTGCGC TCGCGGAGCC TGACAGGACT GGAGAAGCGT 3540
 GTGGAGCAGA TCCGTGACCA CATCAATGGG CGCGTGCTCT ACTATGCCAC CTGCAAGTGA 3600
 TGCTACAGCT TCCAGCCCGT TGCCCCACTC ATCTGCCGCC TTTGCTTTTG GTTGGGGGCA 3660
 GATTGGGTGG GAATGCTTTC CATCTCCAGG AGACTTTCAT GCAGCCTAAA GTACAGCCTG 3720
 GACCAACCCCT GGTGTGTAGC TAGTAAGATT ACCCTGAGCT GCAGCTGAGC CTGAGCCAAT 3780
 GGGACAGTTA CACTTGACAG ACAAGATGG TGGAGATTGG CATGCCATTG AACTAAGAG 3840
 CTCTCAAGT AAGGAAGACA AAACTTAAC AAAAGTGATG TAAAAATGAA AAGCCAAATA 3900
 GGAATCTTGG ACCAAGCACA AAACTTAAC AAAAGTGATG TAAAAATGAA AAGCCAAATA 3960
 AAAATCTTTG G

Seq ID NO: 521 Protein sequence
 Protein Accession #: NP_000219.1

1 11 21 31 41 51
 MRPFLLCFA LFGLLHAQQA CSRGACYPPV GDLVGRTRF LRASSTCGLT KPETYCTQYG 60
 EWQMKCKCD SRQPNHYSH RVENVASSSG PMRWQSQND VNPVSLQLDL DRRFQLQEVN 120
 MEFGMPMPAG MLIERSSDFG KTWVYQYLA ADCTSTFPRV RQGRPQSQWD VRCQSLPQRP 180
 NARLNGGKVQ LNLMDLVSGI PATQSQKIQE VGEITNLRVN FTRLAPVPQR GYHPPSAYYA 240
 VSQRLRQGGC FCHGHADRCR PKPGASAGPS TAVQVHDCV CQHNTAGPNC ERCAPPYNNR 300
 WPRPAEQDQA HECQCDNCG HSETCHFDPA VFAASQAGY GVCNDCRDHT EGKNCERCQL 360
 HYFRNRPRGA SIQETCISCE CDPDGAVPFA PCDPVTGQCV CKEHVQGER DLCKPGFTGL 420
 TYANPQGCNR CDCNLIGRRR DMPDEESGR CLCLPNVVGK KCDQCAPYHW KLASGGCEP 480
 CACDPHNSPQ PTVQPVHRAV PCREGFGLM CSAAAIRQCP DRTYGDVATG CRACDCDFRG 540
 TEGPGCDKAS GRCLCRPGLT GPRCDQCQRG YCNRYPCVA CHPCFQTYDA DLREQALRFG 600
 RLNRNATASLW SQPGLDRGL ASRILDASK IEQIRAVLSS PAVTEQEVQA VASAILSLRR 660
 TLQGLQLDLF LEEETLSLPR DLESIDRSFN GLLTMYQRKR EQFEKISSAD PSGAFRMLST 720
 AYEQSAQAQA QVSDSSRLLD QLRDSRREAE RLVRQAGGGG GTGSPKLVAL RLEMSSLPDL 780
 TPTFNKLCGN SRQMACTPIS CPGELCPQDN GTACGSRRCR VLPRAAGAFI MAGQVAQLR 840
 GFNAQLQRT R QMIRAAEESA SIQSSAQR L ETQVSASRSQ MEEDVRRTRL LIQVRDFLT 900
 DPTDAAATQ EVSEAVLALW LPTDSATVLQ KMEITEQIAA RLNPVDVLVS QTKQDIARAR 960
 RLQAEAEER SRHAVEGQV EDVVGNLRQG TVALQEAQDT MQGTSRSLRL IQDRVAEVQ 1020
 VLRAEKLVT SMTKQLGDFW TRMEELRHQA RQGGAEAVQA QQLAEGASEQ ALGAQEGFER 1080
 IKQKYAELKD RLQSSMLGE QGARIQSVKT EAEELFGETM EMDRMKDME LELLRGSQAI 1140
 MLRSADLTGL EKRVQIRDH INGRVLYYAT CK

Seq ID NO: 522 DNA sequence
 Nucleic Acid Accession #: NM_001944.1
 Coding sequence: 84..3083

1 11 21 31 41 51
 TTTTCTTAGA CATTAACTGC AGACGGCTGG CAGGATAGAA GCACGCGCTC ACTTGGACTT 60
 TTTACCCAGG GAATCAGAG ACAATGATGG GGCTCTTCCC CAGAACTACA GGGGCTCTGG 120
 CCATCTTCGT GGTGTCATA TTGTTTCATG GAGAAATTGG AATAGAGACT AAAGGTCAAT 180
 ATGATGAAGA AGAGATGACT ATGCAACAAG CTAAAAGAG GCAAAAACGT GAATGGGTGA 240
 AATTGTCCAA ACCCTGCAGA GAAGGAGAAG ATAACCTCAA AAGAAACCCA ATTGCCAAGA 300
 TACTTTCAGA TTACCAAGCA ACCCAGAAAA TCACCTACCG AATCTCTGGA GTGGGAATCG 360
 ATCAGCCGCC TTTTGGAAATC TTTGTTGTTG ACAAAAACAC TGGAGATATT AACATAACAG 420
 CTATAGTCGA CCGGGAGGAA ACTCCAAGCT TCCTGATCAC ATGTCGGGCT CTAATGCCCC 480
 AAGGACTAGA TGTAGAGAAA CCACCTTATC TAACGGTTAA AATTTTGGAT ATTAATGATA 540
 ATCTCCAGT ATTTTCACAA CAAATTTTCA TGGGTGAAT TGAAGAAAT AGTGCCCTCA 600
 ACTCACTGTT GATGATACATA AATGCCACAG ATGCAGATGA ACCAAACCCAT TTGAATTCTA 660
 AAATTGCCCT CAAAATTGTC TCTCAGGAAC CAGCAGGCAC ACCCATGTTT CTCCTAAGCA 720
 GAAACACTGG GGAAGTCCGT ACTTTGACCA ATTCTCTTGA CCGAGAGCAA GCTAGCAGCT 780
 ATCGTCTGGT TGTGAGTGGT GCAGACAAAG ATGGAGAAGG ACTATCAACT CAATGTGAAT 840
 GTAATATTAA AGTGAAAGAT GTCAACGATA ACTTCCCAAT GTTTAGAGAC TCTCAGTATT 900
 CAGCAGCTAT TGAAGAAAT ATTTTAAGTT CTGAATTACT TCGATTTCAA GTAACAGATT 960
 TGGATGAAGA GTACACAGAT AATTGGCTTG CAGTATATTT CTTTACCTCT GGAATGAAG 1020
 GAAATTTGGT TGAATACAA ACTGATCCTA GAACTAATGA AGGCATCCTG AAAGTGGTGA 1080
 AGGCTCTAGA TTATGAACAA CTACAAAGCG TGAACCTTAG TATTGCTGTC AAAAAACAAAG 1140
 CTGAATTTCA CCAATCAGTT ATCTCTCGAT ACCGAGTTCA GTCAACCCCA GTCACAATTC 1200
 AGGTAATATA TGTAAAGAGAA GGAATTGCAT TCCGTCCTGC TTCCAAGACA TTACTGTGC 1260
 AAAAAAGCAT CACTGAAACAA AATTTGGTGG ATTATATCTT GGAACATAT CAAGCCATCG 1320
 ATGAGGACAC TAACAAAGCT GCCTCAAATG TCAAAATATG CATGGGACGT AACGATGGTG 1380
 GATACCTAAT GATTGATCTA AAAACGTGCT AAATCAAAAT TGTCAAAAT ATGAACCGAG 1440
 ATTCTACTTT CATAGTTAAC AAAACAATCA CAGCTGAGGT TCTGGCCATA GATGAATACA 1500
 CGGGTAAAC TCTTACAGGC ACGGTATATG TTAGAGTACC CGATTTCAAT GACAATTGTC 1560
 CAACAGCTGT CCGGAAACAA GATGCAAGTT GCAGTTCTTC ACCTTCGCTG GTTGTCTCG 1620
 CTAGAACACT GAATTAATAGA TACACTGGCC CCTATACATT TGCACTGGAA GATCAACCTG 1680
 TAAAGTTGCC TGCGTATGG AGTATCACAA CCCTCAATGC TACCTCGGCC CTCCTCAGAG 1740
 CCCAGGAACA GATACCTCCT GGAGTATACC ACATCTCCCT GGTACTTACA GACAGTCAGA 1800
 ACAATCGGTG TGAGATGCCA CGCAGCTTGA CACTGGAAGT CTGTCAAGTGT GACCAACAGG 1860

	GCATCTGTGG	AACCTCTTAC	CCAACCACAA	GCCTCTGGGAC	CAGGTATGGC	AGGCCGCACT	1920
	CAGGGAGGCT	GGGGCTGCCC	GCCATCGGCC	TGCTGCTCCT	TGGTCTCCTG	CTGCTGCTGT	1980
	TGGCCCCCTT	TCTGCTGTTG	ACCTGTGACT	GTGGGGCAGG	TTCTACTGGG	GGAGTGACAG	2040
5	GTGGTTTAT	CCAGATTCTC	GATGGCTCAG	AAGGAACAA	TCATCAGTGG	GGAAATGAAG	2100
	GAGCCCATCC	TGAAGACAAG	GAAATCACAA	ATATTGTGT	GCCTCCTGTA	ACAGCCAAATG	2160
	GAGCCGATTT	CATGGAAAGT	TCTGAAGTTT	GTACAAATAC	GTATGCCAGA	GGCACAGCGG	2220
	TGGAAGGCAC	TTCAGGAATG	GAAATGACCA	CTAAGCTTGG	AGCAGCCACT	GAATCTGGAG	2280
	GTGCTGCAGG	CTTTGCAACA	GGGACAGTGT	CAGGAGCTGC	TTCAGGATTC	GGAGCAGCCA	2340
10	CTGGAGTTGG	CATCTGTTCC	TCAGGGCAGT	CTGGAACCAT	GAGAACAAGG	CATTCCACTG	2400
	GAGGAACCAA	TAAGGACTAC	GCTGATGGGG	CGATAAGCAT	GAATTTTCTG	GACTCCTACT	2460
	TTTCTCAGAA	AGCATTTGCC	TGTGCGGAGG	AAGACGATGG	CCAGGAAGCA	AATGACTGCT	2520
	TGTTGATCTA	TGATAATGAA	GGCGCAGATG	CCACTGGTTC	TCCTGTGGGC	TCCGTGGGTT	2580
	GTTGCAGTTT	TATTGCTGAT	GACCTGGATG	ACAGCTTCTT	GGACTCACTT	GGACCCAAAT	2640
15	TTAAAAAAT	TGCAGAGATA	AGCCTTGGTG	TTGATGGTGA	AGGCAAGAA	GTTCAGCCAC	2700
	CCTCTAAAGA	CAGCGGTTAT	GGGATTGAAT	CCTGTGGCCA	TCCCATAGAA	GTCCAGCAGA	2760
	CAGGATTGTT	TAAGTGCCAG	AGTTTGTGAG	GAGTCAAGG	AGCTTCTGCT	TTGTCCGCTT	2820
	CTGGGTCTGT	CCAGCCAGCT	GTTTCCATCC	CTGACCCTCT	GCAGCATGGT	AACTATTTAG	2880
	TAACGGAGAC	TTACTCGGCT	TCTGGTTCCT	TCGTGCAACC	TTCCTGCTGA	GGCTTTGATC	2940
20	CACCTTCTAC	CAAAAATGTG	ATAGTGACAG	AAAGGGTGAT	CTGTCCCTAT	TCCAGTGTTC	3000
	CTGGCAACCT	AGCTGGCCCA	ACGCAGCTAC	GAGGGTCACA	TACTATGCTC	TGTACAGAGG	3060
	ATCCTTGCTC	CGCTGGCCCA	TGACCAGAA	GAGCTGGAAT	ACCACACTGA	CCAAATCTGG	3120
	ATCTTTGGAC	TAAAGTATTC	AAAATAGCAT	AGCAAAGCTC	ACTGTATTGG	GCTAATAATT	3180
	TGGCACTTAT	TAGCTTCTCT	CATAAATGTA	TCACGATTAT	AAATTAAATG	TTTGGGTTCA	3240
25	TACCCCAAAA	GCAATATGTT	GTCACTCCTA	ATTCTCAAGT	ACTATTCAAA	TTGTAGTAAA	3300
	TCTTAAAGTT	TTTCAAAACC	CTAAAATCAT	ATTTCGCT			

Seq ID NO: 523 Protein sequence
Protein Accession #: NP_001935.1

30	1	11	21	31	41	51	
	MMGLFPRTTG	ALAIFVVVIL	VHGELEIETK	QYDEEEMTM	QQAQRKQRE	WVKFAKPCRE	60
	GEDNSKRNP	AKITSYQAT	QKITYRISGV	GIDQPPFGIP	VVDKNTGDIN	ITAIVDREET	120
	PSPLITCRAL	NAQGLDVEKP	LILTVKILDI	NDNPPVFSQQ	IFMGEIEENS	ASNSLVMILN	180
35	ATDADEPNHL	NSKIAFKIVS	QEPAGTGMFL	LSRNTGEVRT	LTNSLDRBQA	SSYRLVVSQA	240
	DKDGEGLSTQ	CECNKVKD	NDNPFMFRDS	QYSARIBENI	LSSLELLRFQV	TDLDEEYTDN	300
	WLAVYFETSG	NEGNWFEIQT	DPRTNEGILK	VVKALDYEQ	QSVKLSIAVK	NKAEFHQSVI	360
	SRYRVQSTPV	TIQVINVREG	IAFRPASKTF	TVQKGISSKK	LVDYILGTQY	AIDEDTNKAA	420
	SNVYVMGRN	DGGYLMIDSK	TAEIKFVKNM	NRDSTFIVNK	TITAEVLAI	EYTKTSTGT	480
40	VYVRVPDFND	NCPTAVLEKD	AVCSSSPSVV	VSARTLNNRY	TGPTYFALED	QPVKLPVAVS	540
	ITTLNATSAL	LRAQEQIPFG	VYHISLVLT	SQNNRCMPR	SLTLEVQCQD	NRGICGTSYP	600
	TTSPGTRYGR	PHSGRLGPAA	IGLLLLGLLL	LLLAPELLLT	CDGAGSTGG	VTGGFIPVPD	660
	GSSGTIHQWG	IEGAHPEDKE	ITNICVPPVT	ANGADFMES	EVCTNTYARG	TAVEGTSGME	720
	MTTKLGAATE	SGGAAGFATG	TVSGAASGFG	AATGVGICSS	QSGSTMTRH	STGGTNKDYA	780
45	DGALISMFLD	SYFSQKAFAC	AEEDDQGEAN	DCLLIYDN	ADATGSPVGS	VGCCSPFIADD	840
	LDPSFLDSL	PKFKLAEIS	LGVDDGEGKEV	QPPSKDSGVY	IESCGHPFIEV	QQTGFVKCQT	900
	LSGSQASAL	SASGSVQPAV	SIPDPLQHG	YLVTEYTSAS	GSLVQPSSTAG	FDPLLTQNV	960
	VERTVICPIS	SVPGNLAGPT	QLRGSHTMLC	TEDPCSRLI			

Seq ID NO: 524 DNA sequence
Nucleic Acid Accession #: XM_058069.2
Coding sequence: 1..1413

55	1	11	21	31	41	51	
	ATGAAGTTTC	TTCTAATACT	GCTCCTGCAG	GCCACTGCTT	CTGGAGCTCT	TCCCCTGAAC	60
	AGCTCTACAA	GCCTGGAAAA	AAATAATGTG	CTATTTGGTG	AAAGATACTT	AGAAAAATTT	120
	TATGGCCTTG	AGATAAACAA	ACTTCCAGTG	ACAAAAATGA	AATATAGTGG	AAACTTAAATG	180
	AAGGAAAAAA	TCCAAGAAAT	GCAGCACTTC	TTGGGTCTGA	AAGTGACCGG	GCAACTGGAC	240
60	ACATCTACCC	TGGAGATGAT	GCAGCACCTT	CGATGTGGAG	TCCCGATGTT	CCATCATTTT	300
	AGGGAAATGC	CAGGGGGGCC	CGATGTGGAG	AAACATTATA	TCACCTACAG	AATCAATAAT	360
	TACACACCTG	ACATGAACCG	TGAGGATGTT	GACTACGCAA	TCCGGAAAGC	TTTCCAAGTA	420
	TGGAGTAATG	TTACCCCTTT	GAAATTCAGC	AAGATTAACA	CAGGCATGGC	TGACATTTTG	480
	GTGGTTTTTG	CCCGTGGAGC	TCATGGAGAC	TTCCATGCTT	TTGATGGCAA	AGGTGGAATC	540
65	CTAGCCCATG	CTTTTGGACC	TGGATCTGGC	ATTGGAGGGG	ATGCACATT	CGATGAGGAC	600
	GAATTCCTGA	CTACACATT	AGGAGGCACA	AACTTGTCTC	TCATCTGCTG	TCACGAGATT	660
	GGCCATTCCT	TAGGCTCTGG	CCATTCTAGT	GATCCAAAGG	CCGTAAATGT	CCCCACCTAC	720
	AAATATGTTG	ACATCAACAC	ATTTGCGCTC	TCTGCTGATG	ACATACGTGG	CATTCACTCC	780
	CTGTATGGAG	ACCCAAAAGA	GAACCAACGC	TTGCCAAATC	CTGACAAATC	AGAACCAAGT	840
70	CTCTGTGACC	CCAATTGTAG	TTTTGATGCT	GTCACTACCG	TGGGAAATAA	GATCTTTTTC	900
	TTCAAAGACA	GGTTCTTCTG	GCTGAAGGTT	TCTGAGAGAC	CAAAGACCAG	TGTTAATTTA	960
	ATTTCTTCCT	TATGGCCAAC	CTTGCCATCT	GGCATTGAAG	CTGCTTATGA	AATTGAAGCC	1020
	AGAAATCAAG	TTTTTCTTTT	TAAAGATGAC	AAATACTGGT	TAATTAGCAA	TTTAAGACCA	1080
75	GAGCCAAATT	ATCCCAAGAG	CATACATTCT	TTTGGTTTTT	CTAACTTTGT	GAATAAATTT	1140
	GATGCAGCTG	TTTTTAACCC	ACGTTTTTAT	AGGACCTACT	TCTTTGTAGA	TAACCAAGTAT	1200
	TGGAGGTATG	ATGAAGGAG	ACAGATGATG	GACCTGGTGT	ATCCCAAACT	GATTACCAAG	1260
	AACTTCCAAG	GAATCGGGCC	TAAATTTGAT	GCAGTCTTCT	ACTCTAAAAA	CAAACTACTAC	1320
80	TATTTCTTCC	AAGGATCTAA	CCAATTGAA	TATGACTTCC	TACTCCAAAG	TATCACCAAA	1380
	ACACTGAAAA	GCAATAGCTG	GTTTGGTTGT	TGA			

Seq ID NO: 525 Protein sequence
Protein Accession #: P39900

85	1	11	21	31	41	51	
	MKPLILLILL	ATASGALPLN	SSTSLEKNV	LFGERYLEKF	YGLEINKLPV	TKMKYSGNLM	60
	KEKIQEMQHF	LGLKVVGQLD	TSTLEMMHAP	RCGVDPVHHF	REMPGGPVWR	KHYITYRINN	120

YTPDMNREDEV DYAIRKAFQV WSNVTPKXFS KINTGMADIL VVFARGAGHD FHAFDGGKGI 180
 LAHAFGPGSG IGGDAHFDED EFWTTHSGGT NLFLTAVHEI GHSLGLGHSS DPKAVMFPTY 240
 KYVDINTFRL SADDIRGIQS LYGDPKENQR LPNPDNSEPA LCDPNLSFDA VTTVGNKIFP 300
 FKDRFFWLKV SERPKTSVNL ISSLWPTLPS GIEAAEIEA RNQVFLFKDD KYWLISNLRP 360
 EPNYPKSIHS FGFPNFKKI DAAVFNPRFY RTYFFVDNQY WRYDERRQMM DPGYPLKITK 420
 NFOGIGPKID AVFYSKNKYY YFFQGSNQFE YDFLLQRITK TLKSNSWFGC

Seq ID NO: 526 DNA sequence

Nucleic Acid Accession #: NM_024423.1

Coding sequence: 64..2590

1 11 21 31 41 51
 15 GGCAGGTCTC GCTCTCGGCA CCCTCCCGGC GCCCGCGTTC TCCTGGCCCT GCCCGGCATC 60
 CCGATGGCCG CCGCTGGGCC CCGGCGCTCC GTGCGCGGAG CCGTCTGCCT GCATCTGCTG 120
 CTGACCTCTG TGATCTTCAG TCGTGATGGT GAAGCCTGCA AAAAGGTGAT ACTTAATGTA 180
 CCTTCTAAAC TAGAGGCAGA CAAATAAATT GGCAGAGTTA ATTTGGAGA GTGCTTCAGG 240
 TCTGCAGACC TCATCCGCTC AAGTGATCCT GATTTCAGAG TTCTAAATGA TGGGTCACTG 300
 20 TACACAGCCA GGGCTGTTGC GCTGTCTGAT AAGAAAAGAT CATTTACCAT ATGGCTTTCT 360
 GACAAAAGGA AACAGACACA GAAAGAGGTT ACTGTGCTGC TAGAACATCA GAAGAAGGTA 420
 TCGAAGACAA GACACACTAG AGAACTGTT CTCAGGCGTG CCAAGAGGAG ATGGGCACCT 480
 ATTCCTTGCT CTATGCAAGA GAATTCCTTG GCCCTTTCC CATTGTTTCT TCAACAAGTT 540
 GAATCTGATG CAGCACAGAA CTATACTGTC TTCTACTCAA TAAGTGGACG TGGAGTTGAT 600
 25 AAAGAACCTT TAAATTTGTT TTATATAGAA AGAGACACTG GAAATCTATT TTGCACTCGG 660
 CCTGTGGATG GTGAAGAATA TGATGTTTTT GATTTGATTG CTTATGCGTC AACTGCAGAT 720
 GGATATTTCG CAGATCTGCC CCTCCCCTA CCCATCAGGG TAGAGGATGA AAATGACAAC 780
 CACCTCTGTT TCACAGAAGC AATTATAAAT TTGAAGTTT TGGAAAGTAG TAGACCTGGT 840
 ACTACAGTGG GGGTGGTTTG TGCCACAGAC AGAGATGAAC CGGACACAT GCATACGCGC 900
 30 CTGAATACCA GCATTTTGCA GCAGACACCA AGGTCACTG GGCTCTTTTC TGTGCATCCC 960
 AGCAGAGGCG TAATCACCAC AGTCTCTCAT TATTTGGACA GAGAGGTTGT AGACAAGTAC 1020
 TCATTGATAA TGAAATGATC AGACATGGAT GGCCAGTTTT TTGGATTGAT AGGCACATCA 1080
 ACTTGATACA TAACAGTAAC AGATTCAAAT GATAATGCAC CCATCTTCAG ACAAATGCT 1140
 TATGAAGCAT TTGTAGAGGA AATGTCATT AATGTGGAAA TCTTACGAAT ACCTATAGAA 1200
 35 GATAAGGATT TAATTAACAC TGCCAATTGG AGAGTCAATT TTACCATTTT AAAGGGAAT 1260
 GAAAATGGAC ATTTCAAATC CAGCACAGAC AAAGAACTA ATGAAGGTGT TCTTTCTGTT 1320
 GTAAAGCCAC TGAATTATGA AGAAACCGT CAAGTGAACC TGGAAATTTG AGTAAACAAT 1380
 GAAGCGCCAT TTGCTAGAGA TATTCACAGA GTGACAGCCT TGAACAGAGC CTTGGTTACA 1440
 GTTCATGTGA GGGATCTGGA TGAGGGGCGT GAATGCACCT CTGCAGCCCA ATATGTGCGG 1500
 40 ATTAAGAAAA ACTTAGCAGT GGGTCAAAAG ATCAACGGCT ATAAGGCATA TGACCCCGAA 1560
 AATAGAAATG GCAATGGTTT AAGGTACAAA AAATGTCATG ATCTTAAAGG TTGGATCACC 1620
 ATTGATGAAA TTTCAGGGTC AATCATAACT TCCAAAATCC TGGATAGGGA GGTGGAACAT 1680
 CCCCAAAATG AGTTGTATAA TATTACAGTC CTGGCAATAG ACAAAGATGA TAGATCATGT 1740
 ACTGGAACAC TTGCTGTGAA CATTGAAAGT GTAAATGATA ATCCACCAGA AATACTTCAA 1800
 45 GAATATGTAG TCATTGCAA ACCAAAATG GGGTATACCG ACATTTTAGC TGTGTGCTCT 1860
 GATGAACCTG TCCATGAGC TCCATTTTAT TTCAGTTTGC CCAATACTTC TCCAGAAATC 1920
 AGTAGACTGT GGAGCCTCAC CAAAGTTAAT GATACAGCTG CCCGTCTTTC ATATCAGAAA 1980
 AATGCTGGAT TTCAAGATAA TACCATTCTT ATTACTGTAA AAGACAGGGC CGGCCAAGCT 2040
 GCAACAAAAT TATTCTGTGT TAATCTGTGT GAATGTACTC ATCCAACTCA GTGTCTGTGG 2100
 50 ACTTCAAGGA GTACAGGAGT AATACTTGGG AAATGGGCAA TCCTTGCAAT ATTACTGGGT 2160
 ATAGCACTGC TCTTTTCTGT ATTGCTAAT TTAGTATGTG GAGTTTTTGG TGCAACTAAA 2220
 GGGAAACGTT TTCCTGAAGA TTTAGCACAG CAAAACCTAA TTATATCAAA CACAGAAGCA 2280
 CTTGGAGAGC ATAGAGTGTG CTCTGCCAAT GGATTTATGA CCAAACTAC CAACAACCTC 2340
 AGCCAAGGTT TTGCTGTATC TATGGGATCA GGAATGAAAA ATGGAGGGCA GGAACCACTT 2400
 55 GAAATGATGA AAGGAGGAAA CCAGACCTTG GAATCTGCC GGGGGGCTGG GCATCATCAT 2460
 ACCCTGGACT CCTGCAGGG AGGACACACG GAGGTGGACA ACTGCAGATA CACTTACTCG 2520
 GAGTGGCACA GTTTTACTCA ACCCGTCTC GGTGAAGAA CCATTAGAGG ACACACTGGT 2580
 TAAAAATTA ACATAAAAGA AATTGCATCG ATGTAATCAG AATGAAGACC GCATGCCATC 2640
 CCAAGATTAT TGCTCTACTT ATAACATAGA GGAAGAGGGA TCTCCAGCTG GTTCTGTGGG 2700
 60 CTGCTGCAGT GAAAAGCAGG AAGAAGATGG CCTTGACTTT TTAATAATT TGAACCCCAA 2760
 ATTTATTACA TTAGCAGAAG CATGCACAAA GAGATAATGT CACAGTGCTA CAATTAGGTC 2820
 TTTGTCAGAC ATCTGGAGG TTTCCAAAAA TAATATTGTA AAGTTCAATT TCAACATGTA 2880
 TGTATATGAT GATTTTTC TCAATTTTGA ATTATGCTAC TCACCAATTT ATATTTTAA 2940
 AGCCAGTTGT TGCTTATCTT TTCCAAAAAG TGAAAAATGT TAAACAGAC AACTGGTAAA 3000
 65 TCTCAAACCT CAGCACTGGA ATTAAGGTCT CTAAGCATC TGCTCTTTT TTTTTCACG 3060
 GATATTTTAG TAATAATAT CTGGATAAAA TATTAGTCCA ACAATAGCTA AGTTATGCTA 3120
 ATATCACATT ATTATGTATT CACTTTAAGT GATAGTTTAA AAAATAACA AGAAATATTG 3180
 AGTATCACTA TGTGAAGAAA GTTTTGGAAA AGAAACAATG AAGACTGAAT TAAATTAATA 3240
 70 ATGTTGCAGC TCATAAAGAA TTGGGACTCA CCCCTACTGC ACTACCAAT TCATTTGACT 3300
 TTGGAGGCAA AATGTGTGTA AGTGCCCTAT GAAGTAGCAA TTTTCTATAG GAATATAGTT 3360
 GGAAATAAAT GTGTGTGTGT ATATTATTAT TAATCAATGC AATATTTAAA ATGAAATGAG 3420
 AACAAAGAGG AAAATGTTAA AAACCTGAAA TGAGGCTGGG GTATAGTTTG TCCTACAATA 3480
 GAAAAAAGAG AGAGCTTCTT AGGCCTGGGC TCTTAAATGC TGCATTATAA CTGAGTCTAT 3540
 75 GAGGAAATAG TTCCTGTCCA ATTTGTGTAA TTTGTTTAAA ATTGTAAATA AATTAAACTT 3600
 TTCTGGTTTC TGTGGGAAGG AAATAGGGAA TCCAATGGAA CAGTAGCTTT GCTTTCAGT 3660
 CTGTTTCAAG ATTTCTGCAT CCACAAGTTA GTAGCAAACT GGGGAATACT CGCTGCAGCT 3720
 GGGGTTCCTT GCTTTTGGT AGCAAGGGTC CAGAGATGAG GTGTTTTTT CGGGAGCTA 3780
 ATAACAAAAA CATTTTAAAA CTTACCTTTA CTGAAGTTAA ATCTCTATT GCTGTTTCTA 3840
 80 TTCTCTCTTA TAGTGACCAA CATCTTTTTA ATTTAGATCC AAATAACCAT GTCCCTCTAG 3900
 AGTTTAGAGC CTAGAGGGAG CTGAGGGGAG GATCTTACTG AAAGCACCTT GGGGAGATTG 3960
 ATGTCTCTTA AACCTTAAGC CCACAACTT GACACCTGAT CAGGTCTGGG AGCTACAAAA 4020
 TTTCAATTTT CTCCTCACTG CCCTTCTTCT GAGTGGCATT GGCTGAATC AAGGAAGGCC 4080
 AGGCCTTGTG GGCCCTCTTC TTTGGGCTTT TGCTTAAAGC AACACCTCCA GCAGAGATTC 4140
 CCTTAAGTGA CTCAAGTTT TCCACCATCC TTCAGCGTGA ATTAATTTT AATCAGTTTG 4200
 85 CTTTCTCCAG AGAATCTTTA AAATAATAGA AGAAATAGAA ATTTTGAATG TATAAAGAA 4260
 AAAGATCAAG TTGTCATTTT AGAACAGAGG GAACCTTGGG AGAAAGCAGC CCAAGTAGGT 4320
 TATTTGTACA GTCAGAGGGC AACAGGAAGA TGACGGCCTT CAAGGGCAAG GAGAGGCCAC 4380
 AAGGAATATG GGTGGGACTA AAAGCAACAT CGTCTGCTTC ATACTTTTTC CTAGGCTTGG 4440

	CAC	TGC	CTT	TCT	TC	CA	GG	CCA	TGG	CA	AA	CT	GAG	GGG	AT	CA	4500
	CCA	AC	CT	CT	CT	AT	GG	CT	CAC	CT	TAT	TT	GG	AG	T	CA	4560
	TGC	AT	GA	GT	CT	GA	AG	CT	ATT	TG	CA	GA	CT	GG	T	GC	4620
	AGG	CAT	TC	AT	GA	TT	GT	GT	AT	T	CT	CT	C	TT	CT	GG	4680
5	CT	AT	GA	AT	TA	A	AT	GG	CT	CT	TA	AA	TT	CT	TT	CT	4740
	TG	AC	CT	TAA	AT	CT	AT	GT	GT	TT	AG	CT	TA	TT	AG	CT	4800
	TT	G	AG	CA	GC	GA	CT	CA	AG	G	CT	GG	AG	TG	CA		4860
	CT	GA	AG	CT	C	GC	CT	CC	CG	G	GT	CT	CA	GC	CT	CG	4920
	GAC	TAC	AG	GC	CC	CA	CC	AC	CC	AC	CG	CC	GG	CT			4980
10	TT	CA	CT	GT	T	AG	CC	AG	AT		TG	CT	CG	AT			5040
	TCC	CA	AG	AT	G	CT	GG	AT	TAC		AG	GC	AT	GAC			5100
	GT	CG	CT	CT	T	TT	TA	AT	GT	TA	TC	AT	T	TT	TA		5160
	TC	AT	CT	TT	GA	A	A	A	CT	CA	A	A	AG	AG	CT		5220
	GC	CA	AA	TA	T	TG	GT	CT	GA		AAT	G	GA	AT			5280
15	TG	T	AA	CC	AG	A	GC	CA	GT	AT	CT	A	CC	CA	CT		5340
	CC	CA	CT	C	CA	C	G	AT	CA	A	CT	CC	A	CT	TA		5400
	TC	AA	AG	AG	CA	T	AT	CA	CT	CT	CT	CT	CT	CT	CT		5460
	TG	AA	CT	TG	CT												5520
20	AA	AT	G	AA	AT	T	T	A	T	T	T	A	G	T	A		5580
	TC	CT	T	A	T	A	T	G	T	A	T	G	T	A	T		5640
	AG	CT	T	T	C	C	C	C	A	C							5700
	TT	T	T	C	T	T	A	A	G	A							5760
	TT	T	A	A	C	A	G	A									5820
25	CT	G	T	C	T	T	A	A	A								5880
	A	A	T	A	A	A	A	A	A								5940
	TT	T	C	A	G	A	T										6000
	TT	T	A	G	A	T											6060
	G	A	A	T	A	G	A	A									6120
30	TC	AT	T	A	T	A	T	A									6180
	TT	G	A	G	C	A	C	A									6240
	GT	A	T	T	A	A	A	A									6300
	AC	A	G	G	G	G	T	T									6360
	C	A	G	G	C	A	A	T									6420
35	G	A	C	A	G	A	T	G									6480
	GG	A	G	T	GT	GC	T										6540
	AA	AG	CC	CT	T	A	T										6600
	ACC	A	T	T	T	G	T										6660
	AT	AC	C	G	G	A	T										6720
40	GT	T	G	A	A	G	C										6780
	ACT	T	C	T	G	T											6840
	AT	G	A	A	C	A	A										6900
	AC	A	T	A	G	A	A										6960
	AT	G	T	A	G	T	T										7020
	C	A	T	A	T	A	T										

Seq ID NO: 527 Protein sequence
Protein Accession #: NP_077741.1

50	1	11	21	31	41	51		
	MAAGPRRSV	RGAVCLHLL	TLVIFSRDGE	ACKKVILNVP	SKLEADKIIG	RVNLEECFRS	60	
	ADLRSSDDP	FRVLNDGSVY	TARAVALS	DKRSEPTIWLSD	KRKQTKQKEVT	VLEHQKKVVS	120	
	KTRHRETVL	RRAKRRWAPI	PCSMQENSLG	PFPLFLQQVE	SDAAQNYTVF	YSISGRGVDD	180	
55	EPLNLFYIER	DTGNLFCTRP	VDREEDVFD	LIAYASTADG	YSADLPPLP	IRVEDENDNH	240	
	PVFTEAITYNF	EVLESSRPPT	TGVGVCATDR	DEPDTHMTRL	KYSILQQTSPR	SPGLFSVHPHS	300	
	TGVITTVSHY	LDREVVDKYS	LIMKVQMDRG	QFPGLIGTST	CIIITVTDSDN	NAPTFRQNAV	360	
	EAFVEENAFN	VEILRIPIED	KDLINTANWR	VNFTILKGNE	NGHPKISTDK	ETNNEGVSUVI	420	
60	KPLNYEENRG	VNLEIGVNNE	APPARDIPRV	TALNRALVTV	HVRDLDEGTE	CTPAAGYVVR	480	
	KENLAVGSKI	NGYKAYDPEN	RNGNGLRYKK	LHDPKGWITI	DEISGSIYS	KILDRSEVTP	540	
	KNELYNTVL	AIDKDDRSCT	GTLAVNIEDV	NDNPPPEILQE	YVVICPKPMG	YTVIDLAVDPD	600	
	EPVHGAPFFY	SLPTNSPEIS	RLWSLTKVND	TAARLSYQKN	AGFQETIPTI	TKDRAGQAAV	660	
65	TKLLRVNLCE	CTHPTQCRAT	SRSTGVILGK	WAILAILLGI	ALLFSVLLTL	VCGVFGATKG	720	
	KRFPEDLAQQ	NLIISNTEAP	GDDRVCBSANG	FMTQTTNNSS	QGFCGTMGSG	MKNNGQETIE	780	
	MMKGGNOTLE	SCRGAGHHHT	LDS	CRGGHTE	VDNCRITYSE	WHSTPTQRLG	EESIRGHTG	

Seq ID NO: 528 DNA sequence
Nucleic Acid Accession #: NM_001941.2
Coding sequence: 64..2754

70	1	11	21	31	41	51	
	GGCAGGTCTC	GCTCTCGGCA	CCCTCCCGGC	GCCCGCGTTC	TCCTGGCCCT	GCCCGGCATC	60
	CCGATGGCCG	CCGCTGGGCC	CCGCGCGCTCC	GTGCGCGGAG	CCGCTCGCCT	GCATCTGCTG	120
	CTGACCTCTG	TGATCTTCAG	TCGTGATGGT	GAAGCCTGCA	AAAAGGTGAT	ACTTAATGTA	180
75	CCTTCTAAAC	TAGAGGCAGA	CAAAATAATT	GGCAGAGTTA	ATTTGGAAGA	GTGCTTCAGG	240
	TTCTGCAGAC	TCACTCCGGT	AAGTGAATCCT	GATTTTCAGAG	TTCTAAATGA	TGGGTCACTG	300
	TACACAGCCA	GGGCTGTGTC	GCTGTCTGAT	AAGAAAAGAT	CATTTTACCAT	ATGGCTTTCT	360
	GACAAAAGGA	AACAGACACA	GAAAGAGGTT	ACTGTGCTGC	TAGAACATCA	GAAGAAGGTA	420
	TCGAAGACAA	GACACACTAG	AGAAACTGTT	CTCAGGCGTG	CCAAGAGGAG	ATGGGCACCT	480
80	ATTCTTGCT	CTATGCAAGA	GAATTCCTTG	GGCCCTTTCC	CATTGTTTCT	TCAACAAGTT	540
	GAATCTGATG	CAGCACAGAA	CTATACTGTC	TTCTACTCAA	TAAGTGGACG	TGGAGTTGAT	600
	AAAGAACCTT	TAAATTTGTT	TTATATAGAA	AGAGACACTG	GAAATCTATT	TTGCACTCGG	660
	CCTGTGATCT	TGAAGAATAA	TGATGTTTTT	GATTTGATTG	CTTATGCGTC	AATCGAGAT	720
	GGATATTTAG	CAGATCTGCC	CCTCCCACTA	CCCATCAGGG	TAGAGGATGA	AAATGACAAC	780
85	CACCTGTTG	TCACAGAAGC	AATTTATAAT	TTTGAAGTTT	TGGAAGTAGT	TAGACCTGGT	840
	ACTACAGTGG	GGGTGGTTTG	TGCCACAGAC	AGAGATGAAC	CGGACACAAT	GCATACGCGC	900
	CTGAAATACA	GCATTTTGCA	GCAGACACCA	AGGTCACTTG	GGCTCTTTTC	TGTGCATCCC	960

5

10

15

20

25

30

35

40

45

50

55

60

65

70

75

80

85

AGCACAGGGG TAATCACCAC AGTCTCTCAT TATTGGACA GAGAGGTTGT AGACAAGTAC 1020
 TCATTGATAA TGAAAGTACA AGACATGGAT GGCCAGTTTT TTGGATTGAT AGGCACATCA 1080
 ACTTGTATCA TAACAGTAAC AGATTCAAAT GATAATGCAC CCACCTTTCAG ACAAATGCT 1140
 TATGAAGCAT TTGTAGAGGA AATGGCATT TCTTACGAAT ACCTATAGAA 1200
 GATAAGGATT TAATTAACAC TGCCAAATGG AGAGTCAATT TTACCATTTT AAAGGGAAAT 1260
 GAAATGGAC ATTTCAAAT CAGCACAGAC AAAGAACTA ATGAAGGTGT TCTTCTGTT 1320
 GTAAAGCCAC TGAATTATGA AGAAAACCGT CAAGTGAACC TGGAAATTTGG AGTAAACAT 1380
 GAAGCGCCAT TTGCTAGAGA TATTCCAGAG GTGACAGCCT TGAACAGAGC CTGTTTACA 1440
 GTTCATGTGA GGGATCTGGA TGAGGGGCCCT GAATGCATCT CTGCAGCCCA ATATGTGCGG 1500
 ATTAAGAAA ACTTAGCAGT GGGGTCAAAG ATCAACGGCT ATAAGGCATA TGACCCCGAA 1560
 AATAGAAATG GCAATGGTGT AAGGTACAAA AAATTGCATG ATCCTAAAGG TTGGATCACC 1620
 ATTGATGAAA TTTCAAGGTC AATCATAACT TCCAAATCC TGGATAGGGA GGTGAAACT 1680
 CCCAAAATG AGTTGTATAA TATTACAGTC CTGGCAATAG ACAAAGATGA TAGATCATGT 1740
 ACTGGAACAC TTGTGTGTA CATTGAAGAT GTAAATGATA ATCCACCAGA AATACTTCAA 1800
 GAATATGTAT TCAATTGCAA ACCAAAATG GGGTATACCG ACATTTTAGC TGTGTATCCT 1860
 GATGAACCTG TCCATGGAGC TCCATTTTAT TTCAGTTTGC CCAATACTTC TCCAGAAATC 1920
 AGTAGACTGT GGAGCCTCAC CAAAGTTAAT GATACAGCTG CCCGCTCTTC ATATCAGAAA 1980
 AATGTCTGGT TTCAAGATA TACCATTCTT ATTACTGTAA AAGACAGGGC CGGCCAAGCT 2040
 GCAACAAAAT TATTGAGAGT TAATCTGTGT GAATGTACTC ATCCAACTCA GTGTGTCGG 2100
 ACTTCAAGGA GTACAGGAGT AATACTTGGG AAATGGGCAA TCCTTGCAAT ATTACTGGGT 2160
 ATAGCACTGC TCTTTCTGT TTAGTAACT TTAGTATGTG GAGTTTGTGG TGCACTAAA 2220
 GGGAAACGTT TTCTGAAGA TTTAGCACAG CAAAACCTAA TTATATCAA CACAGAAGCA 2280
 CTTGGAGAGC ATAGAGTGT CTCTGCCAAT GGATTTATGA CCCAACTAC CAACAACCTC 2340
 AGCCAAAGTT TTGTGTGATC TATGGGATCA GGAATGAAAA ATGGAGGGCA GGAAACCAT 2400
 GAAATGATGA AAGAGGAAAA CCAGACCTTG GAATCTGCC GGGGGGCTGG GCATCATCAT 2460
 ACCCTGGACT CCTGCAGGGG AGGACACACG GAGGTGGACA ACTGCAGATA CACTTACTCG 2520
 GAGTGGCACA GTTTTACTCA ACCCGTCTC GGTGAAAAAT TGCATCGATG TAATCAGAAT 2580
 GAAGACCCGA TGCCATCCCA AGATTATGTC CTCACTTATA ACTATGAGGG AAGAGGATCT 2640
 CCAGCTGGTT CTGTGGCTG CTGCAGTGAA AAGCAGGAAG AAGATGGCCT TGACTTTTAA 2700
 AATAAATTTG AACCCAAAT TATTACATTA GCAGAAAGCAT GCACAAAGAG ATAATGTCAC 2760
 AGTGTACAAA TTAGTCTTT CTGCAGACAT CTGGAGGTTT CCAAAAATAA TATTGTAAAG 2820
 TTCAATTTCA ACATGTATGT ATATGATGAT TTTTCTCTCA ATTTTGAATT ATGCTACTCA 2880
 CCAATTTATA TTTTAAAGC CAGTTGTGTC TTATCTTTTC CAAAAGTGA AAAATGTTAA 2940
 AACAGACAAC TGGTAAATCT CAAACTCCAG CACTGGAATT AAGGTCTCTA AAGCATCTGC 3000
 TCTTTTTTTT TTTTACGGAT ATTTTAGTAA TAAATATGCT GGATAAATAT TAGTCCAACA 3060
 ATAGCTAAGT TATGCTAATA TCACATTATT ATGTATTCAC TTTAAGTAT AGTTTAAAAA 3120
 ATAAACAAGA AATATTGAGT ATCACTATGT GAAGAAAGTT TTGAAAGA AACAATGAAG 3180
 ACTGAATTA AATAAAATG TTGCAGCTCA TAAAGAAATG GGACTCACCC CTACTGCATC 3240
 ACCAAATTC TTTGACTTTG GAGGCAAAAT GTGTGAAGT GCCCTATGAA GTAGCAATTT 3300
 TCTATAGGAA TATAGTTGGA AATAAATGTG TGTGTGTATA TTATTATTA TCAATGCAAT 3360
 ATTTAAATG TATGAGAAC AAGAGGAAAA ATGGTAAAAA CTTGAAATGA GGCTGGGGTA 3420
 TAGTTTGTCC TACAATAGAA AAAAGAGAGA GCTTCTAGG CCTGGGCTCT TAAATGCTGC 3480
 ATTATAACTG AGCTATGAG GAAATAGTTC CTGTCCAATT TGTGTAATTT GTTTAAATTT 3540
 GTAAATAAAT TAAACTTTTC TGGTTCTGT GGGAAAGAAA TAGGGAATCC AATGGAACAG 3600
 TAGCTTTGCT TTGCAGTCTG TTTCAAGATT TCTGCATCCA CAAGTTTAGTA GCAAACTGGG 3660
 GAATACTCGC TGACGCTGGG GTTCCCTGCT TTTTGGTAGC AAGGGTCCAG AGATGAGGTG 3720
 TTTTCTCGG GGAGCTAATA ACAAACCAT TTTAAACTT ACCTTTACTG AAGTTAAATC 3780
 CTCTATTGCT GTTCTATTTC TCTCTTATAG TGACCAACAT CTTTTTAATT TAGATCCAAA 3840
 TAACCATGTC CTCTAGAGT TTAGAGGCTA GAGGGAGCTG AGGGGAGGAT CTACTGAAA 3900
 GCACCTCGGG GAGATTGATT GTCTTAAAC CTAAGCCCCA CAAACTTGAC ACCTGATCAG 3960
 GTCTGGGAGC TCAAAAATTT CATTTTCTC CTCAGTCCCT TCTCTGAG TGCCATTGGC 4020
 CTGAATCAAG GAAAGCCAGG CCTTGTGGGC CCCCTTCTTT CGGCTTCTG CTAAAGCAAC 4080
 ACCTCCAGCA GAGATTCTCT TAAGTGACTC CAGGTTTTCC ACCATCTTTC AGCGTGAATT 4140
 AATTTTAAAT CAGTTTGTCT TCTCCAGAGA AATTTTAAAA TAATAGAAGA AATAGAAAT 4200
 TTGAATGTAT AAAAGAAATAT GATCAAGTTG TCATTTTAGA ACAGAGGGA CTTTGGGAGA 4260
 AAGCAGCCCA AGAGGTTTAT TTGTACAGTC AGAGGGCAAC AGGAAGATG AGGCCTTCAA 4320
 GGGCAAGGAG AGGCCACAAG GAATATGGGT GGGAGTAAAA GCAACATCGT CTGCTTCATA 4380
 CTTTCTCTTA GGCCTGGCAC TGCCTTTTCC TTTCTCAGG CAATGGCAAC TGCCATTGGA 4440
 GTCCGGTGAG GGATCAGCCA ACCTCTTCTC TATGGCTCAC CTTATTGGA GTGAGAAATC 4500
 AAGGAGACAG AGCTGACTGC ATGATGAGTC TGAAGGCATT TGCAGGATGA GCCTGAACTG 4560
 GTTGTGCAGA ACAAACAAGG CATTCTAGGG AATTGTTGTA TTCCTTCTGC AGCCCTCCTT 4620
 CTGGGCACTA AGAAGGTCTA TGAATTAAT GCCTATCTAA AATCTGATT TATCTCTACA 4680
 TTTTCTGTTT TCTAATTGGA CCTTAAATC TATGTGTTT AGACTTAGAC TTTTATTGTC 4740
 CCCCCCCCCC TTTTTTTTTG AGACGGAGTC TCGCTCTGAC GCACAGGCTG GAGTGCAGTG 4800
 GCTCCGATCT CTGCTCACTG AAAGCTCCGC CTCGGGGTT CATGCCATT TCCTGCCTCA 4860
 GCCTCCTGAG TAGCTGGGAC TACAGGCGCC CACCACCAG CCCGGCTAAT TTTTGTATT 4920
 TTTAATAGAG ACGGGGTTTC ACTGTGTTAG CCAGGATGGT CTCGATCTCC TGACCTCGTG 4980
 ATCCGCCTGC CTCGGCCTCC CAAAGTGCTG GGATTACAGG CATGACCCAC CGCTCCCGGC 5040
 CTTGTTTCC GTTTAAAGTC GTCTTCTTT AATGTAATCA TTTTGAACAT GTGTGAAAGT 5100
 TGATCATACG AATTGGATCA ATCTTGAAT ACTCAACCA AAGACAGTC AGAAGCCAGG 5160
 GGGAGAAAGA ACTCAGGGCA CAAAATATTG GTCTGAGAA TGAATCTCT GTAAGCCTAG 5220
 TTGCTGAAAT TTCTGCTGT AACCAGAAGC CAGTTTATC TAACGGCTAC TGAACACCC 5280
 ACTGTGTTT GCTCACTCCC TCACTCACCG ATCAAAACCT GCTACCTCCC CAAGACTTTA 5340
 CTAGTGCCGA TAACTTTCT CAAAGAGCAA CCAGTATCAC TTCCCTGTTT AAAAAACCTC 5400
 TAACCATCTC TTTGTTCTT GAACATGCTG AAAACACCT GGTCTGATG TATGCCGAA 5460
 TTTGTAATTC TTTCTCTCA AATGAAATTT TAATTTTAGG GATTCAATTC TATATTTTCA 5520
 CATATGTAGT ATTATATTT CCTTATATGT GTAAGGTGAA ATTTATGTA TTTGAGTGTG 5580
 CAAGAAAAA TATTTTAAAA CTTTCAATTT TTCCCCAGT GAATGATTGA GAATTTTTTA 5640
 TGTAAATATA CAGAAATGTT TTTCTACTT TTATAAGGAA GCAGCTGTCT AAAATGCAGT 5700
 GGGGTTGTT TTGCAATGTT TTTAAGAGG TTTTAGTATT GCTATTAAGA GAAGTTACTT 5760
 TGCTTTAAA GAAACTTGGC TGCTTAAAT AAGCAAAAT TGGATGCATA AAGTAATATT 5820
 TACAGATGTT GGGAGATGTA ATAAAAAAT ATTAACCTGG TTTCTGTTT TTGCTGATT 5880
 TAGAGATTA AATAATTCTAA GATGATCACT TTGCAAAAT ATGCTTATGG CTGGCATGGA 5940
 AATAGAAAT CTCAATATG TCTTTGTTGT ATTAATGGGG AATATTTTGG ACAATGTTTC 6000
 ATTATCAAT GTCCAGATG ATTAATATAT ATTGTAATGT TGGGAAGAGA TCACTATTTT 6060
 GAAGCACAGC TTTACAGATG AGTATCTATG ATACATATGT ATAATAAAT TTGATCGGGT 6120
 ATTAAGAGTA TTAGAGGTG GTTATAATTG CAGAGTATTC CATGAATAGT AACTGACAC 6180

WO 02/086443

PCT/US02/12476

AGGGGTTTTA CTTTGAGGAC CAGTGTAGTC AAGGGAAAAC ATGAGTTAAA AAGAAAAGCA 6240
GGCAATATTG CAGTCTTGAT TCTGCCACTT ACAGGATAGA TAATGCCCTGA ACTTTAATGA 6300
CAAGATGATC CAACCATAAA GGTGCTCTGT GCTTCACAGT GAATCTTTTC CCCATGCAGG 6360
AGTGTGCTCC CCTACAAACG TTAAGACTGA TCATTTCAAA AATCTATTAG CTATATCAAA 6420
AGCCTTACAT TTTAATATAG GTTGAACCAA AATTTCAATT CCAGTAACCT CTATTGTAAC 6480
CATTATTTTT GTGTATGTCT TCAAGAATGT TCATTGGATT TTTGTTTGTG ATAGTAAAAA 6540
ACCGGATACA TTTACAGTGT CCTTCAGTAT TGATTGGTGT GAATATTGGG TCATAATGGT 6600
TGAGAAGCAT GGACACTAGA GCCAGAAATGC TTGGATATGA ATCCTGGATC TGTCACTTAC 6660
TTCTGTGTGA CCTTTGAAAG GCTACTTATT TCCTCTCTTA GCTTTCTCAT TAAAAATCAAT 6720
GAACAAATGCC AGCCTCATGG GGTGTGTGAA TGATTAAAT AGTTAATATA CCTAAAGTAC 6780
ATAGAACACT GCCTGCACAT AGTAAAGAAA TTATAAGTGT GAGGTAGTTG GTAAAAATTAT 6840
GTAGTTGGAT ATACTACCGA ACAATATCTA ATCTCTTTT AGGGAAATAA AGTTTGTGCA 6900
TATATATAAT CCCGAAACAT G

Seq ID NO: 529 Protein sequence
Protein Accession #: NP_001932.1

1 11 21 31 41 51
MAAAGPRRSV RGAVCLHLLL TLVIFSRDGE ACKKVILNVP SKLEADKIIG RVNLEECFRS 60
ADLIRSSDDP FRVLNDGGSVY TARAVALSDK KRSFTIWLSD KRKQTQKEVT VLEHQKKVS 120
KTRHRTETVL RRAKRRWAPI PCSMQENSLG PFPLFLQQVE SDAAQNYTVF YSISGRGVDK 180
EPLNLFYIER DTGNLFCTRP VDREYDVFD LIAYASTADG YSADLPLPLP IRVEDENDNH 240
PVFTEAIYNF EVLESSRPGT TVGVVCAADR DEPDTHMTRL KYSILQQTFR SPGLFSVHPS 300
TGVITTVSHY LDREVVDKYS LIMKVQMDMG QFFGLIGTST CIITVTDSDN NAPTFRQNAY 360
EAFVEENAFN VEILRIPIED KDLINTANWR VNFTILKNGE NGHFKISTDK ETNEGVLVSU 420
KPLNYEENRQ VNLEIGVINE APPARDIPRV TALNRALVTV HVRDLDEGPE CTFAAQYVRI 480
KENLAVGSXI NGYKAYDPEN RENGNGLYKK LHDPKGWITI DEISGSIITS KLLDREVETP 540
KNELYNITVL AIDKDDRSCT GTLAVNIEDV NDNPFPEILQE YVVICKPKMG YTDILAVDPD 600
EPVHGAPFFY SLPNTSPKIS RLWSLTKVND TAARLSYQKN AGFQEYTIPI TVKDRAGQAA 660
TKLLRVNLCE CTHPTQCRAT SRSTGVILGK WAILAILGI ALLFSVLLTL VCGVFGATRG 720
KRFPEDLAQO NLIISNTAP GDDRVCSSANG FMTQTNNSS QGFCGTMGSG MKNGGQETIE 780
MMKGNQNTLE SCRGAQHHT LDCRCGGHTE VDNCRITYSE WHSFTQPRLG EKLHRCNQNE 840
DRMPSQDYVL TYNYEGRGSP AGSVGCCSEK QBEDGLDFLN NLEPKFITLA EACTKR

Seq ID NO: 530 DNA sequence
Nucleic Acid Accession #: NM_016583.2
Coding sequence: 72..842

1 11 21 31 41 51
GGAGTGGGGG AGAGAGAGGA GACCAGGACA GCTGCTGAGA CCTCTAAGAA GTCCAGATAC 60
TAAGAGCAAA GATGTTTCAA ACTGGGGGCC TCATTGTCTT CTACGGGCTG TTAGCCCAGA 120
CCATGGCCCA GTTTGGAGGC CTGCCCCGTC CCTCGGACCA GACCTGCCCC TTGAATGTGA 180
ATCCAGCCCT GCCCTTGAGT CCCACAGGTC TTGCAGGAAG CTTGACAAAT GCCCTCAGCA 240
ATGGCCTGCT GTCTGGGGGC CTGTTGGGCA TTCTGGAAAA CCTTCCGCTC CTGGACATCC 300
TGAAGCCTGG AGGAGGTACT TCTGGTGGCC TCCTTGGGGG ACTGCTTGGG AAAGTGACGT 360
CAGTGATTCC TGGCCTGAAC AACATCATTG ACATAAAGGT CACTGACCCC CAGCTGCTGG 420
AAGTGGCCTT TGTGCAGAGC CCTGATGGCC ACCGTCTCTA TGTCAACATC CCTCTCGGCA 480
TAAAGTCCCA AGTGAATACG CCCCTGGTCC GTGCAAGTCT GTTGAGGCTG GCTGTGAAGC 540
TGACATCAC TGACAGAAATC TTAGCTGTGA GAGATAAGCA GGAGAGGATC CACCTGGTCC 600
TTGGTGACTG CACCAATTC CCTGGAAGCC TGCAAAATTC TCTGCTTGAT GGACTTGGCC 660
CCCTCCCCAT TCAAGGCTCT CTGGACAGCC TCACAGGGAT CTTGAATAAA GTCTGCTGCT 720
AGTTGGTTCA GGGCAACGTG TGCCCTCTGG TCAATGAGGT TCTCAGAGGC TTGGACATCA 780
CCCTGGTGCA TGACATTGTT AACATGCTGA TCCACGGA CTAGTTGTGC ATCAAGGTCT 840
AAGCCTTCCA GGAAGGGGCT GGCCTCTGCT GAGCTGCTTC CCAGTGTCTC CAGATGGCTG 900
GCCCATGTGC TGGAAATGCA CACAGTTGCC TTCTCTCCGA GGAACCTGCC CCCTCTCCTT 960
TCCACCAGG CGTGTGTAAC ATCCCATGTG CCTCACCTAA TAAATGGCT CTCTCTCTGC 1020
AAAAAAAAA AAAAAAAAAA AAAAAAAAAA

Seq ID NO: 531 Protein sequence
Protein Accession #: NP_057667.1

1 11 21 31 41 51
MFQTGGLIVE YGLLAQTMQA FGGLPVPLDQ TLPLNVNPAI PLSPITGLAGS LTNALSNGLL 60
SGLLGILEN LPLLDILKPG GGTSGGLLGG LLGKVTSVIP GLNNIIDIKV TDPQLLELGL 120
VQSPDGHRLY VTIPGLIKLQ VNTPLVGASL LRLAVKLDT AEILAVRDQK ERIHLVLGDC 180
THSPGSLQIS LLDGLGPLFI QGLLDSLTGI LNKVLPPLVQ GNVCPVNEV LRGLDITLVH 240
DIVNMLIHGL QFVIKV

Seq ID NO: 532 DNA sequence
Nucleic Acid Accession #: NM_004363.1
Coding sequence: 115..2223

1 11 21 31 41 51
CTCAGGGCAG AGGGAGGAAG GACAGCAGAC CAGACAGTCA CAGCAGCCTT GACAAAACGT 60
TCCTGGAAC CTAGCTCTTC TCCACAGAGG AGGACAGAGC AGACAGCAGA GACCATTGGAG 120
TCTCCCTCGG CCCTCCGCCA CAGATGGTGC ATCCCTGGCC AGAGGCTCCT GCTCAGAGCC 180
TCACTTCTAA CCTTCTGGAA CCCGCCACAC ACTGCCAAGC TCATATTGTA ATCCAGCCCG 240
TTCAATGTGC CAGAGGGGAA GGAGGTGCTT CTACTTGTCC ACAATCTGCC CCAGCATCTT 300
TTTGGCTACG GCTGGTACAA AGGTGAAAGA GTGGATGGCA ACCGTCAAAT TATAGGATAT 360
GTAATAGGAA CTCAACAAGC TACCCAGGG CCCGCATACA GTGGTCGAGA GATAATATAC 420
CCCAATGCAT CCTGCTGAT CCAGAATATC ATCCAGAATG ACACAGGATT CTACACCCTA 480

5
10
15
20
25
30
35
40
45

CACGTCATAA AGTCAGATCT TGTGAATGAA GAAGCAACTG GCCAGTTCGG GGTATACCCG 540
 GAGCTGCCCA AGCCCTCCAT CTCAGCAAC AACTCCAAAC CCGTGGAGGA CAAGGATGCT 600
 GTGGCCTTCA CCTGTGAACC TGAGACTCAG GACGCAACCT ACCTGTGGTG GGTAAACAAT 660
 CAGAGCCTCC CGGTCAAGTCC CAGGCTGCAG CTGTCCAATG GCAACAGGAC CCTCACTCTA 720
 TTCAATGTCA CAAGAAATGA CACAGCAAGC TACAAATGTG AAACCCAGAA CCCAGTGAGT 780
 GCCAGGCGCA GTGATTCAGT CATCCTGAAT GTCCCTCTATG GCCCGGATGC CCCACCATT 840
 TCCCCTCTAA ACACATCTTA CAGATCAGGG GAAATCTGA ACCTCTCTGT CCACGCAGCC 900
 TCTAACCCAC CTGCACAGTA CTCTTGGTTT GTCAATGGGA CTTTCCAGCA ATCCACCCAA 960
 GAGCTCTTTA TCCCAACAT CACTGTGAAT AATAGTGGAT CCTATACGTG CCAAGCCCAT 1020
 AACTCAGACA CTGGCCTCAA TAGGACCACA GTCACGACGA TCACAGTCTA TGCAGAGCCA 1080
 CCAAAACCTT TCATCACCAG CAACAACCTC AACCCTGTGG AGGATGAGGA TGCTGTAGCC 1140
 TTAACCTGTG AACCTGAGAT TCAGAACACA ACCTACCTGT GGTGGGTAAA TAATCAGAGC 1200
 CTCCCGGTCA GTCCACAGCT GCAGCTGTCC AATGACAACA GGACCCCTAC TCTACTCAGT 1260
 GTCACAAGGA ATGATGTAGG ACCCTATGAG TGTGGAATCC AGAACGAATT AAGTGTGTAG 1320
 CACAGCGACC CAGTCATCCT GAATGTCTCT TATGGCCAG ACACCCCTAC CATTTCCCCC 1380
 TCATACACTT ATTACCGTAT AGGGGTGAAC CTCAGCTCTC CTGCGCATGC AGCCTCTAAC 1440
 CCACCTGCAC AGTATTCTTG GCTGATTGAT GGAACATCC AGCAACACAC ACAAGAGCTC 1500
 TTTATCTCCA ACATCAGTGA GAAGAACAGC GGACTCTATA CCTGCCAGGC CAATAACTCA 1560
 GCGAGTGGCC ACAGCGAGTG TACAGTCAAG ACAATCAGAG TCTCTGCGGA GCTGCCAAG 1620
 CCTCCACTCT CCAGCAACAA CTCCAAACCC GTGGAGGACA AGGATGTCTG GGCCTTCACC 1680
 TGTGAACCTT AGGCTCAGCT CACAACCTAC CTGTGGTGGG TAAATGGTCA GAGCCTCCCA 1740
 GTCAGTCCCA GGCTGCAGCT GTCCAATGGC AACAGGACCC TCACCTCTAT CAATGTCA 1800
 AGAAATGAGC CAAGAGCCTA TGTATGTGGA ATCCAGAACT CAGTGAGTGC AAACCGCAGT 1860
 GACCCAGTCA CCTGTGATGT CCTCTATGGG CCGGACACCC CCATCATTTC CCCCCAGAC 1920
 TGTCTTACCT TTGCGGAGC GAACCTCAAC CTCTCTGCC ACTCGGCCCT TAACCCATCC 1980
 CGCAGTATT CTGCGGTAT CAATGGGATA CCGCAGAAC ACACACAAGT TCTCTTTATC 2040
 GCCAAATCA CGCCAAATAA TAACGGGACC TATGCCTGTT TTGTCTCTAA CTGCGTACT 2100
 GGCCGCAATA ATTCATAGT CAAGAGCATC ACAGTCTCTG CATCTGGAAC TTCTCTCTGT 2160
 CTCTCAGCTG GGGCCAGTGT CGGCATCATG ATTGGAGTGC TGGTGTGGGT TGCTCTGATA 2220
 TAGCAGCCCT GGTGTAGTTT CTTTATTTC GGAAGACTGA CAGTGTGTTT GCTTCTCTCT 2280
 TAAAGCATTT GCAACAGTAT CAGTCTAAAA TTGCTCTTT ACCAAGGATA TTTACAGAAA 2340
 AGACTCTGAC CAGAGATCGA GACCATCTTA GCCAACATCG TGAAACCCCA TCTCTACTAA 2400
 AAATACAAAA ATGAGCTGGG CTGCTGTGGC CGCACCCTGA GTCCAGTTA CTCGGGAGGC 2460
 TGAGGCAGGA GAATCGCTTG AACCCGGGAG GTGGAGATTG CAGTGAGCCC AGATGCGACC 2520
 ACTGCACTCC AGTCTGGCAA CAGAGCAAGA CTCCTCTCA AAAAGAAAAG AAAAGAACAC 2580
 TCTGACCTGT ACTCTGTAAT ACAAGTTTCT GATACCACTG CACTGTCTGA GAATTTCCAA 2640
 AACTTTAATG AACTAATGTA CAGCTTCATG AAACCTCCA CCAAGATCAA GCAGAGAAA 2700
 TAATTAATTT CATGGGACTA AATGAACATA TGAGGATTGC TGATTCCTTA AATGTCTTGT 2760
 TTCCAGATT TCAGGAAACT TTTTCTCTT TAAGCTATCC ACTCTTACAG CAATTTGATA 2820
 AAATATACTT TGTGAACAA AATTGAGAC ATTACATT TCTCCCTATG TGGTCGCTCC 2880
 AGACTTGGGA AACTATTCAT GAATATTAT ATTGTATGGT AATATAGTTA TTGCACAAGT 2940
 TCAATAAAAA TCTGCTCTTT GTATAACAGA AAAA

Seq ID NO: 533 Protein sequence
 Protein Accession #: NP_004354.1

50
55
60

1 11 21 31 41 51
 | | | | |
 MESPSAPPHR WCIPWQRLLL TASLLTFWNP PTTAKLTIES TPFNVABEKE VLLLVLNLPQ 60
 HLFQSWYKQ ERVDGNRQII GYVIGTQAT PGPAYSGREI IYPNASLLIQ NIIQNDTGFPY 120
 TLHVIKSDLV NEEATGQFRV YPELPKPSIS SNNSKPVEDK DAVAFTCEPE TQDATYLWNV 180
 NNQSLFVSPR LQLSNGNRTL TLFNVTRNDT ASYKCTQNP VSARRSDSVI LNVLYGPDAP 240
 TISPLNLSYR SGENLNLSCB AASNPPAQYS WFNVTGFQQS TOELFIPNIT VNNSGSYTCQ 300
 AHNSTDGLNR TTVTTITVYA EPPKPFITSN NSNPVEDEDA VALTCEPEIQ NITYLWNVNN 360
 QSLPVSPRLQ LSNDRNLTL LSVTRNDVGP YECGIQNELS VDHSDPVLIN VLYGPDPTI 420
 SPSYTYRRP VNLDSLCHAA SNPPAQYSWL IDGNIQHTQ ELFISNITEK NSGLYTCQAN 480
 NSAGHSRRT VKTITVSAEL PKPSISSNNS KPVEDKDAVA PTCEPEAQNT TYLWVWNGQS 540
 LPVSPRLQLS NGNRTLTLFN VTRNDARAYV CGIQNSVSN RSDPVTLDVL YGPDPTIISP 600
 PDSSYLSGAN LNLSCHSASN PSPQYSNRIN GIPOQHTQVL FIAKITPNNN GTYACFVSNL 660
 ATGRNNSIVK SITVSASGTS PGLSAGATVG IMIGVLVGVA LI

Seq ID NO: 534 DNA sequence
 Nucleic Acid Accession #: NM_006952.1
 Coding sequence: 11..793

65
70
75
80

1 11 21 31 41 51
 | | | | |
 AATCCCAGACA ATGGCGAAAG ACAACTCAAC TGTTCTGTGC TTCCAGGGCC TGCTGATTTT 60
 TGGAAATGTG ATTATTGGTT GTTGGCGCAT TGCCCTGACT GCGGAGTGCA TCTTCTTTGT 120
 ATCTGACCAA CACAGCCTCT ACCCACTGCT TGAAGCCACC GACAACGATG ACATCTATGG 180
 GGCTGCTCTG ATCGGCATAT TTGTGGGCAT CTGCCTCTTC TGCTGTCTG TTTAGGCAT 240
 TGTAGGCATC ATGAAGTCCA GCAGGAAAAT TCTTCTGGCG TATTTCATTC TGATGTTTAT 300
 AGTATATGCC TTTGAAGTGG CATCTGTAT CACAGCAGCA ACACAACGAG ACTTTTTCAC 360
 ACCCAACCTC TCTCTGAAGC AGATGCTAGA GAGGTACCAA AACACAGCC CTCCAACAA 420
 TGATGACCAG TGGAAAAACA ATGGAGTCAC CAAAACCTGG GACAGGCTCA TGCTCCAGGA 480
 CAATTGCTGT GCGGTAAATG GTCCATCAGA CTGGCAAAAA TACACATCTG CCTTCCGGAC 540
 TGAGAATAAT GATGCTGAGC ATCCCTGGCC TCGTCAATGC TGTGTTATGA ACAATCTTAA 600
 AGAACCTCTC AACCTGGAGG CTTGTAAACT AGGCGTGCCT GGTTTTATCA ACAATCAGG 660
 CTGCTATGAA CTGATCTCTG GTCCAATGAA CCGACACGCC TGGGGGGTTG CCTGGTTTGG 720
 ATTTGCCATT CTCTGCTGGA CTTTTTGGGT TCTCTGGGT ACCATGTCTT ACTGGAGCAG 780
 AATTGAATAT TAAGAA

Seq ID NO: 535 Protein sequence
 Protein Accession #: NP_008883.1

85

1 11 21 31 41 51
 | | | | |

MAKDNSTVRC PQGLLIFGNV IIGCCGIALT AECIFFVSDQ HSLYPLLEAT DNDDIYGAAW 60
 IGIFVIGICLF CLSVLGIVGI MKSSRKILLA YFILMFIVYA FEVASCITAA TQRDFFTPNL 120
 FLKQMLERYQ NNSPPNDDQ WKNNGVKTW DRLMLQDNCC GVNQPSDWQK YTSAPRTENN 180
 DADYPWPRQC CVMNMLKEPL NLEACKLGVP GFYHNQGCYE LISGPMNRHA WGVANFGFAI 240
 LCWTFWVLLG TMFYWSRIEY

Seq ID NO: 536 DNA sequence
 Nucleic Acid Accession #: NM_002638.1
 Coding sequence: 120..473

1 11 21 31 41 51
 | | | | |
 CAATACAGCT | AAGGAATTAT | CCCTTGTAAT | TACCACAGAC | CCGCCCTGGA | GCCAGGCCAA 60
 GCTGGACTGC | ATAAAGATTG | GTATGGCCTT | AGCTCTTAGC | CAAACACCTT | CCTGACACCA 120
 TGAGGGCCAG | CAGCTTCTTG | ATCGTGGTGG | TGTTCCTCAT | CGCTGGGACG | CTGGTTCTAG 180
 AGGCAGCTGT | CACGGGAGTT | CTTGTTAAAG | GTCAAGACAC | TGTCAAAGGC | CGTGTTCAT 240
 TCAATGGACA | AGATCCCGTT | AAAGGACAAG | TTTCACTTAA | AGGTCAAGAT | AAAGTCAAAG 300
 CGCAAGAGCC | AGTCAAAGGT | CCACTCTCCA | CTAAGCCTGG | CTCTGCCCCC | ATTATCTTGA 360
 TCCGGTGGCG | CATGTTGAAT | CCCCCAACC | GCTGCTTGAA | AGATACTGAC | TGCCAGGAG 420
 TCAAGAAGTG | CTGTGAAGGC | TCTTGCAGGA | TGGCCTGTTT | CGTTCCTCCG | TGAAGGGAGC 480
 CGGTCTCTGC | TGCACCTGTG | CCGTCCCGAG | AGCTACAGGC | CCCATCTGGT | CCTAAGTCCC 540
 TGCTGCCCTT | CCCCTTCCCA | CACTGTCCAT | TCTTCTCCC | ATTCAGGATG | CCCACGGCTG 600
 GAGCTGCCCT | TCTCATCCAC | TTTCAATAA | A

Seq ID NO: 537 Protein sequence
 Protein Accession #: NP_002629.1

1 11 21 31 41 51
 | | | | |
 MRASSFLIVV | VFLLIAGTLVL | EAAVTGVPVK | GQDTVKGKRP | FNGQDPVKGQ | VSVKGQDKVK 60
 AQEPVKGPVS | TKPQSCPIIL | IRCAMLNPPN | RCLKDITDCFG | IKKCCGSCG | MACFVPQ

Seq ID NO: 538 DNA sequence
 Nucleic Acid Accession #: NM_001793.2
 Coding sequence: 71..2560

1 11 21 31 41 51
 | | | | |
 AAAGGGGCAA | GAGCTGAGCG | GAACACCGGC | CCGCCGTGCG | GGCAGCTGCT | TCACCCCTCT 60
 CTCTGAGCC | ATAGGGCTCC | CTGCTGGACC | TCTCGCTCT | CTCTCTCTC | TCCAGGTTTG 120
 CTGGCTGCAG | TGCGCGGCTT | CCGAGCCGTG | CCGGGCGGTC | TTCAAGGAGG | CTGAAGTGAC 180
 CTTGGAGGCG | GGAGGCGCGG | AGCAGGAGCC | CGGCCAGGCG | CTGGGGAAG | TATTCATGGG 240
 CTGCCCTGGG | CAAGAGCCAG | CTCTGTTTAA | CACTGATAAT | GATGACTTCA | CTGTGCGGAA 300
 TGGCGAGACA | GTCCAGGAAA | GAAGGTCAT | GAAGGAAAGG | AATCCATTGA | AGATCTTCCC 360
 ATCCAAACCT | ATCTTACGAA | GACACAAGAG | AGATTGGGTG | GTTGCTCCAA | TATCTGTCCC 420
 TGAATAATGC | AAGGTCCTCT | TCCCCAGAG | ACTGAATCAG | CTCAGTCTA | ATAAAGATAG 480
 AGACACCAAG | ATTTTCTACA | GCATCAGCGG | GCGGGGGGCA | GACAGCCCCC | CTGAGGGTGT 540
 CTTGCTGTGA | GAGAAGGAGA | CAGGCTGGTT | GTTGTGAAT | AAGCCACTGG | ACCGGGAGGA 600
 GATTGCCAAG | TATGAGCTCT | TTGGCCACGC | TGTGTCAGAG | AATGGTGCTT | CAGTGGAGGA 660
 CCCCATGAAC | ATCTCCATCA | TCGTGACCGA | CCAGAATGAC | CACAAGCCCA | AGTTTACCCA 720
 GGACACCTTC | CGAGGGAGTG | TCTTAGAGGG | AGTCCTACCA | GGTACTTCTG | TGATGCAGGT 780
 GACAGCCAGC | GATGAGGATG | ATGCCATCTA | CACCTACAT | GGGGTGGTTG | CTTACTCCAT 840
 CCATAGCCAA | GAACCAAGG | ACCCACAGCA | CCTCATGTTT | ACCATTCAAC | GGAGCACAGG 900
 CACCATCAGC | GTCATCTCCA | GTGGCCTGGA | CCGGGAAGAA | GTCCCTGAGT | ACACACTGAC 960
 CATCCAGGCC | ACAGACATGG | ATGGGAGCGG | CTCACCAACC | ACGGCAGTGG | CAGTAGTGGA 1020
 GATCCTTGAT | GCCAATGACA | ATGCTCCCAT | GTTTGACCCC | CAGAAGTACG | AGGCCCATGT 1080
 GCCTGAGAA | GCAGTGGGCC | ATGAGGTGCA | GAGGCTGACG | GTCACTGATC | TGGACGCCCC 1140
 CAACTCACCA | ACCTGGGCGT | CCACCTACCT | TATCATGGGC | GGTGACGACG | GGGACCATTT 1200
 TACCATCACC | ACCCACTCTG | AGAGCAACCA | GGGCATCCTG | ACAACCAAGG | AGGTTTGGGA 1260
 TTTTGAAGCC | AAAAACCAGC | ACACCTCTGA | CGTTGAAGTG | ACCAAGAGG | CCCCTTTTGT 1320
 GCTGAAGCTC | CCAACCTCCA | CAGCCACCAT | AGTGGTCCAC | GTGGAGGATG | TGAATGAGGC 1380
 ACCTGTGTTT | GTCCACCTCT | CCAAAAGTGT | TGAGGTCCAG | GAGGGCATCC | CCACTGGGGA 1440
 GCCTGTGTGT | GTCTACACTG | CAGAAGACCC | TGACAAGGAG | AATCAAAAGA | TCAGCTACCG 1500
 CATCCTGAGA | GACCCAGCAG | GGTGGCTAGC | CATGGACCCA | GACAGTGGGC | AGGTCAACAG 1560
 TGTGGGCACC | CTCGACCGTG | AGGATGAGCA | GTTGTGAGG | AACACATCT | ATGAAGTCAT 1620
 GGTCTTGGCC | ATGGACAATG | GAAGCCCTCC | CACCACTGGC | ACGGGAACCC | TTCTGCTAAC 1680
 ACTGATTGAT | GTCAATGACC | ATGGCCCACT | CCTGAGCCCC | CGTCAGATCA | CCATCTGCAA 1740
 CCAAAGCCCT | GTGCGCCAGG | TGCTGAACAT | CACGGACAAG | GACCTGTCTC | CCCACACCTC 1800
 CCTTTCAG | GCCAGCTCA | CAGATGACTC | AGACATCTAC | TGGACGGCAG | AGGTCAACGA 1860
 GGAAGGTGAC | ACAGTGTGCT | TGTCCCTGAA | GAAGTTCCTG | AAGCAGGATA | CATATGACGT 1920
 GCACCTTTCT | CTGTCTGACC | ATGGCAACAA | AGAGCAGCTG | ACGGTGATCA | GGGCACTGT 1980
 GTGCGACTGC | CATGGCCATG | TCGAAACCTG | CCTTGGACCC | TGGAAGGGAG | GTTTCATCCT 2040
 CCTGTGCTG | GGGGCTGCTG | TGGCTCTGCT | GTTCTCTCTG | CTGGTCTGTC | TTTTGTGTTG 2100
 GAGAAAGAAG | CGGAAGATCA | AGGAGCCCTT | CCTACTCCCA | GAAGATGACA | CCGTGACAA 2160
 CGTCTTCTAC | TATGCGAAG | AGGGGGGTGG | CGAAGAGGAC | CAGGACTATG | ACATCACCCA 2220
 GCTCCACCGA | GGTCTGGAGG | CCAGGCGGGA | GGTGGTTCTC | CGCAATGACG | TGGCACCAC 2280
 CATCATCCCG | ACACCATGAT | ACCGTCTCTG | GCCAGCCAAC | CCAGATGAAA | TCGGCAACTT 2340
 TATAATTGAG | AACCTGAAGG | CGGCTAACAC | AGACCCCAAC | GCCCCGCCCT | ACAGCACCTT 2400
 CTGTGTGTTT | GACTATGAGG | GCAGCGGCTC | CGACCGCCCG | TCCCTGAGCT | CCTCACCTC 2460
 CTCGCGCTCC | GACCAAGACC | AAGATTACGA | TTATCTGAAC | GAGTGGGGCA | GCGCTTCAA 2520
 GAAGCTGGCA | GACATGTACG | GTGGCGGGGA | GGACGACTAG | GCGGCCTGCC | TGCAGGGCTG 2580
 GGGACCAAC | GTCAGGCCAC | AGAGCATCTC | CAAGGGGTCT | CAGTTCCTCC | TTCAGCTGAG 2640
 GACTTCGGAG | TTTCTCAGGA | AGTGGCCGTA | GCAACTTGGC | GGAGACAGGC | TATGAGTCTG 2700
 ACCTTAGAGT | GGTGTCTTCC | TTAGCCTTTC | AGGATGGAGG | AATGTGGGCA | GTTGACTTTC 2760
 AGCACTGAAA | ACCTCTCCAC | CTGGGCCAGG | GTTGCTCAG | AGGCCAAGTT | TCCAGAAGCC 2820
 TCTTACCTGC | CGTAAATGTC | TCAACCTCTG | GTCCCTGGGC | TGGGCCTGCT | GTGACTGACC 2880
 TACAGTGGAC | TTTCTCTCTG | GAATGGAACC | TTCTTAGGCC | TCCTGGTGCA | ACTTAATTTT 2940

TTTTTTAAT GCTATCTTCA AAACGTTAGA GAAAGTTCTT CAAAAGTGCA GCCCAGAGCT 3000
GCTGGGCCCA CTGGCCGTCC TGCATTCTG GTTCCAGAC CCCAATGCCT CCCATTCCGA 3060
TGGATCTCTG CGTTTTTATA CTGAGTGTGC CTAGGTTGCC CCTTATTTT TATTTTCCCT 3120
GTTGCGTTGC TATAGATGAA GGGTGAGGAC AATCGTGAT ATGTACTAGA ACTTTTTTAT 3180
TAAAGAACT TTTCCAGAA AAAAA

Seq ID NO: 539 Protein sequence
Protein Accession #: NP_001784.2

1 11 21 31 41 51
MGLPRGPLAS LLLQVCWLQ CAASEPCRAV FREAEVTLEA GGAEQEPGQA LGKVFPGCPG 60
QEPALFSTDN DDFTVRNGET VQERRSLKER NPLKIPPSKR ILRRHKRDWV VAPISVPENG 120
KGFFPQRLNQ LKSNKDRDTK IFYSITGPGA DSPPEGVPAV EKETGWLILLN KPLDREEIAK 180
YELFGHAYSE NGASVEDPMN ISIIIVTDQND HKPKFTQDFT RGSVLEGLVP GTSVMQVTAT 240
DEDDAIYTYN GVVAYSISQ EPKDPHDLMP TIHRSTGTIS VISSGLDREK VPEYTLTIQA 300
TDMGDGSGTT TAVAVVEILD ANDNAPMFDP QKYEAVHPEN AVGHEVQRLT VTDLDAPNSP 360
AWRATYLMG GDDGDHFTIT THPESNQIL TTRKGLDPEA KNQHTLYVEV TNEAPFVLKL 420
PTSTATIVVH VEDVNEAPVF VPPSKVVEVQ EGIPTGEVPC VYTAEDPDKE NQKISYRILR 480
DPAGWLAMP DSGQVTVAGT LDREDEQFVR NNIEYVMVLA MDNGSPPTTG TGTLLTLID 540
VNDHGFVPEP RQITICNOSP VRQVLNITDK DLSPTSPFQ AQLTDDSDIY WTAEVNEEGD 600
TVVLSLKKPL KQDTYDVHLS LSDHGNKEQL TVIRATVDCD HGHVETCPGP WKGGFILPVL 660
GAVLALLFL LVLVLLVRKK RKIKEPLLLP EDDTRDNVFI YGEEGGGEED QDYDITQLHR 720
GLEARPEVVL RNDVAPTIIP TPMYRPRPAN PDEIGNFIE NLKAANTDPT APPYDITLLVF 780
DYEGSGSDAA SLSSLTSSAS DQDQDYDYLN EWGSRFKKLA DMVGGGEDD

Seq ID NO: 540 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..672

1 11 21 31 41 51
ATGAGGCTCC AAAGACCCCG ACAGGCCCCG GCGGGTGGGA GCGCGCGCGC CCGGGCGGG 60
CGGGGCTCCC CCTACCGGCC AGACCCGGG AGAGGCGCGC GGAGGCTGCG AAGGTTCCAG 120
AAGGGCGGGG AGGGGGCGCC GCGCGCTGAC CCTCCTCGGG CACCGCTGGG GACGATGGCG 180
CTGCTCGCCT TGCTGCTGGT CGTGGCCCTA CCGCGGGTGT GGACAGACGC CAACCTGACT 240
GGGAGACAAC GAGATCCAGA GGACTCCAG CGAACGAGCG AGGGTGACAA TAGAGTGTGG 300
TGTCATGTT GTGAGAGAGA AAACACTTTC GAGTGCCAGA ACCCAAGGAG GTGCAATGG 360
ACAGAGCCAT ACTGCGTTAT AGCGGCCGTG AAAATATTTC CACGTTTTTT CATGTTTGG 420
AAGCAGTGCT CCGCTGTTTG TGCAGCGATG GAGAGACCCA AGCCAGAGGA GAAGCGGTTT 480
CTCTGGAAG AGCCCAACCA CTCTTTTAC CTCAGTGTT GTAAAAATCG CTAAGTCAAT 540
TTAGAGGGGC CACCTATCAA CTCATCAGTG TTCAAAGAA ATGCTGGGAG CATGGGTGAG 600
AGCTGTGGTG GCGTGTGGCT GGCATCCTC CTGCTGCTGG CCTCATTGC AGCCGCGCTC 660
AGCCTGTCTT GA

Seq ID NO: 541 Protein sequence
Protein Accession #: Eos sequence

1 11 21 31 41 51
MRLQRPRQAP AGGRRAPRGG RGSFYRDPDG RGARRLRFPQ KGGEGAPRAD PPWAPLGTMA 60
LLALLLVVAL PRVWTDANLT ARQRPEDSDQ RTDEGDNVW CHVCERENTF ECQNPRRCWK 120
TEPYCVIAAV KIFPRPFMVA KQCSAGCAAM ERPKPEERKF LLEBPMPPFY LKCKIRYCN 180
LEGPPINSSV FKEYAGSMGE SCGGLWLAIL LLLASIAAGL SLS

Seq ID NO: 542 DNA sequence
Nucleic Acid Accession #: XM_035292.2
Coding sequence: 53..1576

1 11 21 31 41 51
GCTCGCTGGG CCGCGGCTCC CGGGTGTCCC AGGCCCGGCC GGTGCGCAGA GCATGGCGGG 60
TGCGGGCCCG AAGCGGCGCG CGCTAGCGGC GCGGCGGGCC GAGGAGAAGG AAGAGGCGCG 120
GGAGAAGATG CTGCGCGCCA AGAGCGCGGA CGGCTCGCGC CCGGCAGGCG AGGGCGAGGG 180
CGTGACCTCG CAGCGGAACA TCACGCTGCT CAACGCGCTG GCCATCATCG TGGGACCAT 240
TATCGGCTCG GGCATCTTCG TGACGCCAC GGGCGTGCTC AAGGAGGCG GCTCGCGGG 300
GCTGGGCTCG GTGGTGTGGG CCGCGTGGG CGTCTTCTCC ATCGTGGGCG CGCTCTGCTA 360
CGCGGAGCTC GGCACCAACA TCTCCAAATC GGGCGGCGAC TACGCCTACA TGCTGGAGGT 420
CTACGGCTCG CTGCGCGCCT TCCTCAAGCT CTGGATCGAG CTGCTCATCA TCGGCGCTTC 480
ATCGCAGTAC ATCGTGGCCC TGGTCTTGG CACCTACCTG CTCAGCGCG TCTTCCCCAC 540
CTGCCCGGTG CCCGAGGAGG CAGCCAAGCT CGTGGCGTGC CTCTGCGTGC TGCTGCTCAC 600
GGCGGTGAAC TGCTACAGCG TGAAGGCGCG CACCGGGTTC CAGGATGCCT TTGCGCGCG 660
CAAGCTCCTG GCCCTGGCCC TGATCATCCT GCTGGGCTTC GTCCAGATCG GAAAGGGTGA 720
TGTGTCCAAT CTAGATCCCA ACTTCTCATT TGAAGGCACC AAACCTGGATG TGGGGAACAT 780
TGTGTGSSCA TTATACAGCG GCCTCTTTGC CTATGGAGGA TGAATTACT TGAATTGCT 840
CACAGAGGAA ATGATCAACC CCTACAGAAA CCTGCCCTG GCCATCATCA TCTCCTTGCC 900
CATCGTAGCG CTGCTGTACG TGCTGACCAA CCTGGCCTAC TTCACCAACC TGTCCACCGA 960
GCAGATGCTG TCGTCCGAGG CCGTGGCGGT GGAATTCGGG AACTATCACG TGGGCGTCAT 1020
GTCTGGATC ATCCCGTCT TCGTGGGCGT GTCTGCTTC GGCTCCGTC ATGGGTCCCT 1080
GTTACATCC TCCAGCTCT TCTTGTGGG GTCCCGGGA GGCACCTGC CCTCCATCCT 1140
TCCCATGATC CACCCACAGC TCCTCACCCC CGTGGCGTCC CTCGTGTCA CGTGTGTGAT 1200
GACGCTGCTC TAGCCTTCT CCAAGGACAT CTCTCCGTC ATCAACTTCT TCAGCTTCTT 1260
CAACTGGCTC TACGCTGCCC TGGCCATCAT CGGCATGATC TGGCTGCGCG ACAGAAAGCC 1320
TGAGCTTAG CGGCCATCA AGGTGAACCT GGCCCTGCCT GTGTCTTCA TCTGGCCTG 1380
CCTCTTCTG ATCGCGTCT CTCTCTGAA GACACCGTG GAGTGTGGCA TCGGCTTCA 1440
CATCATCCTC AGCGGGCTGC CCGTCTACTT CTCTGGGGTC TGGTGGAAAA ACAAGCCCA 1500
GTGGCTCCTC CAGGCGATCT TCTCCACGAC CGTCTGTGT CAGAAGCTCA TGCAGTGTG 1560

CCCCCAGGAG ACATAGCCAG GAGGCCGAGT GGCTGCCGGA GGAGCATGC

Seq ID NO: 543 Protein sequence
Protein Accession #: XP_035292.2

1	11	21	31	41	51	
MAGAGPKRRA	LAAPAAEKE	EAREKMLAAK	SADGSAPAGE	GEGVTLQRNI	TLLNGVAIIV	60
GTIIGSGIFV	TPTGVLKEAG	SPGLALVWVA	ACGVFSIVGA	LCYAEIGTTI	SKSGGDYAYM	120
LEVYGSLLPAP	LKLWIELLII	RPSSQYIVAL	VFATYLLKPL	FPTCPVPEEA	AKLVACLCLV	180
LLTAVNCYSV	KAATRVQDAF	AAAKLLALAL	IILLGFVQIG	KGDVSNLDPN	FSFEGTKLDV	240
GNIVLALYSG	LPAYGGWNYL	NFVTEEMINP	YRNLPALIII	SLPIVTLVYV	LTNLAYFTTL	300
STEQMLSSSEA	VAVDFGNHYL	GVMWSIIPVF	VGLSCFGSVN	GSLEPTSSRLF	FVGSREGHLP	360
SLLSMIHPQL	LTPVPSLVFT	CVMTLLYAFS	KDIFSVINFF	SFFNWLVCAL	AIIGMIWLRH	420
RKPELERPIK	VNLALPVFFI	LACLFLIAVS	PWKTPVECGI	GFTIILSGLP	VYFFGVWKN	480
KPKWLLQGIF	STTVLCQKLM	QVVPQBT				

Seq ID NO: 544 DNA sequence
Nucleic Acid Accession #: NM_005268.1
Coding sequence: 168..989

1	11	21	31	41	51	
TAAAAAGCAA	AAGAATTCGC	GGCCGCGTCG	ACACGGGCTT	CCCCGAAAAC	CTTCCCCGCT	60
TCTGATATG	AAATTCAGC	TGCTTGTCTGA	GTCTTATTGC	CGGCTGTCTG	GAGCCAGGAG	120
AGCCCTGAGG	AGTAGTCACT	CAGTAGCAGC	TGACGCGTGG	GTCCACCATG	AACCTGGAGTA	180
TCTTTGAGGG	ACTCTGAGT	GGGTCAACA	AGTACTCCAC	AGCCTTTGGG	CGCATCTGGC	240
TGCTCTGGT	CTTCATCTTC	CGCGTGTCTG	TGTACTCTGT	GACGGCCGAG	CGTGTCTGGA	300
GTGATGACCA	CAAGGACTTC	GACTGCAATA	CTCGCCAGCC	CGGCTGTCTC	AACGTCTGCT	360
TTGATGAGTT	CTTCCCTGTG	TCCCATGTGC	GCCTCTGGGC	CCTGCAGCTT	ATCCTGTGTA	420
CATGCCCTTC	ACTGCTGTG	GTCATGCACG	TGGCCTACCG	GGAGGTTTCA	GAGAAGAGGC	480
ACCGAGAAGC	CCATGGGGAG	AACAGTGGGC	GCCTCTACCT	GAACCCCGGC	AAGAAGCGGG	540
GTGGGCTCTG	GTGGACATAT	GTCTGCAGCC	TAGTGTTCAA	GGCGAGCGTG	GACATCGCCT	600
TTCTCTATGT	GTTCACCTCA	TTCTACCCCA	AATATATCCT	CCCTCTGTGT	GTCAAGTGCC	660
ACGCAGATCC	ATGTCCTAAT	ATAGTGGACT	GCTTCTATCT	CAAGCCCTCA	GAGAAGAACA	720
TTTTACCCCT	CTTCTGTG	GCCACAGCTG	CCATCTGCAT	CCTGCTCAAC	CTCGTGGAGC	780
TCATCTACCT	GGTGAGCAAG	AGATGCCACG	AGTGCTGGC	AGCAAGGAAA	GCTCAAGCCA	840
TGTGCACAGG	TCATCACCCC	CACGGTACCA	CCTCTTCTCT	CAACAAGAC	GACCTCTCTT	900
CGGGTGACCT	CATCTTTCTG	GGCTCAGACA	GTCATCTCTC	TCTCTTACCA	GACCGCCCCC	960
GAGACCATGT	GAAGAAACC	ATCTTGTGAG	GGGCTGCCTG	GACTGTGCTG	GCAAGTTGGG	1020
CCTGGATGGG	GAGGCTCTAG	CATCTCTCAT	AGGTGCAACC	TGAGAGTGGT	GGAGCTAAGC	1080
CATGAGGTAG	GGGCAGGCAA	GAGAGAGGAT	TCAGACGCTC	TGGGAGCCAG	TTCTAGTCC	1140
TCAACTCCAG	CCACCTGCCC	CAGCTCGACG	GCACTGGGCC	AGTTCCTCC	CTGCTCTGCA	1200
GCTCGGTTTC	CTTTCTAGA	ATGGAAATAG	TGAGGGCCAA	TGC		

Seq ID NO: 545 Protein sequence
Protein Accession #: NP_005259.1

1	11	21	31	41	51	
MNWSIFEGLL	SGVNVKYSTAF	GRWLSLVFI	FRVLVYLVA	ERVWSDDHKD	FDCNTRQPGC	60
SNVCFDEFPF	VSHVRLWALQ	LILVTCPSLL	VVMHVAYREV	QEKRRHREAHG	ENSGRLYLNP	120
GKKRGGWLWT	YVCSLVFKAS	VDIAFLVVFH	SFYPKYILEP	VVKCHADPCP	NIVDCTFISKP	180
SEKNIFTLFM	VATAICILL	NLVELIYLV	KRCHECLAAR	KAQAMCTGHH	PHGTTSSCKQ	240
DDLSSGDLIF	LGSDSHPLLL	PDRPRDHVKK	TIL			

Seq ID NO: 546 DNA sequence
Nucleic Acid Accession #: NM_002391.1
Coding sequence: 26..457

1	11	21	31	41	51	
CGGGCGAAGC	AGCGCGGGCA	GCGAGATGCA	GCACCGAGGC	TTCCTCTCTC	TCACCTCTCT	60
CGCCCTGCTG	GCGCTCACCT	CCGCGGTGCG	CAAAAAGAAA	GATAAGGTGA	AGAAGGGCGG	120
CCCGGGGAGC	GAGTGCCTG	AGTGGGCTG	GGGCGCTG	ACCCCGAGCA	GCAAGGATTG	180
CGGCGTGGGT	TTCCGCGAGG	GCACCTGCGG	GGCCCGAGCC	CAGCGCATCC	GGTGCAGGGT	240
GCCCTGCAAC	TGGAAGAAGG	AGTTTGGAGC	CGACTGCAAG	TACAAAGTTG	AGAACTGGGG	300
TGCGTGTGAT	GGGGGACAG	GCACCAAGT	CCGCCAAGGC	ACCCTGAAGA	AGGCGCGCTA	360
CAATGCTCAG	TGCCAGGAGA	CCATCCGCGT	CACCAAGCCC	TGCACCCCCA	AGACCAAGGC	420
AAAGGCCAAA	GCCAAGAAAG	GGAAGGGAAA	GGACTAGACG	CCAAGCCTGG	ATGCCAAGGA	480
GCCCTGGTGT	TCACATGGGG	CCTGGCCACG	CCCTCCCTCT	CCCAGGCCCC	AGATGTGACC	540
CACCAAGTCC	TTCTGTCTGC	TGTTAGCTT	TAATCAATCA	TGCCCTGCCT	TGTCCCTCTC	600
ACTCCCGAGC	CCACCCCTTA	AGTGGCCAAA	GTGGGGAGGG	ACAAGGGATT	CTGGGAAGCT	660
TGAGCCTCCC	CCAAAGCAAT	GTGAGTCCCA	GAGCCCGCTT	TTGTTCTTCC	CCACAATCC	720
ATTACTAAGA	AACACATCAA	ATAAAGTGAC	TTTTTCCCCC	CAATAAAAGC	TCTTCTTTT	780
TAATAT						

Seq ID NO: 547 Protein sequence
Protein Accession #: NP_002382.1

1	11	21	31	41	51	
MQHRGFLLLT	LLALLAL TSA	VAKKKDKVKK	GGPGSECAEW	AWGPCTPSSK	DCGVGFREGT	60
CGAQTQRI RC	RVPCNWKKEF	GADCKYKFEN	WGACDGGTGT	KVRQGTLLKA	RYNAQCQETI	120
RVTKPCTPKT	KAKAKAKGK	GKD				

Seq ID NO: 548 DNA sequence

PCT/US02/12476

1	11	21	31	41	51	
ATGGATTGGG	GGACGCTGCA	CAC TTTCATC	GGGGGTGTCA	ACAAACACTC	CACCGAGCATC	60
GGGAAGTGTT	GGATCACAAGT	CATCTTTATT	TTCGAGTCA	TGATCCTAGT	GGTGGCTGCC	120
CAGGAAGTGT	GGGGTGACGA	GCAAGAGAGC	TTCGCTGTCA	ACACACTGCA	ACCGGGATGC	180
AAAAATGTGT	GCTATGACCA	CTTTTTCGCG	GTGTCACACA	TCGGCGTGTG	GGCCCTCAG	240
CTGATCTTCG	TGCAACCCCC	CGCTGCTGTC	GTGGCCATGC	ATTTGGCCCTA	CTACAGGCAC	300
GAACCACTC	GCAATTCAGC	GCAGAGAGAG	AAGAGGAATG	ATTGTCAAAG	CATAGAGGAC	360
ATTA AAAAGC	ACAAGTTTCG	GATAGAGGGG	TCGCTGTGGT	GGACGTACAC	CAGCAGCATC	420
TTTTTCCGAA	TCATCTTTGA	AGCAGCCTTT	ATTGATGTGT	TTTACTCTCT	TTACAGATGG	480
TACCACTGTC	CTCGGTTGTT	GAAATGTGGG	ATTGACCCCT	CGCCCAACCT	TGTTGACTGC	540
TTTATTCTA	GGCCAACAGA	GAAAGACCTG	TTTACCAATT	TGATGATTC	TGGGCTCTGTG	600
ATTGTCATGC	TGCTTAACTG	GGCAGAGTTG	TGCTACCTGC	TTGTGAAAGT	GTGTTTGAAG	660
AGATCAAGA	GAGCAAGAC	GCAAAAAAAT	CACCCCAATC	ATGCCCTAAA	GGAGAGTAAG	720
CAGAAATGAA	TGAAATGAGCT	GATTTTCAGAT	AGTGGTCAAA	ATGCAATCAC	AGGTTTCCCA	780
AGCTAA						

1	11	21	31	41	51	
MDWGTLHTFI	GGVKNKHSI	GKVNITVIFI	FRVMILVAA	QEVWGDEQED	FVCNTLQPGC	60
KQVCYDHFFI	VSHIRLWALQ	LIPVSTPAAL	VAMVAVAYRH	YHLTKFRFRGE	KRNFDFKDIED	120
IKKHVKVRIEG	SLWWTYTSSI	FPRIIEFAAF	MYVPYPLYNG	ETHLPVNLKCG	IDPCPNLVLD	180
FISRPTEKTV	FTFPMISASV	ICMLLNVAEL	CYLLLVKVCFR	RSKRAQTQKN	HPNHALKESK	240
QENMNELISD	SGONAITGPF	S				

1	11	21	31	41	51	
CATCCCTCTG	GCTCCAGAGC	TCAGAGCCAC	CCACAGCCGC	AGCCATGCTG	TGCCCTCTGC	60
TCACCCCTGGG	CGTGCGCCCTG	GTCTGTGGTG	TCCCGGCCAT	GGACATCCCC	CAGACCAAGC	120
AGGACCTGGA	GCTCCCAAAG	TGGCAGGGA	CCTGGCCATC	GATGGCCATC	GCGACCAACA	180
ACACTCTCCCT	CATGCGCGCA	CTGAGGCCCT	CTCTGAGGGT	CCACATCACC	TCACTGTGTC	240
CCAGCAAGCTG	GGACAACTCG	GAGATCGTTT	TGCAACAGAT	GAGGACCAAC	AGCTGTGTTG	300
ACAGAAGGCT	CTCTGGAGAG	AAGACTGGGA	ATCCAAGAA	TTCACAGAT	AACTATACGG	360
TGGCGAACGA	GGCCACGCTG	CTCGATACTG	ACTACGACAA	TTTCTGTGTT	CTCTGCTTAC	420
AGGACACCCAC	GACCCCCCATC	CATGACATGA	TGTGCCAGTA	GCTCGGCCAC	GTCCTGGTGG	480
AGGACGATGA	GATCATCGAG	CGAGTTCATCA	GGGCTTTTCAG	GCCCTCGCCC	AGGCACCTAT	540
GGTACTTGCT	GGACTTGAAA	CAGATGGAAG	AGCCGTCGCC	TTTGTGAGTC	ACTCCGCGCT	600
CCAGGAAGAC	GAGACTCCCA	CCCTTCCACA	CTCCAGAGC	ATTGCGACCT	CCCTCTGCC	660
TTTCAAAGAA	TAACACAGC	TCAGAGGAGC	ATGACGTGGT	CATCTGTGTC	GCCATCCCCT	720
TCCTGTGCTCA	CACCTGCAAC	ATTGCCATGT	GGAGGCTGCT	CCCTCGGGGC	AGAGTCTCTG	780
GCAGAGGTGA	TTAATAAACC	CTTGAGAGC	G			

1	11	21	31	41	51	
MDIPQTKQDL	ELPKLAGTWH	SMAMATNNIS	LMATLKAPLR	VHITSLLPTP	EDNLEIVLHR	60
WENNSCVEKK	VLGEKGTGNF	KFKINYTVAN	EATLLDTDYD	NFLPFLCLQDT	TTPIQSMMCQ	120
YLARVLVEDD	EIMOGFIRAF	RPLPRHLWYL	LDLQKMEEPC	RF		

1	11	21	31	41	51	
ACTTGCCTCT	CGCCCTCCGG	CCAAGCATGG	GGCTTCCCAG	GCTGGTCTGC	GCCTTCTTGC	600
TGCGCCGCTG	CTGCTGTGCT	CCTCGCGCTG	CGGGTGTGCC	CGGAGAGGCT	GAGCAGCCTG	1200
CGCCTGAGCT	GGTGGAGGCT	GAAGTGGGCA	GCACAGCCTT	CTTGAAGTGC	GAGCCTTCCC	1800
AGTCCCAAGG	CAACCTCAGC	CATGTCCAGT	GGTTTTCTGT	CCACAGAGTA	AAGCGACGCG	2400
TCATCTTCCG	TGTGCGCCAG	GCGCCAGGGC	AGAGCGAAGC	TGCGGAGTAC	GAGCAGGAGC	3000
TCAGCCTCCA	GACAGACAGG	GCTACTCTGG	CCCTGACTCA	AGTACCCCCC	CACAGACGAG	3600
GCACTCTCTT	GTGCGCAGGG	AAGCGCCCTC	GGTGCCAGGA	GTACCGCATC	CAGCTCCCGG	4200
TCATCAAAAG	TCGCGAGAGT	CCAAACATCC	AGGTCAACCC	CTTGGGCATC	CCGTGTGAAC	4800
GTAAGGAGCC	TGAGGAGGTC	GCTACTCTGT	TAGGGAGGAA	CGGATACCCC	ATTCTCTAAG	5400
TCATCTGGTA	CAAGAATGSC	CGGCTCTCGA	AGGAGGAGAA	GAAACGGGCT	CACATTCAGT	6000
CGTCCCAGAC	TGTGAGTGCT	AGTGGTTTTG	ACACCTTGCA	GAGTATTCTG	AAGGCACAGC	6600
TGGTTTAAAG	AGCAAAAGAT	GCCGCAAGTT	ACTGTGAGCT	CAACTACCCG	CTGCCCCAGT	7200
GGAACCACTA	GAAAGAGTCC	GAGGAAGTGC	CGCTCCGCTG	TTTCTACCGG	ACAGAAATAAG	7800
TGTGGCTGGA	AGTGAGAGCC	GTGGGAATGC	TGAAGGAAGG	GGACCCCGTG	GAAATCAGGT	8400
GGTTGGCTGA	TGGCAACCTC	CCACCAATCT	TCAGACTCAG	CACGACAGAC	CCGACGACCA	9000
GGGAGGCAGA	GGAAGAGACA	ACCAACGACA	ACGGGGTCTT	GGTGCTGGAG	CCTGCCGTCG	9600
AGGAAGACAG	TGGGCGCTAT	GAAATGTGAG	CTGTGAACTT	GGACCCAGTG	ATATCCCTGC	10200
TGGAGTAAAC	ACAGGAACTA	TGTTGTAAC	ATGTGTCCTG	GTGTCGAGAT	AGTCCGCGAG	10800
CCCTGTGAGAG	ACAGGAAGTG	AGAGACCTCA	CCCTGACCTC	TGAGGACAGAG	AGTATGAGCC	11400
ACCTCTGAGTT	CCAGTGGGCT	AGGAGAGAGA	CAGACCAAGT	CTGTGGAAGG	GGGCGCTGTC	12000

	TTCAAGTTGCA	TGACCTGA	CGGGAGGCAG	GAGGCGGCTA	TCGCTGCGTG	GGCTCTGTGC	1260
	CCAGCATACC	CGGCTGAAC	CGCACACAGC	TGGTCAAGCT	GGCCATTTTT	GGCCCCCCTT	1320
	GGATGGCATT	CAAGGAGAGG	AAGGTGTGGG	TGAAAGAGAA	TATGGTGTG	AATCTGTCTT	1380
5	GTGAAGCGTC	AGGGCACCCC	CGGCCCACCA	TCTCTGGAA	CGTCAACGGC	ACGGCAAGTG	1440
	AACAAGACCA	AGATCCACAG	CGAGTCTCTGA	GCACCCGTAA	TGTCTCTGTG	ACCCCGGAGC	1500
	TGTTGGAGAC	AGGTGTGAA	TGCAACGGCT	CCAAACGACCT	GGGCAAAAAC	ACCAGCATCC	1560
	TCTTCTGTGA	GCTGTCTAAT	TTAACCACCC	TCACACCAGA	CTCCAACACA	ACCACTGGCC	1620
	TCAGCACTTC	CACCTGCCAGT	CCTCATACCA	GAGCCACACG	CACCTCCACA	GAGAGAAAGC	1680
10	TGCCGGAGCC	GGAGAGCCGG	GGCGTGGTCA	TCGTGGCTGT	GATTGTGTGC	ATCCTGGTCC	1740
	TGGCGTGTCT	GGGCGCTGTC	CTCTATTTC	TCGTATAAGAA	GGGCAAGCTG	CCGTGCAGGC	1800
	GCTCAGGGAA	GCAGGAGATC	ACGCTGCCCC	CGTCTCGTAA	GACCGAACTT	GTAGTTGAAG	1860
	TTAAGTCAGA	TAAGTCCCA	GAAGAGATGG	GCCTCTCTGA	GGGCAGCAGC	GGTGACAAGA	1920
	GGGCTCCGGG	AGACCAGGGA	GAGAAATACA	TCGATCTGAG	GCATTAGCCC	CGAATCACTT	1980
15	CAGCTCCCTT	CCCTGCCTGG	ACCATTCCCA	GCTCCCTGCT	CACCTCTCTC	TCAGCCAAAG	2040
	CTCTCAAAAG	GACTAGAGAG	AAGCTCCTG	CTCCCTCAC	CTGCACACCC	CCTTTCAGAG	2100
	GGCCACTGGG	TAGGAGCTG	AGGACCTCAC	TTGGCCCTGC	AAGCCGCTTT	TCAGGGACCA	2160
	GTCACACACC	ATCTCTCTCA	CGTTGAGTGA	AGCTCATCCC	AAGCAAGSAG	CCCCAGTCTC	2220
	CCGAGCGGGT	ACGAGAGTGT	CTTGCAAGAAC	GTGTTTTTTC	TTTACACACA	TTATGGCTGT	2280
20	AAATACCTGG	CTCTGCCAG	CAGCTGAGCT	GGTAGCCTC	TCTGAGCTGG	TTTCTGCCCC	2340
	CAAGAGCTGG	CTTCCACCAT	CCAGGTGCAC	CACCTGAAGT	AGGACACACC	GGAGCCAGGC	2400
	GCCTGTCTAT	GTGGAAGTGC	GCTGTTTACA	CCCGCTCCGG	AGAGCACCCC	AGCGGCATCC	2460
	AGAAGCAGCT	GCAAGTGTGC	TGCCACACCC	CTCTGCTCG	CCTCTTCAAA	GTCTCTCTGT	2520
	ACATTTTTTC	TTTGTCTAGA	AGCCAGGAAC	TGGTGTCTAT	CCTTAAAGAA	TACGTGCCGG	2580
25	GGCCAGGTGT	GGTGGCTCAC	GCCTGTAATC	CCAGCACTTT	GGGAGGCCGA	GGCGGGCGGA	2640
	TCACAAAGTC	AGGACGAGAG	CATCTGGCT	AACACGGTGA	AACCTGTCTC	CTACTAAAAA	2700
	TACAAAAAAA	AATTAGCTAG	GGTAGTGGT	TGGCACCTAT	AGTCCCAAGT	ACTCGGAAGG	2760
	CTGAAGCAGC	AGAATGGTAT	GAATCCAGGA	GGTGGAGCTT	GCACTGAGCC	GAGACCGTGC	2820
	CACCTGCTGC	CAGCCTGGGC	AACACACGCA	GACTCCGTCT	CGAGGAAAAA	AAAAGAAAAA	2880
30	ACGCGTACCT	GGGTGAGGA	AGCTGGGCGC	TGTTTTCSAG	TTAGGTGAA	TTAGCCTCAA	2940
	TCGCCGTGTT	CACCTGTCTC	CATAGCCCTC	TTGATGGATC	ACGTAAAACT	GAAAGGCAGC	3000
	GGGAGCAGCA	CAAAAGCTAG	GTCTACACTG	TCCTTCTATG	GGATTAAAGC	TATGGTTATA	3060
	TTAGACACAA	ACTTCTACAA	ACCAAGCTCA	GGGCCCCAAC	CCTAGAAAGG	CCCAAAATGAG	3120
	AGAATGGTAT	TTAGGGATGG	AAAACGGGGC	CTGGCTAGAG	CTTCGGGTGT	GTGTGTCTGT	3180
35	CTGTGTGTAT	GCATACATAT	GTGTGTATAT	ATGGTTTTGT	CAGGTGTGTA	AATTTGCAAA	3240
	TTGTTTCCTT	TATATATGTA	TGTATATATA	TATATGAAAA	TATATATATA	TATGAAAAAT	3300
	AAAGCTTAAT	TGTCACAGAA	AATCATACAT	TGCTTTTTTA	TTCTACATGG	GTACCCAGG	3360
	AACTGGGGG	CCTGTGAAC	TACAACCAAA	AGGCACACAA	AACCGTTTCC	AGTTGGCAGC	3420
	AGAGATCAGG	GGTTACTCTC	GCTTCTGAGC	AAATGGCTCA	AGCTCTACCA	GAGCAGACAG	3480
40	CTACCCTACT	TTTACGACG	AAAACGTCCT	GTATGACGCA	GCACGAAGGG	CCTGGCAGGC	3540
	TGTTAGCAGG	AGCTATGTCC	CTTCTATCG	TTTCCGTCCA	CTT		

Seq ID NO: 553 Protein sequence
Protein Accession #: NP_006491.1

45	1	11	21	31	41	51	
	GLPRLVCAFL	LAACCCPRV	AGVPGEAEQP	APELVEVEVG	STALLKCGLS	QSQGNLSHVD	60
	WFSVHKEKRT	LIFRVQQGG	QSEFGEYEQR	LSLQDRGATL	ALTQVTPQDE	RIFLCQKRP	120
	RSQERYIQLR	VVKAPPEPNI	QVNPLGIPVN	SKPEPEVATC	VGRNGYPIPO	VIWYKNGRPL	180
50	KEEKVRVHIQ	SSQTVESSGL	YTLQSLKAAQ	LVKEDKDAQF	YCELNYRLPS	GNHMKESREV	240
	TVPVFPYTEK	VNLEVEPVMG	LKEGDRVEIR	CLADGNPPPH	FSISKQNPST	REAEETITND	300
	NGVLVLEPAR	KEHSGRYECQ	AWNLDTMISL	LSEPOELLVN	YVSDVRVSPA	APERQEGSSL	360
	TLTCEAESST	DLEFQWLREE	TDQVLERGPV	LQLHDLKREA	GGGYRCVASV	PSIPGLNRTQ	420
	LVKLAIFGPP	WMAFKERKVV	VKENMVLNLS	CEASGHPRPT	ISWNVNGTAS	EQDQDPQVRL	480
55	STLNVLVTPB	LELETGVECTA	SNDLGKNTSI	LFLELVNLIT	LTPDSNTTGT	LSTSTASPHT	540
	RANSTSTERK	LPEPESRGVV	IVAVIVCILV	LAVLGAVLYP	LYKKGKLPCR	RSQKQBITLP	600
	PSRKTELVEV	VKSDKLPEEM	GLLQSSGSDK	RAPGDQGEKY	IDLRH		

Seq ID NO: 554 DNA sequence
Nucleic Acid Accession #: NM_003183.3
Coding sequence: 165..2639

65	1	11	21	31	41	51	
	TCGAGCCTGG	CGGTAGAATC	TTCCCACTAG	GCGGCGCGGG	AGGGAAAAAG	GGATTGAGGG	60
	GCTAGGCCGG	GCGGATCCCG	TCCTCCCCCG	ATGTGAGCAG	TTTTCCGAAA	CCCGCTCAGG	120
	CGAAGCTGCG	CCAGAGAGGT	GGAGTCGGTA	GCGGGGCCGG	GAACATGAGG	CAGTCTCTCC	180
	TATTCTGTAC	CAGCGTGGTT	CCTTTCGTGC	TGGCGCGCGG	ACCTCCGGAT	GACCCGGGCT	240
70	TCGCCCCCA	CCAGAGACTC	GAGAAGCTTG	ATTCTTTGCT	CTCAGACTAC	GATATTCTCT	300
	CTTTATCTAA	TATCCAGCAG	CATTCCGTAA	GAAAAAGAGA	TCTACAGACT	TCAACACATG	360
	TAGAAACACT	ACTAACTTTT	TCAGCTTTGA	AAAGGCATTT	TAAATTATAC	CTGACATCAA	420
	GTACTGAACG	TTTTTCACAA	AATTTCAAGG	TCGTGGTGGT	GGATGGTAAA	AACGAAAGCG	480
	AGTACACTGC	AAAATGGCAG	GACTTCTTCA	CTGGACACGT	GGTTGGTGGG	CCTGACTCTA	540
	GGGTCTTAGC	CCACATAAGA	GATGATGATG	TTAATATCAG	AATCAACACA	GATGGGGCCG	600
75	AAATATAACAT	AGAGCCACTT	TGGAGATTGG	TTAATGATAC	CAAAAGACAAA	AGAATGTTAG	660
	TTTATAAATC	TGAAGATATC	AAGAATGTTT	CACGTTTGCA	GTCTCCAAAA	GTGTGTGGTT	720
	ATTTAAAGT	GGATAATGAA	GAGTTGCTCC	CAAAAGGTTT	AGTAGACAGA	GAACCACTG	780
	AAGAGCTTGT	TCATCGAGTG	AAAAGAAGAG	CTGACCCAGA	TCCCATGAAG	AACACGTGTA	840
	AAATTATTGGT	GGTAGCAGAT	CATCGCTTCT	ACAGATACAT	GGGCAGAGGG	GAAGAGAGTA	900
80	CAACTACAAA	TACTTAATA	GAGCTAATTG	ACAGAGTTGA	TGACATCTAT	CGGAACACTT	960
	CATGGGATTA	TGCAAGTTTT	AAAGGCTATG	GAATACAGAT	AGAGCAGATT	CGCAATCTCA	1020
	AGTCTCCACA	AGAGGTAAAA	CCTGGTGAAA	AGCACTACAA	CATGGCAAAA	AGTTACCCAA	1080
	ATGAAGAAAA	GGATGCTTGG	GATGTGAAGA	TGTTGCTAGA	GCAATTATAG	TTTGATATAG	1140
	CTGAGGAAGC	ATCTAAAGTT	TGCTTGGCAC	ACCTTTTCAC	ATACCAAGAT	TTTGATATGG	1200
85	GAACCTCTTG	ATTAGCTTAT	GTTGGCTCTC	CCAGAGCAAA	CAGCCATGGA	GGTGTTTGTC	1260
	CAAAGGCTTA	TTATAGCCCA	GTTGGGAAGA	AAAATATCTA	TTTGAATAGT	GGTTTGACGA	1320
	GCACAAAGAA	TTATGGTAAA	ACCATCCTTA	CAAAGGAAGC	TGACCTGGTT	ACAACTCATG	1380

AATTGGGACA TAATTTTGGG GCAGAACATG ATCCCGATGG TCTAGCAGAA TGTGCCCCGA 1440
 ATGAGGACCA GGGAGGGAAA TATGTCATGT ATCCCATAGC TGTGAGTGGC GATCAGCAGA 1500
 ACAATAAGAT GTTTTCAAAC TGCAGTAAAC AATCAATCTA TAAGACCATT GAAAGTAAGG 1560
 CCCAGGAGTG TTTTCAAGAA CGCAGCAATA AAGTTTGTGG GAACCTGAGG GTGGATGAAG 1620
 GAGAAAGATG TGATCCTGGC ATCATGTATC TGAACAAACA CACCTGCTGC AACAGCGACT 1680
 GCACGTTGAA GGAAGGTGTC CAGTGCACTG ACAGGAACAG TCCTTGCTGT AAAAACTGTC 1740
 AGTTTGAGAC TGCCACAGAG AAGTGCCAGG AGGCGATTAA TGCTACTTGC AAAGGCGTGT 1800
 CCTACTGCAC AGGTAATAGC AGTGAGTGCC CGCTCCAGG AAATGCTGAA AATGACACTG 1860
 TTTGCTTGA TCTTGGCAAG TGTAAAGGAT GGAAATGCAT CCCTTCTGTC GAGAGGGAAAC 1920
 AGCAGCTGGA GTCCTGTGCA TGTAAATGAAA CTGCAAACTC CTGCAAGGTG TGCTGACAGG 1980
 ACCTTCTCG CCGCTGTGTG CCCTATGTCT ATGCTGAACA AAAGAAGCTA TTTTGTAGGA 2040
 AAGGAAAGCC CTGTACAGTA GGATTTTGTG ACATGAATGG CAAATGTGAG AACCGAGTAC 2100
 AGGATGTAAT TGAACGATTT TGGGATTTCA TTGACCAGCT GAGCATCAAT ACTTTTGGAA 2160
 AGTTTTTAGC AGACAAATC GTTGGGTCTG TCCTGGTTTT CTCCTTGATA TTTTGGATTG 2220
 CTTTCAAGAT TCTTGTCCAT TGTGTGGATA AGAAATTTGA TAAACAGTAT GAATCTCTGT 2280
 CTCTGTTTCA CCCAGTTAAC GTGAAAATGC TGAGCAGCAT GGATTCGTGA TCGGTTTCGA 2340
 TTATCAAACC CTTTCTCTCG CCCAGACTC CAGGCCGCTC GCAGCCTGCC CCTGTGATCC 2400
 CTTGCGCGCC AGCAGCTCCA AAACCTGGACC ACCAGAGAAT GGACACCATC CAGGAAGACC 2460
 CCAGCACAGA TCCCAATAG GACGAGGATG GGTTTGAGAA GGACCCCTTC CCAAAATAGCA 2520
 GCACAGCTGC CAAGTCATTG GAGGATCTCA CGGACCATCC GGTGCGCAGA AGTGAAGAGG 2580
 CTGCTCTCTT TAACTGTGAG GTGCAAGTAC GTGTTAACAG CAAAGAAACA GAGTGCTAAT 2640
 TTAGTTCTCA GCTCTTCTGA CTTAAGTGTG CAAATATTTT TTATAGATTT GACCTACAAA 2700
 TCAATCACAG CTGTGATTTT GTGAAGACTG GGAAGTGACT TAGCAGATGC TGGTCATGTC 2760
 TTTGAACTTC CTGCAAGTAA ACAGTTCTTG TGTGTTTGG CCCTTCTCCT TTTGAAAAGG 2820
 TAAGGTGAAA GTGAATCTAC TTATTTTGTG GCTTTCAGT TTTAGTTTTC AAAATATCTT 2880
 TTGACCTGTA TGAATCTTAA AGAAAATACA GCTGGATTGG GTTATGAATA TTTACGTTTT 2940
 TGTAAATTA TCTTTTATAT TGAACACAGC ACTGACTAGG GAAATGATCA GTTTTTTTTT 3000
 ATACACTGTA ATGAACCGCT GAATATGAAG CATTTGGCAT TTATTTGTGA GAAAAGTGA 3060
 ATAGTTTTTT TTTTCTTCTG CTTCAACTAA AAAACAAAGG GATAAATTTA 3120
 GTATACATG TATCTAAATG GTGGGTCTAT TTCTAGTTAT TACCAGAGT TTTTATGTAG 3180
 CAGGGAATAT ATATATCTAA ATTTAGAAAT CATTTGGGTT AATATGGCTC TTCATAATTC 3240
 TAAGACTAAT GCTCAGAAC TAACCACTAC CTTACAGTGA GGGCTATACA TGGTAGCCAG 3300
 TTGAATTTAT GGAATCTACC AACTGTTTAG GGCCCTGATT TGCTGGGCAG TTTTCTGTGA 3360
 TTTTATAAGT ATCTTCATGT ATCCCTGTTA CTGATAGGGA TACATGTCTT AGAAAATTC 3420
 CTATTGGCTG GGAGTGGTGG CTCATGCTCG TAATCCAGC ACTTGGAGAG GCTGAGGTG 3480
 CGCCACTACA CTCAGCCTG GGTGACAGG TGAGATCTGC CTC

Seq ID NO: 555 Protein sequence
 Protein Accession #: NP_003174.2

1 11 21 31 41 51
 MRQSLFLTS VVFFVLAPRP PDDPGFGPHQ RLEKLDLSLS DYDILSLSNI QHHSVRKRD 60
 QSTHVETLL TFSALKRHFK LYLTSSSTERF SQNFKVVVD GKNESEYAK WQDFFTGHHV 120
 GEPDSRVLAH IRDDDVIRI NTDGAENYIE PLWRPVNDTK DKRMLVYKSE DIKNVSRLLQS 180
 PKVCGYLKVD NEELLPKGLV DREPPEELVH RVKRRADPDF MKNTCKLLV ADHRFPYRYM 240
 RGEESTTNY LLELIDRVDD IYRNTSWDNA GFKGYGIQIE QIRILKSPQE VKPGEKHYNM 300
 AKSYFNEEKD AWDVLMLELQ PFPDIAEEAS KVCLAHLEPT QDFDMGTGLL AYVGSPPRNS 360
 HGGVCPKAYY SPVGGKNIYL NSGLTSTKNY KTIILTKEAD LVTTHELGHV FGAEHDPDGL 420
 AECAPNEDQG GYVMYPIAV SGDHENNKMF SNCSKQSIYK TIESKAQECF QERSNKVCGN 480
 SRVDEGEEDC PGIMVLNNDT CCNSDCTLKE GVQCSDRNSP CCKNCQFETA QKCKQBAINA 540
 TCKGVSCTYG NSSECPPPGN AENDTVCLDL GKCKDGKCIPI FCEREQQLS CACNETDNNSC 600
 KVCRRDLGR CVPYVDAQK NPLFRKGKPC TVGFCDMNGK CEKRVQDVIE RFNDFIDQLS 660
 INTFGKFLAD NIVGSVLVFS LIFWIPFSIL VHCVDKLLDK QYESLSLFHP SNVEMLSMD 720
 SASVRIKPP PAPPTGRLQ PAPVIPSAPA APKLDHQRMD TIQEDPSTDS HMDGDFEKO 780
 PPFNSSTAAR SPEDLTDFHV ARSEKAASPK LQRQNRVNSK ETEC

Seq ID NO: 556 DNA sequence
 Nucleic Acid Accession #: NM_021832.1
 Coding sequence: 164..2248

1 11 21 31 41 51
 TCGAGCCTGG CGGTAGAATC TTCCAGTAG GCGGCGCGGG AGGAAAAGAG GATTGAGGGG 60
 CTAGGCCGGG CGGATCCCGT CCTCCCGGGA TGTGAGCAGT TTTCCGAAAC CCGTCAGGC 120
 GAAGGCTGCC CAGAGAGGTG GAGTCGGTAG CGGGGCCGGG AACATGAGGC AGTCTCTCCT 180
 ATTCTGAGCC AGCGTGGTTC CTTTCTGTCT GCGCCCGCGA CCTCCGGATG ACCCGGGCTT 240
 CGGCCCCAC CAGAGACTCG AGAAGCTTGA TTCTTTGCTC TCAGACTACG ATATTCTCTC 300
 TTTATCTAAT ATCCAGCAGC ATTCGGTAAG AAAAGAGAT CTACAGACTT CAACACATGT 360
 AGAAACACTA CTAACTTTTT CAGCTTTGAA AAGGCATTTT AAATTATACC TGACATCAAG 420
 TACTGAACGT TTTTCAAAA ATTTCAAGGT CGTGGTGGTG GATGGTAAAA ACGAAAGCGA 480
 GTACACTGTA AAATGGCAGG ACTTCTTCAC TGGACACGTG GTTGGTGAGC CTGACTCTAG 540
 GGTCTAGGCC CACATAAGAG ATGATGATGT TATAATCAGA ATCAACACAG ATGGGGCCGA 600
 ATATAACATA GAGCCACTTT GGAGATTGT TAATGATACC AAAGACAAA GAATGTTAGT 660
 TTATAAATCT GAAGATATCA AGAATGTTT ACCTTTGCG TCTCCAAAAG TGTGTGGTTA 720
 TTTAAAAGTG GATAATGAAG AGTTGCTCCC AAAAGGGTTA GTAGACAGAG AACCACTGA 780
 AGAGCTTGT CATCAGTGA AAAGAAGAGC TGACCCAGAT CCCATGAAGA ACACGTGTAA 840
 ATTATTGGTG GTAGAGATC ATCGCTTCTA CAGATACATG GGCAGAGGGG AAGAGAGTAC 900
 AACTACAAAT TACTTAATAG AGCTAATTGA CAGAGTTGAT GACATCTATC GGAACACTTC 960
 ATGGGATAAT GCAGGTTTTA AAGGCTATGG AATACAGATA GAGCAGATTG GCATTCTCAA 1020
 GTCTCCACAA GAGGTAAAC CTGGTGAAAA GCACTACAAC ATGGCAAAA GTTACCCAAA 1080
 TGAAGAAAAG GATGCTTGGG ATGTGAAGAT GTTGCTAGAG CAATTTAGCT TTGATATAGC 1140
 TGAGGAAGCA TCTAAAGTTT CTTTGGCACA CTTTTCACA TACCAAGATT TTGATATGGG 1200
 AACTCTTGA TTAGCTTATG TTGGCTCTCC CAGAGCAAAC AGCCATGGAG GTGTTTGTCC 1260
 AAAGGCTTAT TATAGCCGAG TTGGGAAGAA AAATATCTAT TTGAATAGTG GTTTGACGAG 1320
 CACAAAGAA TATGTAATAA CCATCCTTAC AAAGGAAGCT GACCTGGTTA CAATCATGA 1380
 ATTTGGGACAT AATTTTGGAG CAGAACATGA TCCGATGGT CTAGCAGAA GTGCCCCGAA 1440

	TGAGGACCAAG	GGAGGGAAAT	ATGTCAATGTA	TCCCATAGCT	GTGAGTGGCG	ATCACGAGAA	1500
	CAATAAGATG	TTTTCAAAC	GCAGTAAACA	ATCAATCTAT	AAGACCATTG	AAAGTAAGGC	1560
	CCAGGAGTGT	TTTCAAGAAC	GCAGCAATAA	AGTTTGTGGG	AACTCGAGGG	TGGATGAAGG	1620
5	AGAAGAGTGT	GATCCTGGCA	TCATGTATCT	GAACAACGAC	ACCTGCTGCA	ACAGCGACTG	1680
	CACGTTGAAG	GAAGGTGTCC	AGTGCACTGA	CAGGAACAGT	CCTTGCTGTA	AAAACGTGTA	1740
	GTTTGAGACT	GCCCAAGAAG	AGTGCCAGGA	GGCGATTAA	GCTACTTGCA	AAGGCGGTGC	1800
	CTACTGCACA	GGTAATAGCA	GTGAGTGCCC	GCCTCCAGGA	AATGCTGAAG	ATGACACTGT	1860
	TTGCTTGGAT	CTTGGCAAGT	GTAAAGGATG	GAAATGCATC	CCCTTCTGCG	AGAGGGGAACA	1920
10	GCAGCTGGAG	TCCTGTGCAT	GTAAATGAAAC	TGACAACTCC	TGCAAGGTGT	GCTGCAGGGA	1980
	CCCTTCCGGC	CGCTGTGTGC	CCTATGTGCA	TGCTGAACAA	AAGAAGTTAT	TTTGTAGGAA	2040
	AGGAAAGCCC	TGTACAGTAG	GATTTTGTGA	CATGAATGGC	AAATGTGAGA	AACGAGTACA	2100
	GGATGTAATT	GAACGATTTT	GGGATTTTCT	TGACCAGCTG	AGCATCAATA	CTTTTGGAAA	2160
	GTTTTTAGCA	GACAACTATG	TTGGGTCTGT	CCTGGTTTTC	TCCTTGATAT	TTTGGATTCC	2220
	TTTCAGCATT	CTGTGTCAAT	GTGTGTAAAC	TCGAAATGCT	GAGCAGCATG	GATTCTGCAT	2280
15	CGGTTTCGAT	TATCAAAACC	TTTCTGCGC	CCGAGACTCC	AGGCGCGCTG	CAGCCTGCCC	2340
	CTGTGATCCC	TTCCGCGCCA	CGAGCTCCAA	AACTGGACCA	CCAGAGAATG	GACACCATCC	2400
	AGGAAGACCC	CAGCACAGAC	TCACATATGG	ACGAGGATGG	GTTTGAGAAG	GACCCCTTCC	2460
	CAAAATAGCAG	CACAGCTGCC	AAGTCATTTG	AGGATCTCAC	GGACCATCCG	GTCAACAGAA	2520
20	GTGAAAAGGC	TGCTCTCTTT	AACTGCAGC	GTCAAGATCG	TGTTGACAGC	AAAGAAACAG	2580
	AGTGCTAATT	TAGTCTCTAG	CTCTTCTGAC	TTAAGTGTGC	AAAAATTTT	TATAGATTG	2640
	ACCTACAATT	TATATTTTGT	GAAGACTGGG	AAGTGACTTA	GCAGATGCTG		2700
	GTCAATGTGT	TGAATCTCT	GCAGGTAAAC	AGTCTCTGTG	TGGTTTGGCC	CTTCTCTTT	2760
	TGAAAAGGTA	AGGTGAAGGT	GAATCTAGCT	TATTTTGAAG	CTTTCAGGTT	TTAGTTTTTA	2820
25	AAATATCTTT	TGACCTGTGG	TGCAAAAGCA	GAAAATACAG	CTGGATTGGG	TTATGAGTAT	2880
	TACGTTTTTT	GTAAATTAAT	CTTTTATATT	GATAACAGGC	ACTGACTAGG	GAAATGATCA	2940
	GTTTTTTTTT	ATACACTGAT	ATGAACCGCT	GAATATGAAG	CATTGGGCAT	TTATTTGTGA	3000
	GAAAAGTGGA	ATAGTTTTTT	TTTTTTTTTT	TTTTTTTTTG	CTTCAACTAA	AAACAAAGGA	3060
	GATAAATTTA	GTATACATTT	TATCTAAATT	GTGGGTCTAT	TTCTAGTTAT	TACCCAGAGT	3120
30	TTTTATGTAG	CAGGGAATAA	ATATATCTAA	ATTTAGAAAT	CATTGGGTTT	AATATGGCTC	3180
	TTCAATAATC	TAAGACTAAT	GCTCAGAAC	TAACCACTAC	CTTACAGTGA	GGGCTATACA	3240
	TGGTAGCCAG	TTGAATTTAT	GGAACTCTAC	AACTGTTTAG	GGCCCTGATT	TGCTGGGCAG	3300
	TTTTTCTGTA	TTTTATAAGT	ATCTTCATGT	ATCCCTGTTA	CTGATAGGGA	TACATGTCTT	3360
	AGAAAATTTCA	CTATTGGCTG	GGAGTGGTGG	CTCATGCCCT	TAATCCAGC	ACTTGGAGAG	3420
35	3421	GCTGAGGTTG	CGCCACTACA	CTCCAGCTCG	GGTGACAGAG	TGAGATCTGC	CTC

Seq ID NO: 557 Protein sequence
Protein Accession #: NP_068604.1

	1	11	21	31	41	51	
40	MRQSLFLTS	VVPFVLAPRP	PDDPGFGPHQ	RLEKLDLSLS	DYDILSLSN	QQHSVRKRDL	60
	QTSTHVETLL	TFSALKRHF	LYLTSSTERF	SONFKVVVD	GKNESEYTVK	WQDFFTGHVV	120
	GPDSRVLAH	IRDDVDIIRI	NTDGAENIE	PLWRFVNDTK	DKRMLVYKSE	DIKNVSRLOS	180
45	PKVGYLKV	NEELLPKGLV	DREPEELVH	RVKRRADPDF	MKNTCKLLV	ADHRFYRYMG	240
	RGEESTTNY	LIELIDRVDD	IYRNTSWDNA	GFKGYGIQIE	QIRILKSPQE	VKPGKHYNM	300
	AKSYNNEED	AWDVLMLEQ	FSFDIAEAS	KVCLAHLFY	QDFDMGTLEL	AYVGSPRANS	360
	HGGVCKKAY	SPVGKKNY	NSGLTSTKNY	GKTLTKEAD	LVTTHLELGH	FGAEHDPDGL	420
	AECAPNEDQ	GKYMYPYIAV	SGDHNNKMF	SNCSKQSIYK	TIESKAQECF	QERSNKVCGN	480
50	SRVDEGEED	PGIMYLNNDT	CCNSDCTLKE	GVQCSDRNSP	CCNKQCFETA	QKKCQEAINA	540
	TCKGVSCTG	NSSECPPEGN	AEDDTVCLDL	GKCKDGKICP	FCEREQQLS	CACNETDNCS	600
	KVCCRDLGR	CVFYVDAEQK	NFLRKGKPC	TVGFCDMNGK	CEKRVQDVIE	RFNDFIDQLS	660
	INTFGKPLAD	NIVGSVLVFS	LIFWIPFSIL	VHCV			

Seq ID NO: 558 DNA sequence
Nucleic Acid Accession #: NM_004994.1
Coding sequence: 20..2143

	1	11	21	31	41	51	
60	AGACACCTCT	GCCTCACCA	TGAGCCTCTG	GCAGCCCTCG	GTCCTGGTGC	TCCTGGTGCT	60
	GGGTGCTGCG	TTTGTCTGCC	CCAGACAGCG	CCAGTCCACC	CTTGTGCTCT	TCCCTGGAGA	120
	CCTGAGAAC	AATCTCACCG	ACAGGCAGCT	GGCAGAGGAA	TACCTGTACC	GCTATGGTTA	180
	CACCTCGGTG	GCAGAGATGC	GTGGAGAGTC	GAAATCTCTG	GGGCTGCGC	TGCTGCTTCT	240
65	CCAGAAGCAA	CTGTCCCTGC	CCGAGACCGG	TGAGCTGGAT	AGCGCCACGC	TGAAGGCCAT	300
	GCGAACCACA	CGGTGCGGGG	TCCAGACCT	GGCAGATTTC	CAAACTTTTG	AGGGCGACCT	360
	CRAAGTGGAC	CACCACAACA	TCACCTATTG	GATCCAAAAC	TACTCGGAAG	ACTTGCCGGG	420
	GGCGGTGATT	GACGACGCTT	TTGCCCGCGC	CTTCGCACTG	TGGAGCGCGG	TGACGCGGCT	480
	CACCTTCACT	CGCTGTATAC	GCCGGGACGC	AGACATCGTC	ATCCAGTTTG	GTGTGCGGGA	540
70	GCAAGGAGAC	GGGTATCCCT	TGACGGGAA	GGACGGGCTC	CTGGCACACG	CCCTTCTCTC	600
	TGGCCCGGCG	ATTGAGGGAG	ACGCCCATTT	CGACGATGAC	GAGTTGTGGT	CCCTGGGCAA	660
	GGGCGTCTGT	GTTCCAACTC	GGTTTGGAAA	CGCAGATGGC	GCGGCGTGGC	ACTTCCCTTT	720
	CATCTTCGAG	GGCCGCTCCT	ACTCTGCTGT	CACCACCGAC	GGTCTGCTCG	ACGGCTTGCC	780
	CTGGTGCATT	ACCACGGCCA	ACTACGACAC	CGACGACCGG	TTTGGCTTCT	GCCCCAGCGA	840
75	GAGACTCTAC	ACCCGGGACG	GCAATGCTGA	TGGGAAACCC	TGCCAGTTTC	CATTCTCTTT	900
	CCAAGGCCAA	TCCTACTCCG	CCTGCACCAC	GGACGGTCCG	TCCGACGGCT	ACCGCTGGTG	960
	GCCACCAACC	GCCAACTACG	ACCGGGACAA	GCTCTTCGGC	TTCTGCCCGA	CCCGAGCTGA	1020
	CTCGACGGTG	ATGGGGGACA	ACTCGGCGGG	GGAGCTGTGC	GTCTTCCCTT	TCACCTTCTT	1080
	GGGTAAGGAG	TACTCTGACT	TACCAACGGA	GGGCGCGGGA	GATGGGCGCC	TCTGGTGCGC	1140
80	TACCACCTCG	AACTTTGACA	GCGACAAGAA	GTGGGGCTTC	TGCCCGGACC	AAGGATACAG	1200
	TTTGTTCCTC	GTGGCGGCGC	ATGAGTTCTG	CCACGCGCTG	GGCTTAGATC	ATTCTCTAGT	1260
	CCCGAGGGCG	CTCATGTACC	CTTCACTGAG	GGGCCCCCTT	TGCATAAGGA		1320
	CGACGTGAAT	GGCATCCGGC	ACCTCTATGG	TCTCTGCCCT	GAACTCTGAG	CAGGCGCTCC	1380
	AACCAACCA	CCACGGCTCC	CCGACGCTCC	CCGACGCTCC	TGCCCCACCG	GACCCCCAC	1440
85	TGTCCACCCC	TCAGAGCGCC	CCACAGCTGG	CCCCACAGGT	CCCCCTCAG	CTGGCCCCAC	1500
	AGGTCCCCCC	ACTGCTGGCC	CTTCTACGGC	CCTACTGTG	CCTTTGAGTC	CGGTGGACGA	1560
	TGCCTGCAAC	GTGAACATCT	TCGACGCCAT	CGCGGAGATT	GGGAACACG	TGTATTGTGT	1620
	CAAGGATGGG	AAGTACTGGC	GATTCTCTGA	GGGCGGGGG	AGCGCGCCCG	AGGGCCCCCT	1680

5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85

CCTTATCGCC GACAAGTGGC CCGCGCTGCC CCGCAAGCTG GACTCGGTCT TTGAGGAGCC 1740
GCTCTCCAAG AAGCTTTTCT TCTTCTCTGG GCGCCAGGTG TGGGTGTACA CAGGCGCGTC 1800
GGTCTGGGC CCGAGGCGTC TGGACAAGCT GGGCGTGGGA GCGGACGTGG CCCAGGTGAC 1860
CGGGCCCTC CGAGTGTGCA GGGGGAAGAT GCTGCTGTTC AGCGGGCGGC GCCTCTGGAG 1920
GTTGAGCGTG AAGGCGCAGA TGGTGGATCC CCGGAGCGCC AGCGAGGTGG ACCGGATGTT 1980
CCCCGGGGTG CCTTTGGACA CGCACGACGT CTTCAGTAC CGAGAGAAAG CCTATTTCTG 2040
CCAGGACCGC TTCTACTGGC GCGTGAAGTC CCGGAGTGAG TTGAACCAAG TGGACCAAGT 2100
GGGCTACGTG ACCTATGACA TCCTGCAGTG CCCTGAGGAC TAGGGCTCCC GTCCTGCTTT 2160
CGAGTGCAT GTAAATCCCC ACTGGGACCA ACCCTGGGGA AGGAGCCAGT TTGCCGGATA 2220
CAAACTGGTA TTCTGTTCTG GAGGAAAGGG AGGAGTGGAG GTGGGCTGGG CCCTCTCTTC 2280
TCACCTTTGT TTTTGTGTGG AGTGTTCTA ATAACTTGG ATTCTCTAAC CTTT

Seq ID NO: 559 Protein sequence
Protein Accession #: NP_004985.1

1 11 21 31 41 51
MSLWQPLVLV LLVLGCCFAA PRQRQSTLVL FPGDLRLNLT DRQLAEELYLY RYGYTRVAEM 60
RGESKSLGPA LLLLLQKLSL PETGELDSAT LKAMRTPRCG VPDLRGFTQF EGDLEKWHHN 120
ITWYIQNYSE DLPRVIDDA FARAFALWSA VTPLTFTRVY SRDADIVIQF GVAEHGDGYP 180
FDGKDGLLAH AFPPGPGIQQ DAHFDDDELW SLGKGVVVPF RFGNADGAAC HFPFIFEGRS 240
YSACTTDGRS DGLPWCSTTA NYDTDDRFGF CPSELYTRD GNADGKPCQF PFIFQQQSYS 300
ACTTDGRSDG YRWCATTANY DRDKLFGFCP TRADSTVMGG NSAGELCVFP FTFLGKEYST 360
CTSEGRGDGR LWCATTSNFD SDDKWWGFCPD QGYSFLVAA HEFGHALGLD HSSVPEALMY 420
PMYRFTGPPS LHKDDVNGIR HLYGPRPEPE PRPPTTTTPQ PTAPPTVCTP GPPTVHPSER 480
PTAGFTGPPS ACPTGPPTAG PSTATTVPLS PVDDACNVNI FDAIAEIGNQ LYLKDKGKYW 540
RFSEGRGSRP QGFILADKW PALPRKLDV FEEPLSKLE FFSGRQVWVY TGASVLGPRR 600
LDKLGGLADV AQVTGALRSV RGKMLLFSGR RLWRFDVKAQ MVDPRSASEV DRMFPGVPLD 660
THDVFYQYREK AYFCQDRFYW RVSSRSELNQ VDQVGYVTYD ILQCPED

Seq ID NO: 560 DNA sequence
Nucleic Acid Accession #: NM_000213.1
Coding sequence: 127..5385

1 11 21 31 41 51
CGCCCGCGCG CTGCAGCCCC ATCTCCTAGC GGCAGCCGAG GCGCGGAGGG AGCGAGTCCG 60
CCCCGAGGTA GGTCCAGGAC GGGCGCACAG CAGCAGCCGA GGCTGGCCGG GAGAGGGAGG 120
AAGAGGATG CAGGCCACG CCCCAGCCCA TGGGCCAGGC TGCTCCTGGC AGCCTTGATC 180
AGCGTCAGCG TCTCTGGGAC CTTGGCAAAC CGCTGCAAGA AGGCCCCAGT GAAGAGCTGC 240
ACGAGTGTG TCCGTGTGGA TAAGGACTGC GCCTACTGCA CAGACGAGAT GTTCAGGGAC 300
CGGCGCTGCA ACACCCAGGC GGAGCTGCTG GCCCGGGGCT GCCAGCGGGA GAGCATCGTG 360
GTGATGGAGA GCAGCTTCCA AATCACAGAG GAGACCCAGA TTGACACCAC CTGCGGCGC 420
AGCCAGATGT CCCCCAAGG CCTGCGGGTC CGTCTGCGGC CCGGTGAGGA GCGGCATTTT 480
GAGCTGGAGG TGTTTGAGCC ACTGGAGAGC CCGGTGGACC TGTACATCCT CATGGAATTC 540
TCCAACTGTA TCTGGACAAC CTCAAGAAGA TGGGGCAGAA CCTGGCTCGG 600
GCTCTGAGCC AGCTCAGGAC GAGTACACT ATTGGATTG GCAAGTTTGT GGACAAAGTC 660
AGCGTCCCGC AGACGGACAT GAGGCTGAG AAGCTGAAGG AGCCCTGGCC CAACAGTGAC 720
CCCCCTTCT CTTCAAGAA CGTCATCAGC CTGACAGAAG ATGTGGATGA GTTCCGGAAT 780
AAATGTCAGG GAGAGCGGAT CTCAGGCAAC CTGGATGCTC CTGAGGGCGG CTTGATGACC 840
ATCCTGCAGA CAGCTGTGTG CACGAGGGAC ATTGGCTGGC GCCCGGACAG CACCCACCTG 900
TGTGTTCTT CCACCGAGTC AGCCTTCCAC TATGAGGCTG ATGGCGCCAA CGTGTGCGCT 960
GGCATCATGA GCGGCAACGA TGAACGGTGC CACCTGGACA CCACGGGCAC CTACACCCAG 1020
TACAGGACAC AGGACTACCC GTCGGTGCCT ACCCTGGTGC GCCTGCTCGC CAAGCAACAC 1080
ATCATCCCA TCTTTGCTGT CACCAACTAC TCCTATAGCT ACTACGAGAA GCTTCACACC 1140
TATTTCCCTG TCTCCTACT GGGGTGCTG CAGGAGGACT CGTCCAACAT CGTGGAGCTG 1200
CTGGAGGAGG CTTCAATCG GATCCGCTCC AACCTGGACA TCGGGGCCCT AGACAGCCCC 1260
CGAGGCTTTC GCAGCAGAGT CACCTCCAAG ATGTTCCAGA AGACGAGGAG TGGGTCTTTT 1320
CACATCCGCG GGGGGGAAGT GGTATATAT CAGGTGCAGC TGCGGGCCCT TGAGCACGTG 1380
GATGGGACGC ACGTGTGCCA GCTGCCGGAG GACCAGAAGG GCAACATCCA TCTGAAACCT 1440
TCCTTCTCG ACCTGCTCAA GATGGACGCG GGCATCATCT GTGATGTGTG CACTGCGGAG 1500
CTGCAAAAG AGGTGCGGTC AGCTCGCTGC AGCTTCAAG GAGACTTCGT GTGCGGACAG 1560
TGTGTGTGCA GCGAGGGCTG GAGTGGCCAG ACCTGCAACT GCTCCACCGG CTCTCTGAGT 1620
GACATTGACG CTTGCTGCGG GAGGGGCGAG GACAAGCCGT GCTCCGGCGG TGGGAGTGC 1680
CAGTGCGGGC ACTGTGTGTG CTACGGCGAA GGCCGCTACG AGGGTCAGTT CTGCGAGTAT 1740
GACAACCTCC AGTGTCCCG CACTTCCGGG TTCTCTGCA ATGACCGAGG ACGCTGCTCC 1800
ATGGGCGAGT GTGTGTGTGA GCCTGGTGTG ACAGGCCCAA GCTGTGACTG TCCCCCTCAGC 1860
AATGCCACCT GCATGCTGCA CAATGGGGGC ATCTGTAATG GACGTGGGCC CTGTGAGTGT 1920
GGCGCTGCGC ACTGCCACCA GCACTGCTC TACACGGACA CCATCTGCGA GATCAACTAC 1980
TCGGCGATCC ACCCGGGCCT CTGCGAGGAC CTACGCTCCT GCGTGCAGTG CCAGGCGGTG 2040
GGCACGCGCG AGAAGAAGGG GCGCACGTGT GAGGAATGCA ACTTCAAGGT CAAGATGGTG 2100
GACGAGCTTA AGAGAGCCGA GGAGGTGGTG GTGCGCTGCT CTTTCCGGGA CGAGGATGAC 2160
GACTGCACCT ACAGCTACAC CATGGAAGGT GACGGCGCCC CTGGGCCCAA CAGCACTGTC 2220
CTGGTGACCA AGAAGAAGGA CTGCCCTCGG GGCTCCTTCT GGTGGCTCAT CCCCCTGCTC 2280
TCTCTCTCTC TCGCGCTCCT GGCCTTGCTA CTGCTGCTAT GCTGGAAGTA CTGTGCTCTC 2340
TGCAAGGCTT GCCTGGCACT TCTCCGTCG TGCAACCGAG GTGCATGGT GGGCTTTAAG 2400
GAAGACCACT ACATGCTGCG GGAGAACCTG ATGGCCTCTG ACCACTTGGA CACGCCCATG 2460
CTGCGCACG GCAACCTCAA GGGCCGTGAC GTGGTCCGCT GGAAGGTGAC CAACAACATG 2520
CAGCGGCGCT GCTTTGCCAC TCATGCCGCC AGCATCAACC CCACAGAGCT GGTGCCCTAC 2580
GGGCTGTCTT TGCCTGTGGC CGGCTTTGAC ACCGAGAACC TGCTGAAGCC TGACACTCGG 2640
GAGTGCAGCC AGTGCGCCA GGAGGTGGAG GAGAACCCTGA ACGAGGTCTA CAGGCAGATC 2700
TCCGTGTGAC ACAAGCTTCA GCAGACCAAG TTCCGGCAGC AGGCCAATGC CGGGAAGAG 2760
CAAGACCAAC CATTGTGGA CACAGTGTG ATGGCGCCCC GCTCGGCCCA CGCCGCCCTG 2820
CTGAAGCTTA CAGAGAAGCA GGTGGAACAG AGGGCCTTCC ACAGACTCAA GGTGGCCCCC 2880
GGCTACTACA CCTCACTGC AGACCAGGAC GCCCGGGGCA TGGTGGAGTT CCAGGAGGCG 2940
GTGGAGCTGG TGGACGTACG GGTGCCCTC TTTATCCGGC CTGAGGATGA CAGCAGAGAG 3000
CAGCTGTCTG TGGAGGCCAT CGACGTGCCC GCAGGCACTG CCACCTCGG CCGCGCCTG 3060

5	GTAACATCA	CCATCATCAA	GGAGCAAGCC	AGAGACGTGG	TGTCCTTTGA	GCAGCCTGAG	3120
	TTCTCGGTCA	GCCGCGGGGA	CCAGGTGGCC	CGCATCCCTG	TCATCCGGCG	TGTCTGGGAC	3180
	GGCGGGAAGT	CCCAGGTCTC	CTACCGCACA	CAGGATGGCA	CCGCGCAGGG	CAACCGGGAC	3240
	TACATCCCCG	TGGAGGGTGA	GCTGCTGTTC	CAGCCTGGGG	AGGCCTGGAA	AGAGCTGCAG	3300
	GTGAAGCTCC	TGAGAGCTGA	AGAAGTTGAC	TCCCTCCTGC	GGGGCCGCCA	GGTCCGCCCT	3360
	TTCCACGTCC	AGCTCAGCAA	CCTAAGTTT	GGGGCCCAAC	TGGGCCAGCC	CCACTCCACC	3420
	ACCATCATCA	TCAGGGACCC	AGATGAACGT	GACCGGAGCT	TCACGAGTCA	GATGTTGTCA	3480
	TCACAGCCAC	CCCCTCACGG	CGACCTGGGC	GCCCCGCGAG	ACCCCAATGC	TAAGGCCGCT	3540
10	GGGTCCAGGA	AGATTCATTT	CAACTGGCTG	CCCCCTTCTG	GCAAGCCAAT	GGGGTACAGG	3600
	GTAAAGTACT	GGATTCAAGG	TGACTCCGAA	TCCGAAGCCC	ACCTGCTCGA	CAGCAAGGTG	3660
	CCCTCAGTGG	AGCTCAGCAA	CCTGTACCCG	TATTGCGACT	ATGAGATGAA	GGTGTGCCCC	3720
	TACGGGGCTC	AGGGCGAGGG	ACCCTACAGC	TCCCTGGTGT	CCTGCCGCAC	CCACCAGGAA	3780
	GTGCCAGCG	AGCCAGGGCG	TCTGGCCTTC	AATGTCGTCT	CCTCCACGGT	GACCCAGCTG	3840
	AGCTGGGCTG	AGCCGGCTGA	GACCAACGGT	GAGATCACAG	CCTACGAGGT	CTGCTATGGC	3900
15	CTGGTCAACG	ATGACAACCG	ACCTATTGGG	CCCATGAAGA	AAGTGCTGGT	TGACAACCTT	3960
	AAGAACCGGA	TGCTGCTTAT	TGAGAACCTT	CGGGAGTCCC	AGCCCTACCG	CTACACGGTG	4020
	AAGGCGCGCA	ACGGGGCCGG	CTGGGGCCCT	GAGCGGGAGG	CCATCATCAA	CCTGGCCACC	4080
	CAGCCCAAGA	GGCCCATGTC	CATCCCATAT	ATCCCTGACA	TCCCTATGCT	GGACGCCCAG	4140
	AGCGGGGAGG	ACTACGACAG	CTTCCTTATG	TACAGCGATG	ACGTTCTACG	CTCTCCATCG	4200
20	GGCAGCCACA	GGGCCAGCGT	CTCCGATGAC	ACTGAGCACC	TGGTGAATGG	CCGGATGGAC	4260
	TTTGCTTCC	CGGGCCGAC	CAACTCCCTG	CACAGGATGA	CCACGACCAG	TGCTGCTGCC	4320
	TATGGCAGCC	ACCTGAGCCC	ACACGTGCCC	CACCGCGTGC	TAAGCACATC	CTCCACCTTC	4380
	ACACGGGACT	ACAACCTACT	GACCCGCTCA	GAACACTCAC	ACTCGACCAC	ACTGCCGAGG	4440
25	GACTACTCCA	CCCTCACCTC	CGTCTCCTCC	CACGACTCTC	GCCTGACTGC	TGGTGTGCCC	4500
	GACACGCCCA	CCGCGCTGGT	GTTCTCTGCC	CTGGGGCCCA	CATCTCTCAG	AGTGAGCTGG	4560
	CAGGAGCCGG	GGTGGCAGCG	CGCGCTGCAG	GGCTACAGTG	TGGAGTACCA	GCTGCTGAAC	4620
	GGCGGTGAGC	TGCATCGGCT	CAACATCCCC	AACCTGCCCC	AGACCTCGGT	GGTGTGGGAA	4680
	GACCTCCTGC	CCAACCACTC	CTACGTGTTT	CGCGTGCGGG	CCCAGAGCCA	GGAAGGCTGG	4740
30	GGCCGAGAGC	GTGAGGGTGT	CATCACCATT	GAATCCCAGG	TGCACCCGCA	GAGCCCACTG	4800
	TGTCCTCTGC	CAGGCTCCGC	CTTCACTTTG	AGCACTCCCA	GTGCCCCAGG	CCCGCTGGTG	4860
	TTCACTGCCC	TGAGCCCAAG	CTCGCTGCAG	CTGAGCTGGG	AGCGGCCACT	GAGGCCCAAT	4920
	GGGGATATCG	TCCGCTACCT	GGTGACCTGT	GAGATGGCCC	AAGGAGGAGG	GCCAGCCACC	4980
	GCATTCCGGG	TGGATGGAGA	CAGCCCCGAG	AGCCGGCTGA	CCGTGCCGGG	CCTCAGCGAG	5040
35	AACGTGCCCT	ACRAAGTTCAA	GGTGACGGCC	AGGACCACTG	AGGGCTTCGG	GCCAGAGCGC	5100
	GAGGGCATCA	TCACCATAGA	GTCCCAGGAT	GGAGGACCTT	TCCCGCAGCT	GGGACGCCGT	5160
	CGCGGGCTCT	TCCAGCACCC	CGTGCAAAAG	GAGTACAGCA	GCATCACCAC	CACCCACACC	5220
	AGCGCCACCG	AGCCCTTCTT	AGTGGATGGG	CCGACCTCTG	GGGCCACGCA	CCTGGAGGCA	5280
	GGCGGCTCCC	TCACCCGGCA	TGTGACCCAG	GAGTTTGTGA	GCCGGACACT	GACCAACGAC	5340
40	GGAAACCTTA	GCACCCACAT	GGACCAACAG	TTCTTCCAAA	CTTGACCGCA	CCCTGCCCCA	5400
	CCCCCGCCAT	GTCCCACTAG	CGGTCTCTCC	GACTCTCTCT	CCGGAGCCTC	CTCAGCTACT	5460
	CCATCTTGG	ACCCCTGGGG	GCCCAAGCCA	CCCGCATGCA	CAGAGCAGGG	GCTAGGTGTC	5520
	TCTGGGAGG	CATGAAGGGG	GCAAGGTCCG	TCCTCTGTGG	GCCCAACCTT	ATTTGTAACC	5580
45	AAAGAGCTGG	GAGCAGCACA	AGGACCCAGC	CTTTGTTCTG	CATTATATAA	ATGGTTTTGC	5640
	TACTG						

Seq ID NO: 561 Protein sequence
Protein Accession #: NP_000204.1

50	1	11	21	31	41	51	
	MAGPRPSPWA	RLLLAALISV	SLSGTLANRC	KKAPVKSCTE	CVRVKDKCAY	CTDEMFRDRR	60
	CNTQAEELAA	GCQRESIVVM	ESSFQITEET	QIDTTLRRSQ	MSPGGLRVRL	RPGBERHFEL	120
	EVFEPLSPGV	DLVILMDFSN	SMSDDLNLK	KMGQNLARVL	SQLTSDYITIG	FGKFDVKVSV	180
55	PQTDMPREKL	KEPWFNSDPP	FSFKNVISLT	EDVDEFNRKL	QGERISGNLD	APEGGFDAIL	240
	QTAVCTRDIG	WRPDSTHLLV	FSFESAFHYE	ADGANVLAGI	MSRNDERCHL	DTTGYTQYR	300
	TQDYPSPVTL	VRLLAKNII	PIFAVTNYSY	SYEKLHTYF	PVSSILGVLQE	DSSNIVELLE	360
	BAFNIRIRSNL	DIRALDSFRG	LRTEVTSKMF	QKTRTGSFHI	RRGEVGIYQV	QLRALEHVDG	420
	THVQLPEDQ	KGNHILKPSF	SDGLKMDAGI	ICDVCTCELQ	KEVRSARCSF	NGDFVCGQCV	480
60	CSBWSGGQTC	NCSTGSLSDI	QPCLREGEDK	PCSGRGECQC	GHCVCYGEGR	YEGQFCEYDN	540
	PQCPRTSGLF	CNDRGRCSMG	QCVCPEPGWTG	PSCDCPLSNA	TCIDSNGGIC	NGRGHCCEGR	600
	CHCHQSSLYT	DTICEINYSY	IHPGLCEDLR	SCVQCQAWGT	GEKKGRITCEE	CNFKVKMVDK	660
	LKRAEEVVVR	CSFRDEDDDC	TYSYTMEDGD	APGPNSTVLV	HKKKDCPPGS	FWWLIFLLLL	720
	LLPLALLLLL	LCWKYCACCK	ACLALLPCCN	RGHMVGPKED	HYMLRENLM	SDHLDTPLMR	780
65	SGNLKGRDVG	RWKVTNNMQR	PGFATHAASI	NPTELVPYGL	SLRLARLCTE	NLLKPDTRC	840
	AQLRQEVEEN	LNEVYRQISG	VHKLQQTFR	QQFNAGKKQD	HTIVDTVLMA	PRSAKPALLK	900
	LTEKQVEQRA	FHDLKVAPGY	YTLTADQDAR	GMVEPQEGVE	LVDVRVPLFI	RPEDDDEKQL	960
	LVEAIDVPAG	TATLGRRLVN	ITIIKEQARD	VVSFEQPEFS	VSRGDQVARI	PVIRRVLDGG	1020
	KSQVSYRTQD	GTAQGNRDYI	PVEGELLFQP	GEAWKELQVK	LLELQEVDSL	LRGRQVRRFH	1080
70	VQLSNPKFGA	HLGQPHSTTI	IIRDPDELDR	SFTSQMLSSQ	PPPHGDLGAP	QNPNAKAAGS	1140
	RKIHPNWLPP	SGKPMGYRVK	YWIQDSESE	AHLDSKVPS	VELTNLYPYC	DYEMKVCAYG	1200
	AQGEPPYSSL	VSCRTHQEVF	SEPGRLAFNV	VSSVTYQLSW	AEPAETNGEI	TAYEVCYGLV	1260
	NDDNRPPIGPM	KKVLVDNPKN	RMLLIENLRE	SQPYRYTVKA	RNGAGWGPER	EAIINLATQP	1320
	KRPMISPIIP	DIPIVDAQSG	EDYDSFLMYS	DDVLRSPSGS	QRPVSDDTE	HLVNGRMDFA	1380
75	FPGSTNSLHR	MTTTSAAAYG	THLSPHVPHR	VLSTSTSLTR	DYNSLTRSEH	SHSTTLPRDY	1440
	STLTSVSSHD	SRLTAGVPDT	PTSLRVSAAG	PTSLRVSAAG	PRCERPLQGY	SVEYQLLNGG	1500
	ELHRLNIPNP	AQTSVVVEDL	LPNHSYVFRV	RAQSQEGNRR	EREGVITIES	QVHPQSPLCP	1560
	LPGSAFTLST	PSAPGPLVFT	ALSPDSLQLS	WERPRRPNGD	IVGYLVTCME	AQGGGPATAP	1620
	RVDGDSFESR	LTVGLGSEN	PKYFKVQART	TEGFGPEREG	IITIESQDGG	PPFQLGSRNV	1680
80	LFQHPLOQSEY	SSITTTHTSA	TEPFLVDGPT	LGAQHLEARG	SLTRHVTQEF	VSRTLTTSST	1740
	LSTHMDQQFP	QT					

Seq ID NO: 562 DNA sequence
Nucleic Acid Accession #: NM_013332.1
Coding sequence: 1..63

85	1	11	21	31	41	51

5
10
15
20

```

GCACGAGGGC GCTTTTGTCT CCGGTGAGTT TTGTGGCGGG AAGCTTCTGC GCTGGTGTCT 60
AGTAACCGAC TTTCTCCGG ACTCCTGCAC GACCTGCTCC TACAGCCGGC GATCCACTCC 120
CGGCTGTTC CCCGAGGGGT CCAGAGGCCT TTCAGAAGGA GAAGGCAGCT CTGTTTCTCT 180
GCAGAGGAGT AGGTCCTTT CAGCCATGAA GCATGTGTTG AACCTCTACC TGTTAGGTGT 240
GGTACTGACC CTACTCTCCA TCTTCGTTAG AGTGTAGGAG TCCTAGAAAG GCTTACTAGA 300
GAGCCCATCG CCTGGGACCT CTTGGACCC CAGAAGCCAA CTAGCCACA CAGAGCCAC 360
CAAGGSCCTT CCAGACCATC CATCCAGAAG CATGTGATAA GACCTCCTTC CATACTGGCC 420
ATATTTTGA ACACGTGACCT AGACATGTCC AGATGGGAGT CCCATTCTTA GCAGACAAGC 480
TGAGCACCGT TGTAAACAGA GAACATTATC TAGGCCTTGA AGAACCTGTC TAACTGGATG 540
CTCATTGCCT GGGCAAGGCC TGTTTAGGCC GGTTCGGGTG GCTCATGCCT GTAATCCTAG 600
CACTTTGGGA GGTGAGGTG GGTGGATCAC CTGAGGTGAG GAGTTCGAGA CCAGCCTCGC 660
CAACATGGCG AAACCCATC TCTACTAAA ATACAAAAGT TAGCTGGGTG TGGTGGCAGA 720
GGCCTGTAAT CCCAGTTCCT TGGGAGGCTG AGGCGGGAGA ATTGCTTGA CCCGGGGACG 780
GAGGTTGCGAG TGAACCGAGA TCGCACTGCT GTACCCAGCC TGGGCCACAG TGCAAGACTC 840
CATCTCAAAA AAAAAAAGAA AAAAAAAGC CTGTTTAATG CACAGGTGTG AGTGGATTGC 900
TTATGGCTAT GAGATGAGTT GATCTCGCCC TTACCCCGGG GTCTGGTGTG TGCTGTGCTT 960
TCCTCAGCAG TATGGCTCTG ACATCTCTTA GATGTCCCAA CTTGAGTGTG TGGGAGATGG 1020
TGATATTTTC AACCTACTT CCTAAACATC TGTCTGGGTG TCCTTTAGTC TTGAATGTCT 1080
TATGCTCAAT TATTTGGTGT TGAGCCTCTC TTCCACAAGA GCTCCTCCAT GTTTGGATAG 1140
CAGTTGAAGA GGTGTGTGG GTGGGCTGTT GGGAGTGAGG ATGGAGTGT CAGTGCCCAT 1200
TTCTCATTTT GAGTTTAAA TCGTTCTCTC CAACATAGTG TGTATTGGTC TGAAGGGGGT 1260
GGTGGGATGC CAAAGCCTGC TCAAGTTATG GACATTGTGG CCACCATGTG GCTTAAATGA 1320
TTTTTCTAA CTAATAAAGT GGAATATATA TTTCAAAAAA AAAAAAAAAA AA

```

Seq ID NO: 563 Protein sequence
Protein Accession #: NP_037464.1

30

```

1      11      21      31      41      51
|      |      |      |      |      |
MKHVLNLYLL GVVLTLISIF VRVMSLEGL LESPSPGTSW TTRSQLANTE PTKGLPDHPS 60
RSM

```

Seq ID NO: 564 DNA sequence
Nucleic Acid Accession #: NM_023915.1
Coding sequence: 250..1326

35
40
45
50
55
60

```

1      11      21      31      41      51
|      |      |      |      |      |
GGCAGAGGGG TTTCTTTTTC ATGCTTTACC AGAAAAATCCA CTTCCCTGCC GACCTTAGTT 60
TCAAAGCTTA TTCTTAATTA GAGACAAGAA ACCTGTTTCA ACTTGAAGAC ACCGTATGAG 120
GTGAATGAGC AGCCAGCCAC CACAATGAAA GAAATCAAAC CAGGAATAAC CTATGCTGAA 180
CCACGCGCTC AATCGTCCCC AAGTGTTCCT TGACACGCAT CTTTGTCTAC AGTGCATCAC 240
AACTGAAGAA TGGGGTTCAA CTTGACGCTT GCAAAATTAC CAAATAACGA GCTGCACGGC 300
CAAGAGAGTC ACAATTCAGC CAACAGGAGC GACGGGCCAG GAAAGAACAC CACCCTTCAC 360
AATGAATTTG ACACAATGT CTTGCCGGTG CTTTATCTCA TTATATTGTG GGCAAGCATC 420
TTGCTGAATG GTTTAGCAGT GTGGATCTTC TTCCACATTA GGAATAAAAC CAGCTTCATA 480
TTCTATCTCA AAAACATAGT GGTTCAGAGC CTCATAATGA CGCTGACATT TCCATTTCGA 540
ATAGTCCATG ATGCAGGATT TGGACCTTGG TACTTCAAGT TTATTCTCTG CAGATACACT 600
TCAGTTTTGT TTTATGCAA CATGTATACT TCCATCGTGT TCCTTGGGCT GATAAGCATT 660
GATCGCTATC TGAAGGTGGT CAAGCCATTT GGGGACTCTC GGATGTACAG CATAACCTTC 720
ACGAAGGTTT TATCTGTTTG TGTTTGGGTG ATCATGGCTG TTTTGTCTTT GCCAAACATC 780
ATCCTGACAA ATGCTCAGCC AACAGAGGAC AATATCCATG ACTGCTCAAA ACTTAAAGT 840
CCTTTGGGGG TCAAATGGCA TACGGCAGTC ACCTATGTGA ACAGCTGCTT GTTTGTGGCG 900
GTGCTGGTGA TTCTGATCGG ATGTTACATA GCCATATCCA GGTACATCCA CAAATCCAGC 960
AGGCAATTCA TAAGTCAGTC AAGCCGAAAG CGAAAAATA ACCAGAGCAT CAGGGTTGTT 1020
GTGGCTGTGT TTTTACCTG CTTTCTACCA TATCACTGTG GCAGAATTCC TTTTACTTTT 1080
AGTCACTTAG ACAGGCTTTT AGATGAATCT GCACAAAAAA TCCTATATTA CTGCAAGAA 1140
ATTACACTGT TCTGTCTGTC GTGTAATGTT TGCCCTGGATC CAATAATTTA CTTTTCATG 1200
TGTAAGTCAT TTTCAAGAAG GCTGTTCAAA AAATCAAATA TCAGAACCAAG GAGTGAAGC 1260
ATCAGATCAC TGCAAAGTGT GAGAAGATCG GAAGTTCGCA TATATTATGA TTACACTGAT 1320
GTGTAGGCCT TTTATTGTTT GTTGAATCG ATATGTACAA AGTGTAATAA AATGTTTCTT 1380
TTCATTATCC TTAATAAAAA AA

```

Seq ID NO: 565 Protein sequence
Protein Accession #: NP_076404

65
70
75

```

1      11      21      31      41      51
|      |      |      |      |      |
MGFNLTLAKL PNNEHGGQES HNSGNRSDGP GKNTTLHNEF DTIVLPVLYL IIFVASILLN 60
GLAVWIFFHI RNKTSFIFYL KNIVVADLIM TLTFFPRIVH DAGFGPWYFK FILCRYTSVL 120
FYANMYTSIV FLGLISIDRY LKVVKPPGDS RMYSTFTKV LSVCVWVIMA VLSLPNIILT 180
NQOPTEDNIH DCSKLKSPLG VKWHTAVTYV NSCLFVAVLV ILIGCYIAIS RYIHKSSRQF 240
ISQSSRRKRKH NQIRVVVVAV FFTCFLPYHL CRIPFTFSLH DRLLDESAQK ILYYCKEITL 300
PLSACNVCLD PIIFYFMCRS FSRRLFKKSN IRTRESIRS LQSVRRSEVR IYYDYTDV

```

Seq ID NO: 566 DNA sequence
Nucleic Acid Accession #: NM_005365.1
Coding sequence: 1..948

80
85

```

1      11      21      31      41      51
|      |      |      |      |      |
ATGTCTCTCG AGCAGAGGAG TCCGCACTGC AAGCCTGATG AAGACCTTGA AGCCCAAGGA 60
GAGGACTTGG GCCTGATGGG TGACACAGAA CCCACAGGCG AGGAGGAGGA GACTACCTCC 120
TCCTCTGACA GCAAGGAGGA GGAGGTGTCT GCTGCTGGGT CATCAAGTCC TCCCCAGAGT 180
CCTCAGGAG GCGCTTCTCT CTCCATTTC GTCTACTACA CTTTATGGAG CCAATTGAT 240
GAGGGCTCCA GCAGTCAAGA AGAGGAAGAG CCAAGCTCCT CGGTCCAGCC AGCTCAGCTG 300
GAGTTTATGT TCCAAGAAGC ACTGAAATTG AAGGTGGCTG AGTTGGTTCA TTTCTGCTC 360

```

5
10

```

CACAAATATC GAGTCAAGGA GCCGGTCACA AAGGCAGAAA TGCTGGAGAG CGTCATCAAA 420
AATTACAAGC GCTACTTTCC TGTGATCTTC GGCAAAGCCT CCGAGTTCAT GCAGGTGATC 480
TTTGGCACTG ATGTGAAGGA GGTGGACCCC GCCGGCCACT CCTACATCCT TGTCACTGCT 540
CTTGGCCCTC CGTGGCATAG CATGCTGGGT GATGGTCATA GCATGCCCAA GGCCGCCCTC 600
CTGATCATTG TCCTGGGTGT GATCCTAACC AAAGACAACT GCGCCCCCTGA AGAGGTTATC 660
TGGGAAGCGT TGAGTGTGAT GGGGGTGTAT GTTGGGAAGG AGCACATGTT CTACGGGGAG 720
CCCAGGAAGC TGCTACCCA AGATTGGGTG CAGGAAAAC ACCTGGAGTA CCGGCAGGTG 780
CCCCGCAGTG ATCCTGCGCA CTACGAGTTC CTGTGGGGTT CCAAGGCCCA CGCTGAAACC 840
AGCTATGAGA AGGTCATAAA TTATTGGTTC ATGCTCAATG CAAGAGAGCG CATCTGCTAC 900
CCATCCCTTT ATGAAGAGGT TTTGGGAGAG GAGCAAGAGG GAGTCTGA

```

Seq ID NO: 567 Protein sequence
Protein Accession #: NP_005356.1

15
20

```

1 11 21 31 41 51
MSLEQRSPHC KPDEDELEAQQ EDLQLMGAQE PTGEEETTS SSDSKEEEVs AAGSSPPQs 60
PQGGASSSIS VYITLWSQPD EGSSSQEEEE PSSSVDPAPL EFMFQEALKL KVAELVHPLL 120
HKYRVKEPVT KAEMLESVIK NYKRYFPVIF GKASEFMQVI PGTDVKEVDP AGHSYILVTA 180
LGLSCDSMLG DGHSMFKAAL LIIVLGVILT KDNCAPEEVI WEALSVMGVY VGKEHMFYGE 240
PRKLLTQDMV QENYLEYRQV PGSDPAHYEF LWGSKAHAET SYEKVINYL VMLNAREPICY 300
PSLYEEVLGE EQEGV

```

Seq ID NO: 568 DNA sequence
Nucleic Acid Accession #: NM_014400
Coding sequence: 86..1126

25
30
35
40
45
50
55

```

1 11 21 31 41 51
GGTTACTCAT CCTGGGCTCA GGTAAAGAGG CCCGAGCTCG GAGGCGGCAC ACCCAGGGGG 60
GAGCCCAAGG GAGCAGGACG GAGCCATGGA CCCCGCCAGG AAAGCAGGTG CCCAGGCCAT 120
GATCTGGACT GCAGGCTGGC TGCTGCTGCT GTGCTTCGCG GAGGAGAGCG AGGCCCTGGA 180
GTGCTACAGC TGCGTGCAGA AAGCAGATGA CGGATGCTCC CCGAACAAGA TGAAGACAGT 240
GAAGTGCGCG CCGGCGGTGG ACGTCTGCAC CGAGGCCGTG GGGGCGGTGG AGACCATCCA 300
CGGACAATTC TCGCTGGCAG TGCSGGGTGG CGGTTCGGGA CTCGCCGCGA AGAATGACCG 360
CGGCCTGGAT CTTACGGGCG TTCTGGCGTT CATCCAGCTG CAGCAATGCG CTCAGGATCG 420
CTGCAACGCC AAGCTCAACC TCACCTCGCG GCGCTCGAC CCGGCAGGTA ATGAGAGTGC 480
ATACCCGCCC AAGCGCGTGG AGTGCTACAG CTGTGTGGGC CTGAGCCGGG AGGCGTGCCA 540
GGGTACATCG CGCCCGGTGG TGAGCTGCTA CAACGCCAGC GATCATGTCT ACAAGGGCTG 600
CTTCGACGCG AACGTCACTT TGACGGCAGC TAATGTGACT GTGTCTTTCG CTGTCCGGGG 660
CTGTGTCCAG GATGAATTTCT GCACCTCGGA TGGAGTAACA GGCCCAAGGT TCACGCTCAG 720
TGGCTCCTGT TGCCAGGGGT CCCGCTGTAA CTCTGACCTC CGCAACAAGA CCTACTTCTC 780
CCCTCGAATC CCACCCCTTG TCCGGCTGCC CCCTCCAGAG CCCACGACTG TGGCCTCAAC 840
CACATCTGTC ACCACTTCTA CCTGGGCCCC AGTGAGACCC ACATCCACCA CCAAACCCAT 900
GCCAGCGCCA ACCAGTCAGA CTCGAGAGCA GGGAGTAGAA CACGAGGCTT CCGGGATGA 960
GGAGCCCAAG TTGACTGAGC GCGCCGCTGG CCACAGGAC CGCAGCAATT CAGGGCAGTA 1020
TCCTGCAAAA GGGGGGCCCC AGCAGCCCCA TAATAAAGGC TGTGTGGCTC CCACAGCTGG 1080
ATTGGCAGCC CTTCTGTGG TCTCTGGCCC TGGGTACCCC TCTTCTCATC ACTTCTGTG 1200
AAATTTCCCT CTCACCTACT CTCACGCCCC TGTTTTTCCA ACATTCCTCA GTATCCCCAG 1260
CTTCTGCTGC GCTGGTTTGC GGCTTTGGGA AATAAAATAC CGTTGTATAT ATTCTGGCAG 1320
GGGTGTTCTA GCTTTTGGAG GACAGCTCCT GTATCCTTCT CATCCTTGTC TCTCCGCTTG 1380
TCCTCTTGTG ATGTTTGGAC AGAGTGAGAG AAGTCAGCTG TCACGGGGAA GGTGAGAGAG 1440
AGGATGCTAA GCTTCTACT CACTTTCTCC TAGCCAGCCT GGACTTTGGA GCGTGGGGTG 1500
GGTGGGACAA TGGCTCCCCA CTCCTAAGCAC TGCCCTCCCT ACTCCCCGCA TCTTTGGGGA 1560
ATCGGTTCCC CATATGCTCT CTTTACTAGA CTGTGAGCTC CTCGAGGGCA GGGACCGTGC 1620
CTTATGCTCG TGTGTGATCA GTTTCTGGCA CATAAATGCC TCAATAAAGA TTTAATTACT 1680
TTGTATAGTG AAAAAAAA

```

Seq ID NO: 569 Protein sequence
Protein Accession #: NP_055215

60
65
70

```

1 11 21 31 41 51
MDPARKAGAQ AMIWTAGWLL LLLLRRGAQA LECYSCVQKA DDGCSFNKMK TVKCAPGVDV 60
CTEAVGAVET IHGQPSLAVX GCGSGLPGRN DRGLDLHGLL AFIQLQCAQ DRCAKLNLT 120
SRALDPAGNE SAYFPNGVEC YSCVGLSREA CQGTSPPVVS CYNASDHVYK GCFDGNVTLT 180
AANVTYSLPV RGCVDDEFCT RDGVTGPFT LSGSCCGSR CNSDLRNKTY FSPRIPLVLR 240
LPPPEPTTVA STTSVTTS TS APVRPTSTK PMPAPTSQTP RQGVHEASR DEEPRLTGGA 300
AGHQDRNSNG QYPKGGPQQ PHNKGCVAPT AGLAALLLAV AAGVLL

```

Seq ID NO: 570 DNA sequence
Nucleic Acid Accession #: NM_005329.1
Coding sequence: 1..1662

75
80
85

```

1 11 21 31 41 51
ATGCCGGTGC AGCTGACGAC AGCCCTGCGT GTGGTGGGCA CCAGCCTGTT TGCCCTGGCA 60
GTGCTGGGTG GCATCCTGGC AGCCTATGTG ACGGGCTACC AGTTCATCCA CACGGAAAAA 120
CACTACCTGT CCTTGGGCT GTACGGCGCC ATCTGGGCC TGCACCTGCT CATTCAGAGC 180
CTTTTTGCTC TCCTGGAGCA CCGGCGCATG CGACGTGCCG GCCAGGCCCT GAAGCTGCC 240
TCCCCCGCGC GGGGCTCGGT GGCACGTGTC ATTGCCGCGT ACCAGGAGGA CCCTGACTAC 300
TTGCGCAAGT GCTGCGCTC GGCCAGCGC ATCTCCTTCC CTGACCTCAA GGTGGTCTAG 360
TGGTGGATG GCAACCGCGA GGAGGAGGCC TACATGCTGG ACATCTTCCA CGAGGTGCTG 420
GGCGGCACCG AGCAGGCGCG CTTCTTTGTG TGGCGCAGCA ACTTCCATGA GGCAGGCGAG 480
GGTGAGACCG AGGCCAGCCT GCAGGAGGGC ATGGACCGTG TGCGGATGT GGTGCGGGCC 540
AGCACCTTCT CGTGATCAT GCAGAGGTG GGAGGCAAGC GCGAGGTGAT GTACACGGCC 600

```


TCAAGGCC TCGGCGATTC GGTGGACTAC ATCCAGGTGT GCGACTCTGA CACTGTGCTG 660
 GATCCAGCCT GCACCATCGA GATGCTTCGA GTCCCTGGAGG AGGATCCCCA AGTAGGGGGA 720
 GTCGGGGGAG ATGTCCAGAT CCTCAACAAG TACGACTCAT GGATTTCCCTT CCTGAGCAGC 780
 GTGCGGTACT GGATGGCCTT CAACGTGGAG CGGGCCTGCC AGTCTACTT TGGCTGTGTG 840
 CAGTGTATTA GTGGGCCCTT GGGCATGTAC CGCAACAGCC TCCTCCAGCA GTTCTCGGAG 900
 GACTGGTACC ATCAGAAGTT CCTAGGCAGC AAGTGCAGCT TCGGGGATGA CCGGCACCTC 960
 ACCAACCGAG TCCTGAGCCT TGGCTACCGA ACTAAGTATA CCGCGCGCTC CAAGTGCCTC 1020
 ACAGAGACCC CCACTAAGTA CCTCCGGTGG CTCAACCAGC AAACCCGCTG GAGCAAGTCT 1080
 TACTTCCGGG AGTGGCTCTA CAACTCTCTG TGGTTCCTA AGCACCACTC CTGGATGACC 1140
 TACGAGTCAG TGGTCACGGG TTTCTTCCCC TTCTTCTCTA TTGCCACGGT TATACAGCTT 1200
 TTCTACCGGG GCCGCATCTG GAACATTCTC CTCTTCTCTG TGACGGTGCA GCTGGTGGGC 1260
 ATTATCAAGG CCACCTACGC CTGCTTCTCT CCGGGCAATG CAGAGATGAT CTTCATGTCC 1320
 CTCTACTCCC TCCTCTATAT GTCCAGCCTT CTGCGGGCCA AGATCTTTGC CATTGCTACC 1380
 ATCAACAAT CTGGCTGGGG CACCTCTGGC CGAAAAACCA TTGTGGTGAA CTTTATGGC 1440
 CTCATTCTCT TGTCCATCTG GGTGGCAGTT CTCTGGGAG GGCTGGCCTA CACAGCTTAT 1500
 TGGCAGGAC TGTTCAGTGA GACAGAGCTA GCCTTCTCTG TCTCTGGGGC TATACTGTAT 1560
 GGCTGCTACT GGTGGGCCCT CCTCATGCTA TATCTGGCCA TCATCGCCCC GCGATGTGGG 1620
 AAGAAGCCGG AGCAGTACAG CTTGGCTTTT GCTGAGGTGT GA

Seq ID NO: 571 Protein sequence
 Protein Accession #: NP_005320.1

1 11 21 31 41 51
 MPVQLTTLAL VVGTSLFALA VLGGILAAV TGYQFIHTEK HYLSPGLYGA ILGLHLIIQS 60
 LFAFLHRRM RRAQOAKLKP SPRRGSVALC IAAYQEDPDY LRKCLRSAQR ISFPDLKVV 120
 VVDGNRQEDA YMLDIFHEVL GGTEQAGFFV WRSNFHEAGE GETEASLQEG MDRVRDVVRA 180
 STFSCIMQKW GKGREVMYTA FKALGDSVDY IQVCDSDTVL DPACTIEMLR VLEEDPQVGG 240
 VGGDVQILNK YDSWISFLSS VRYWMAFNVE RACQSYFGCV QCSGGLPMY RNSLLQQFLE 300
 DWYHQKPLGS KCSFGDDRHL TNRVLSLGYR TKYTARSKCL TETPTKYLRW LNQQTRWSKS 360
 YFRWLYNSL WFHKHHLWMT YESVVTGFFP FFLIATVIQL FYRGRINWIL LFLLLTVQLVG 420
 IIKATYACFL RGNAMFPM LYSLLYMSL LPAKIFAIAT INKSGWGTSG RKTIVVNFIG 480
 LIPVSIWVAV LLGGLAYTAY CQDLFSETEL APLVSGAILY GCYVVALML YLAIIARRCG 540
 KKPEQYSLAF AEV

Seq ID NO: 572 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 148-7095

1 11 21 31 41 51
 CACACATACG CACGCACGAT CTCACCTCGA TCTATACACT GGAGGATTAA AACAAACAAA 60
 CAAAAAAAC ATTTCCCTTCG CTCCCGCTCC CTCTCCACTC TGAGAAGCAG AGGAGCCGCA 120
 CGGCGAGGGG CGGCAGACCG TCTGGAAATG CGAATCCTAA AGCGTTTCTT CGCTTGCACT 180
 CAGCTCCTCT GTGTTTGGCG CTCTGGATTG GCTAATGGAT ACTACAGACA ACAGAGAAAA 240
 CTGTGTTAAG AGATTGCTCG GTCTATACA GGAGCACTGA ATCAAAAAA TTGGGGAAAG 300
 AAATATCCAA CAGTAATAG CCCAAAACAA TCTCTATCA ATATTGATGA AGATCTTACA 360
 CAAGTAAATG TGAATCTTAA GAAACTTAAA TTTCAGGGTT GGGATAAAAC ATCATGGGAA 420
 AACACATTCA TTCATAACAC TGGGAAAACA GTGGAATAA ATCTCACTAA TGACTACCGT 480
 GTCAGCGGAG GAGTTTTCAGA AATGGTGTIT AAAGCAAGCA AGATAACTTT TCACTGGGGA 540
 AAATGCAATA TGTATCTGTA TGGATCAGAG CATAGTTTAG AAGGACAAAA ATTTCCACTT 600
 GAGATGCAAA TCTACTGCTT TGATGCGGAC CGATTTTCAA GTTTTGAGGA AGCAGTCAAA 660
 GGAAAAGGGA AGTTAAGAGC TTATCCATT TTGTTTGAGG TTGGGACAGA AGAAAATTG 720
 GATTTCAAAG CGATTATTGA TGGAGTCGAA AGTGTTAGTC GTTTTGAGGA GCAGGCTGCT 780
 TTAGATCCAT TCATACTGTT GAACCTTCTG CCAAACTCAA CTGACAAGTA TTACATTTAC 840
 AATGGCTCAT TGACATCTCC TCCTGCACA GACACAGTTG ACTGGATTGT TTTTAAAGAT 900
 ACAGTTAGCA TCTCTGAAAG CCAAGTTGGCT GTTTTGTGTG AAGTTCTTAC AATGCAACAA 960
 TCTGGTTATG TCATGCTGAT GGACTACTTA CAAAACAATT TTGAGAGCA ACAGTACAAG 1020
 TTCTCTAGAC AGGTGTTTTC CTCATACACT GGAAGGAAG AGATTCTATGA AGCAGTTTGT 1080
 AGTTCAGAAC CAGAAAATGT TCAGGCTGAC CCAGAGAATT ATACCAGCCT TCTTGTATCA 1140
 TGGGAAAGAC CTCGAGTCGT TTATGATACC ATGATTGAGA AGTTTGCACT TTTGTACCAG 1200
 CAGTTGGATG GAGAGGACCA AACCAAGCAT GAATTTTGA CAGATGGCTA TCAAGACTTG 1260
 GGTGCTATTG TCAATAATTT GCTACCCAAT ATGAGTTATG TTCTTCAGAT AGTAGCCATA 1320
 TGCATAATG GCTTATATGG AAAATACAGC GACCAACTGA TTGTCGACAT GCCTACTGAT 1380
 AATCCTGAAC TTGATCTTTT CCCTGAATTA ATTGGAAGT AAGAAATAAT CAAGGAGGAG 1440
 GAAGAGGGAA AAGACATTGA AGAAGGCGCT ATTGTGAATC CTGGTAGAGA CAGTGCTACA 1500
 AACCAATCA GGAAGGACCA ACCCCAGATT TCTACCACAA CACACTACAA TCGCATAGGG 1560
 ACGAAATCA ATGAAGCCAA GACTAACCAG TCCCCAACAA GAGGAAGTGA ATTCTCTGGA 1620
 AAGGGTGATG TTCCCAATAC ATCTTAAAT TCCACTTCCC AACCACTCAC TAAATTAGCC 1680
 ACAGAAAAAG ATATTTCTCT GACTTCTCAG ACTGTGACTG AACTGCCACC TCACACTGTG 1740
 GAAGGTACTT CAGCTCTTTT AAATGATGGC TCTAAAACCT TTCTTAGATC TCCACATATG 1800
 AACTTGTGCG GGACTGCAGA ATCTTAAAT ACAGTTTCTA TAACAGAATA TGAGGAGGAG 1860
 AGTTTATTGA CCACTTTCAA GCTTGATACT GGAGCTGAAG ATTCTTCAGG CTCCAGTCCC 1920
 GCAACTCTG CTATCCCAT TATCTCTGAG AACATATCCC AAGGGTATAT ATTTTCTCTC 1980
 GAAAAACCA AGACAATAA ATATGATGTC CTTATACCAG AATCTGCTAG AAATGCTTCC 2040
 GAAGATTCAA CTTATCAGG TTCAGAAGAA TCACTAAAGG ATCCTTCTAT GGAGGGAAAT 2100
 GTGTGTTTTC CTAGCTCTAC AGACATAACA GCACAGCCCG ATGTTGGATC AGGCAGAGAG 2160
 AGCTTTCTCT CAGGCCAGT GATGTACAG GGTCCCTCAG TTACAGATCT GGAATGCCA 2220
 TCTTTTCTG CATTATTCTA CTTTGGCCTA CTTCCCAACT CTCATGCTTT TACCCATCC 2280
 TCCAGACAAC AGGATTGGT CTCCAGGCTC AACGTGGTAT ACTCGCAGAC AACCCACCG 2400
 GTATACAATG GTGAGACACC TCTTCAACCT TCCTACAGTA GTGAAGTCTT TCCTCTAGTC 2460
 ACCCTTTGT TGCTTGACAA ACACATACCC CTGCTGCTTC AAGTAGTGAT 2520
 TCGGCTTGG ATGCTAGGCC TGTATTCCC AGTGTGATG TGTCAATTGA ATCCATCTG 2580
 TCTTCTATG ATGCTGACCC TTTGCTTCCA TTTTCTCTG CTTCTCTCAG TAGTGAAATG 2640
 TTTGCGCATC TGCATACAGT TTCTCAAATC CTTCCACAAG TTACTTCAGC TACCGAGAGT 2700
 GATAAGGTGC CTTTGCATGC TTCTCTGCCA GTGCTGGGG GTGATTGCT ATTAGAGCCC 2760

	AGCCTTGCTC	AGTATTCTGA	TGTGCTGTCC	ACTACTCATG	CTGCTTCAGA	GACGCTGGAA	2820
	TTTGGTAGTG	AATCTGGTGT	TCCTTATAAA	ACGCTTATGT	TTTCTCAAGT	TGAACCAACC	2880
	AGCAGTGATG	CCATGATGCA	TGCACGTTC	TCAGGGCCTG	AACCTTCTTA	TGCCTTGTCT	2940
5	GATAATGAGG	GCTCCCAACA	CATCTTCACT	GTTTCTTACA	GTTCTGCAAT	ACCTGTGCAT	3000
	GATTCTGTGG	GTGTAACCTA	TCCAGGTTCC	TTATTTAGCG	GCCCTAGCCA	TATACCAATA	3060
	CCTAAGTCTT	CGTTAACTAC	CCCAACTGCA	TCATTACTGC	AGCCTACTCA	TGCCCTCTCT	3120
	GGTGATGGGG	AATGGTCTGG	AGCCTCTTCT	GATAGTGAAT	TTCTTTTACC	TGACACAGAT	3180
	GGGCTGACAG	CCCTTAACAT	TTCTTCACCT	GTTTCTGTAG	CTGAATTTAC	ATATACAACA	3240
10	TCTGTGTTTG	GTGATGATAA	TAAGGCGCTT	TCTAAAAGTG	AAATAATATA	TGGAATGAG	3300
	ACTGAACCTG	AAATTCCTTC	TTTCAATGAG	ATGGTTTACC	CTTCTGAAAG	CACAGTCATG	3360
	CCCAACATGT	ATGATAATGT	AAATAAGTTG	AATGCGTCTT	TACAAGAAAC	CTCTGTTTCC	3420
	ATTTCTAGCA	CCAAGGGCAT	GTTTCCAGGG	TCCCTTGCTC	ATACCACCAC	TAAGGTTTTT	3480
	GATCATGAGA	TTAGTCAAGT	TCCAGAAAA	AACCTTTTCA	TTCAACCTAC	ACATACTGTC	3540
15	TCTCAAGCAT	CTGGTGACAC	TTGCTTAA	CCTGTGCTTA	GTGCAAACTC	AGAGCCAGCA	3600
	TCCTCTGACC	CTGCTTCTAG	TGAAATGTTA	TCTCCTTCAA	CTCAGCTCTT	ATTTTATGAG	3660
	ACCTCAGCTT	CTTTTAGTAT	TGAAATGTTA	CTACAACCTT	CCTTTCAGGC	TTCTGATGTT	3720
	GACACCTTGC	TTAAACTCTG	TCTTCCAGCT	GTGCCAGTG	ATCCAATATT	GGTTGAAACC	3780
	CCCAAGTTG	ATAAAATTAG	TTTACAATG	TTGCATCTCA	TTGTATCAAA	TTCTGCTTCA	3840
20	AGTGAAAAACA	TGCTGCATC	TACATCTGTA	CCAGTTTTTG	ATGTGTCGCC	TACTTCTCAT	3900
	ATGCACTCTG	CTTCACTTCA	AGGTTTGACC	ATTTCTTATG	CAAGTGAGAA	ATATGAACCA	3960
	GTTTGTGTTA	AAATGATGAG	TTCCCAACCA	GTGGTACCTT	CTTTGTACAG	TAATGATGAG	4020
	TGTTTCCAAA	CGGCCAATTT	GGAGATTAA	CAGGCCATC	CCCCAAAGG	AAGGCATGTA	4080
	TTTGCTACAC	CTGTTTTATC	AATTGATGAA	CCATTAAATA	CACATAATAA	TAAGCTTATA	4140
25	CATTCCGATG	AAATTTTAA	TCCACCAAA	AGTTCTGTTA	CTGGTAAGGT	ATTTGCTGGT	4200
	ATTCCAACAG	TGCTTCTGTA	TACATTGTA	TCTACTGATC	ATTCTGTTCC	TATAGGAAAT	4260
	GGGCATGTTG	CCATTACAGC	GTGTTCTCCC	CACAGAGATG	GTTCTGTAAC	CTCAACAAAG	4320
	TGCTGTGTTT	CTTCTAAGGC	AACCTTCTGAG	CTGAGTCATA	GTGCCAAATC	TGATGCCGGT	4380
	TTAGTGGGTG	GTGGTGAAGA	TGGTGACACT	GATGATGATG	GTGATGATGA	TGATGATGAC	4440
30	AGAGGTAGTG	ATGGCTTATC	CATTCTAAG	TGTATGTCAT	GCTCATCCTA	TAGAGAATCA	4500
	CAGGAAAAAG	TATGATGTA	TTTCAAGACC	CACGAAAAACA	GTCTTATGGA	TCAGAAATAT	4560
	CCAATCTCAT	AACTCACTAT	TGAGAAATCT	GAAGAAAGATA	ATAGAGTCAC	AAGTGTATCC	4620
	TCAGACAGTC	AACTGGTAT	GGACAGAAAT	CCTGGTAAAT	CACCATCAGC	AAATGGGCTA	4680
	TCCCAAAAGC	ACAATGATGG	AAAAGAGGAA	AATGACATTC	AGACTGGTAG	TGCTCTGCTT	4740
35	CCTCTCAGCC	CTGAATCTAA	AGCATGGGCA	GTTCTGACAA	GTGATGAAGA	AAGTGGATCA	4800
	GGGCAGGATA	CCTCAGATAG	CCTTAATGAG	AATGAGACTT	CCACAGATTT	CAGTTTGTGC	4860
	GACACTAATG	AAATGATGTC	TGATGGGATC	CTGGCAGCAG	GTGACTCAGA	AATAACTCCT	4920
	GGATTCCCA	AGTCCCAAC	ATCATCTGTT	ACTAGCAGGA	ACTCAGAAAT	GTTCCACGTT	4980
	TCAGAGGAG	AGGCCAGTAA	TAGTAGCCAT	GAGTCTGTA	TTGGTCTAGC	TGAGGGGTTG	5040
40	GAATCCGAGA	AGAAGGCAGT	TATACCCCTT	GTGATCGTGT	CAGCCCTGAC	TTTATCTGTT	5100
	CTAGTGGTTC	TTTGGGTAT	TCTCATCTAC	TGGAGGAAAT	GCTTCCAGAC	TGCACACTTT	5160
	TACTTAGAGG	ACAGTACATC	CCTAGAGTT	ATATCCACAC	CTCAACACC	TATCTTTCCA	5220
	ATTTCAGATG	ATGTCCGAGC	AATTCCAATA	AAGCACTTTC	CAAAGCATGT	TGCAGATTTA	5280
	CATGCAAGTA	GTGGGTTTAC	TGAAGAAAT	GAGACACTGA	AAGAGTTTTA	CCAGGAAGTG	5340
45	CAGAGCTGTA	CTGTTGACTT	AGGTATTACA	GCAGACAGCT	CCAACCAACC	AGACAACAAG	5400
	CACAGAATATC	GATACATAAA	TATCGTTGCC	TATGATCATA	GCAGGGTTAA	GCTAGCACAG	5460
	CTTGCTGAAA	AGGATGACAA	ACTGACTGAT	TATATCAATG	CCAATTATGT	TGATGGCTAC	5520
	AACAGACCAA	AAGCTTATAT	TGCTGCCCAA	GGCCCACTGA	AATCCACAGC	TGAAGATTTC	5580
	TGGAGAAATG	TAGGGGAACA	TAAATGGA	GTTATTGTCA	TGATAACAAA	CCTCGTGGAG	5640
50	AAAGGAAGGA	GAAATGTGA	TCAGTACTGG	CCTGCCGATG	GGAGTGAGGA	GTACGGGAAC	5700
	TTTCTGGTCA	CTCAGAAAG	TGTGCAAGTG	CTTGCCCTATT	ATACTGTGAG	GAATTTTACT	5760
	CTAAGAAACA	CAAAATATAA	AAAGGGCTCC	CAGAAAGGAA	GACCCAGTGG	ACGTGTGGTC	5820
	ACACAGTATC	ACTACAGGCA	GTGGCCTGAC	ATGGGAGTAC	CAGAGTACTC	CCTGCCAGTG	5880
	CTGACCTTTG	TGAGAAAGGC	AGCCTATGCC	AAGCGCCATG	CAGTGGGGCC	TGTTGTCTGT	5940
	CACTGCAAGT	CTGGAGTTGG	AGAACAGGC	ACATATATTG	TGCTAGACAG	TATGTTGCAG	6000
55	CAGATTCAAC	ACGAAGGAAC	TGTCAACATA	TTTGGCTTCT	TAAACACAT	CCGTTCAACA	6060
	AGAAATTATT	TGGTACAAAC	TGAGGAGCAA	TATGTCTTCA	TTTATGATAC	ACTGGTTGAG	6120
	GCCATACTTA	GTAAGAAAC	TGAGGTGCTG	GACAGTCATA	TTTATGCTTA	TGTTAATGCA	6180
	CTCTCATTC	CTGGACAGC	AGGCAAAACA	AAGCTAGAGA	AACAATTCCA	GCTCCTGAGC	6240
	CAGTCAATA	TACAGCAGAG	TGACTATTCT	GCAGCCCTAA	AGCAATGCAA	CAGGGAAAG	6300
60	AATCGAATT	CTTCTATCAT	CCCTGTGGAA	AGATCAAGGG	TTGGCATTTC	ATCCCTGAGT	6360
	GGAGAAAGCA	CAGACTACAT	CAATGCCCTC	TATATCATGG	GCTATTACCA	GAGCAATGAA	6420
	TTTATCATTA	CCAGCAGCCC	TCTCCTTCT	ACCATCAAGG	ATTTCTGGAG	GATGATATGG	6480
	GACCATATG	CCCAACTGGT	GGTTATGATT	CCTGATGGCC	AAAACATGGC	AGAAGATGAA	6540
65	TTTGTTTACT	GGCCAAATAA	AGATGAGCCT	ATAAATTGTG	AGAGCTTTAA	GGTCACTCTT	6600
	ATGGCTGAAG	AACACAAAT	TCTATCTAAT	GAGGAAAAAC	TTATAATTCA	GGACTTTATC	6660
	TTAGAAGCTA	CACAGGATGA	TTATGTACTT	GAAGTGAGGC	ACTTTCAGTG	TCCTAAATGG	6720
	CCAAATCCAG	ATAGCCCCAT	TAGTAAACT	TTTGAACCTA	TAAGTGTAT	AAAAGAAGAA	6780
	GCTGCCAATA	GGGATGGGCC	TATGATTGTT	CATGATGAGC	ATGGAGGAGT	GACGGCAGGA	6840
70	ACTTCTGTG	CTCTGACAA	CCTTATGCAC	CAACTAGAAA	AAGAAATTC	CGTGGATGTT	6900
	TACCAGGTAG	CCAAGATGAT	CAATCTGATG	AGGCCAGGAG	TCTTTGCTGA	CATTGAGCAG	6960
	TATCAGTTTC	TCTACAAAGT	GATCCTCAGC	CTTGTGAGCA	CAAGGCAGGA	AGAGAATCCA	7020
	TCCACCTCTC	TGGACAGTAA	TGGTGACGCA	TTGCCCTGAT	GAAATATAGC	TGAGAGCTTA	7080
	GAGTCTTTAG	TTTAAACAG	AAAGGGGTGG	GGGGACTCAC	ATCTGAGCAT	TGTTTTCTCT	7140
75	TTCTTAAAT	TAGGCAGGAA	AATCAGTCTA	GTTCTGTAT	CTGTTGATTT	CCCATCACTT	7200
	GACAGTAAT	TTTATGATAT	AGGATTCTGC	CGCCAAATTT	ATATCATTTA	CAATGTGTGC	7260
	CTTTTTCGAA	GACTTGTAA	TTACTTATTA	TGTTTGAAC	AAAATGATTG	AATTTTACAG	7320
	TATTTCTAAG	AATGGAATG	TGGTATTTT	TTCTGTATTG	ATTTTAAAC	AAAATTTCAA	7380
	TTTATAGAG	TTAGGAATTC	CAAACTACAG	AAAATGTTTG	TTTTTAGTGT	CAAAATTTTA	7440
80	CGCTGATTG	TAGCAATAT	CAGGTTTGCT	AGAAATATAA	CTTTTAAATC	AGTAGCCCTG	7500
	AAATAAAACA	CTCTTCCATA	TGATATTCAA	CATTTTACAA	CTGCAGTATT	CACCTAAAGT	7560
	AGAAATAATC	TGTTACTTAT	TGTAAATAC	GCCCTAGTGT	CTCCATGGAC	CAAAATTTATA	7620
	TTTATAATTG	TAGATTTTTA	TATTTTACTA	CTGAGTCAAG	TTTTCTAGTT	CTGTGTAATT	7680
	GTTTAGTTTA	ATGACGTAGT	TCATTAGCTG	GTCTTACTCT	ACCAGTTTTC	TGACATTGTA	7740
	TTGTGTTACC	TAGTTCATTA	ACTTTGTTTC	AGCATGTAAT	TTTAACTTTT	GTGGAAAAAT	7800
85	GAAATACCTT	CATTTTGAAA	AGAGTTTTTA	TGAGAATAAC	ACCTTACCAA	ACATTGTTCA	7860
	AATGTTTCTT	ATCCAAGGAA	TTGCAAAAA	AAATATAAAT	ATTGCCATTA	AAAAAATAAA	7920
	AAAAAATAAA	AAAAAATAAA	AAAA				

Seq ID NO: 573 Protein sequence:
Protein Accession #: Eos sequence

5	1	11	21	31	41	51	
	MRILKRFLAC	IQLLCVCRLD	WANGYYRQQR	KLVEEIGWSY	TGALNQKNWG	KKYPTCNSPK	60
	QSPINIDEDL	TQVNVNKKL	KFQGWDKTSL	ENTFIHNTGK	TVEINLTNDY	RVSGGVSEMV	120
10	FKASKITPHW	GKCNMSDGS	EHSLEGQKFP	LEMQIYCFDA	DRFSSPEEAV	KGKGKLRALS	180
	ILFEVGTSEN	LDFKAIIDGV	ESVSRFGKQA	ALDPFILLNL	LPNSTDKYYI	YNGSLTSPPC	240
	TDTVDMIVPK	DTVSISESQ	AVFCEVLTMQ	QSGYVLMMDY	LQNNFREQQY	KFSRQVFSSY	300
	TGKEEIEHAV	CSSEPEENVQA	DPENYTSLLV	TWERPRVVYD	TMIEKFAVLV	QQLDGEDQTK	360
	HEPLTDGYQD	LGAILNNLLP	NMSYVLQIVA	ICTNGLYGYK	SDQLIVDMPT	DNPELDLPPE	420
15	LIGTEETIKE	EEEGKDIEEG	AIVNPGRDSA	TNQIRKKEPQ	ISTTTHYNRI	GTKYNEAKTN	480
	RSPTRGSEFS	GKGDVNTSL	NSTSQPVTKL	ATEKDILSTS	QTVTELPPH	VEGTSASLND	540
	GSKTVLRSPH	MNLSGTAEHL	NTVSITEYEE	ESLLTSFKLD	TGAEDSSGSS	PATSAIPFIS	600
	ENISQGYIFS	SENPETITYD	VLIPESARNA	SEDSTSSGSE	ESLKDPSMEG	NVWFPSSTDI	660
	TAQPDVSGSR	ESFLQNTYTE	IRVDESEKTT	KSPSAGPVMS	QGPSVTDLEM	PHYSTFAFYP	720
20	TEVTPHAFTT	SSRQGDVST	VNVVYSQTTQ	PVYNGETPLQ	PSYSSEVPFL	VTPLLLDNQI	780
	LNTTPAASSS	DSALHATPVF	PSVDVSFESI	LSSYDGAPLL	PFSSASFSSS	LFRHLHTVSQ	840
	ILPQVTSATE	SDKVPILHASL	PVAGGDLLLE	PSLAQYSDVL	STTHAASETL	EFGSESGVLV	900
	KTLMFPSQVEP	PSSDAMMHAR	SSGPEPSYAL	SDNEGSQHIF	TVSYSSAIPV	HDSVGVTVYQ	960
	SLFSGPSHIP	IPKSSLITPT	ASLLQPTHAL	SGDGEWSGAS	SDSEFLLPDT	DGLTALNISS	1020
25	PVSVAEFTYT	TSVFGDDNKA	LKSEIIYGN	ETELQIPSPN	EMVYPSESTV	MPNMYDNVVK	1080
	LNASLOETSV	SISSTKGMFP	GLAHTTTKV	FDHEISQVPE	NNFSVQPTH	VSQASGDTSL	1140
	KPVLSEANSEP	ASDDPASSEM	LSPSTQLLEY	ETSASFSTEV	LQPSFQASD	VDTLTKTVLP	1200
	AVPSDPILVE	TPKVDKISST	MLHLIVSNSA	SSENMLHSTS	VPVFDVSPTS	HMHASLQGL	1260
	TISYASEKYE	LVHLKSESSH	QVPSLYSND	ELFQTANLEI	NQAHPPKGRH	VFATPVLSID	1320
30	EPLNTLNLKL	IHSDELLTST	KSSVTGKVFA	GIPTVASDTP	VSTDHSPVPI	NGHVAITAVS	1380
	PHRDGVSST	KLLFPKSKAT	ELSHSAKSDA	GLVGGGDEGD	TDDGDGDDDD	DRGSDGLSIH	1440
	KCMSCSYRE	SQKVMNDSD	THENGLMDQN	NPISYSLSEN	SEEDNRVTSV	SSDSQTGMDR	1500
	SPGKSPSANG	LSQKHNDCKE	ENDIQTGSAL	LPLSPESKAW	AVLTSDEESG	SGQQTSDSLN	1560
	ENETSTDPSF	ADTNEKDADG	ILAAAGDSEIT	PGFPQSPSTS	VTSENSEVPH	VSEAEASNS	1620
35	HESRIGLAEG	LVSEKKAQIP	LVIVSALTPI	CLVVLVGLIL	YWRKCFQTAH	FYLEDSTSPR	1680
	VISTPPTPIF	PISDDVGAIP	IKHFPKHVAD	LHASSGPTTE	FETLKEFYQE	VQSCVTDLGI	1740
	TADSNHPND	KHNRYINIV	ADHRSRVKLA	QLAEKDGKLT	DYINANYVDG	YNRPKAYIAA	1800
	QGPKLSTAED	FWRMIWEHNV	EVIVMITNLV	EKGRRKGDQY	WPADGSEEVG	NFLVTQKSVQ	1860
	VLAYTYVRNF	TLRNTKIKKG	SQKGRPSGRV	VTQYHYTQWP	DMGVPEYSLP	VLTFFVRKAA	1920
40	AKRHAVGPVV	VHCSAGVGR	GTIYVLDLML	QQIQHEGTVN	IFGFLKHIRS	QRNYLVQTTE	1980
	QYVFIHDTLV	EALSLKETEV	LDSHIHAYVN	ALLIPGPAGK	TKLEKQFQLL	SQSNIQQSDY	2040
	SAALKQCNRE	KNRTSSIPV	ERSRVGISSL	SSEGTDYINA	SYIMGYQSN	EFITQHPHLL	2100
	HTIKDFWRMI	WDNNAQLVVM	IPDQGNMAED	EFVYWPKNDE	PINCSEFKVT	LMAEHEKCLS	2160
	NEEKLIQDQF	ILEATQDDYV	LEVRFHQCPK	WPNPDSPISK	TPELISVIKE	EAANRDGPMI	2220
45	VHDEHGGVTA	GTFCALTTL	HQLEKENSVD	VYQVAKMINL	MRPGVFADIE	QYQFLYKVIL	2280
	SLVSTRQEEN	PSTSLDSNGA	ALPDGNIAES	LESIV			

Seq ID NO: 574 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 148-4518

50	1	11	21	31	41	51	
	CACACATACG	CAGCAGCAT	CTCACTTCGA	TCTATACACT	GGAGGATTAA	AACAAACAAA	60
55	CAAAAAAAC	ATTTCCTTCG	CTCCCCCTCC	CTCTCCACTC	TGAGAAGCAG	AGGAGCCGCA	120
	CGGCGAGGGG	CCGACAGCCG	CTCGGAAATG	CGAATCTCAA	AGCGTTTCCT	CGCTTGCAAT	180
	CAGCTCCTCT	GCTGTTGCGC	CCTGGATTGG	GCTAATGGAT	ACTACAGACA	ACAGAGAAAA	240
	CTTGTTGAAG	AGATTGGCTG	GTCCTATACA	GGAGCACTGA	ATCAAAAAAA	TTGGGGAAAG	300
	AAATATCCAA	CATGTAATAG	CCCAAAACAA	TCTCTATCA	ATATTGATGA	AGATCTTACA	360
60	CAAGTAAATG	TGAATCTTAA	GAAACTTAAA	TTTCAGGGTT	GGGATAAAAC	ATCATTGGAA	420
	AACACATTCA	TTCATTAACAC	TGGGAAAACA	GTGGAAATTA	ATCTCACTAA	TGACTACCGT	480
	GTCAAGCGAG	GAGTTTCAGA	AATGGTGTTT	AAAGCAAGCA	AGATAACTTT	TCAGTGGGGA	540
	AAATGCAATA	TGTCACTCTG	TGGATCAGAG	CATAGTTTAG	AAGGACAAAA	ATTTCCACTT	600
	GAGATGCAAA	TCTACTGCTT	TGATGCGGAC	CGATTTTCAA	GTITTTGAGGA	AGCAGTCAAA	660
65	GGAAAAGGGA	AGTTAAGAGC	TTTATCCATT	TTGTTTGAGG	TTGGGACAGA	AGAAAATTTG	720
	GATTTCAAAG	CGATTATTGA	TGGAGTCGAA	AGTGTTAGTC	GTITTTGGGA	GCAGGCTGCT	780
	TTAGATCCAT	TCTACTGTGT	GAACCTTCTG	CCAAACTCAA	CTGACAAGTA	TTACATTTAC	840
	AATGGCTCAT	TGACATCTCC	TCCCTGCACA	GACACAGTTG	ACTGGATTGT	TTTTAAAGAT	900
	ACAGTTAGCA	TCTCTGAAAG	CCAGTTGGCT	GTTTTTTGTG	AAGTTCCTAC	AATGCAACAA	960
70	TCTGGTTATG	TCTATGCTGAT	GGACTACTTA	CAAAACAATT	TTGAGAGCA	ACAGTACAAG	1020
	TTCTCTAGAC	AGGTGTTTTT	CTCATACTCT	GGAAAGGAAG	AGATTCATGA	AGCAGTTTGT	1080
	AGTTTCAGAAC	CAGAAAATGT	TCAAGCTGAC	CCAGAGAATT	ATACCAGCCT	TCTTGTTACA	1140
	TGGGAAAGAG	CTCGAGTCGT	TTATGATACC	ATGATTGAGA	AGTTTGACGT	TTTGTACACC	1200
	CAGTTGGATG	GAGAGGACCA	AACCAAGCAT	GAATTTTGA	CAGATGGCTA	TCAAGACTTG	1260
75	GGTGCTATTC	TCAATAATTT	GCTACCCCAT	ATGAGTTATG	TTCTTCAGAT	AGTAGCCATA	1320
	TGCACTAATG	GCTTATATGG	AAAATACAGC	GACCAACTGA	TTGTCGACAT	GCCTACTGAT	1380
	AATCCTGAAC	TTGATCTTTT	CCCTGAATT	ATTGGAACCT	AAGAAATAAT	CAAGGAGGAG	1440
	GAAGAGGGAA	AAGACATTGA	AGAAGGCGCT	ATTGTGAATC	CTGGTAGAGA	CAGTGCTACA	1500
	AACCAATACA	GAAAGGAGGA	ACCCAGATT	TCTACCACAA	CACACTACAA	TCGCATAGGG	1560
80	ACGAAATACA	ATGAAGCCAA	GACTAACCGA	TCCCAACAA	GAGGAAGTGA	ATTCCTGGA	1620
	AAGGGTGATG	TTCCCAATAC	ATCTTTAAAT	TCCACTTCCC	AACCAAGTCA	TAAATTAGCC	1680
	ACAGAAAAAG	ATATTTCCTT	GACTTCTCAG	ACTGTGACTG	AACCTGCCAC	TCACACTGTG	1740
	GAAGGTACTT	CAGCCTCTTT	AAATGATGGC	TCTAAAACCT	TTCTTAGATC	TCCACATATG	1800
	AACCTGTCGG	GAGCTCAGAG	ATCCTTAAAT	ACAGTTTCTA	TAACAGAAATA	TGAGGAGGAG	1860
	AGTTTATTGA	CCAGTTTCAA	GCTTGATACT	GGAGCTGAAG	ATTCTTCAGG	CTCCAGTCCC	1920
85	GCAACTTCTG	CATCTCTGAG	AACATATCCC	AAGGGTATAT	ATTTCTCTCC		1980
	GAAAAACCCAG	AGACAATAAC	ATATGATGTC	CTTATACCAG	AATCTGCTAG	AAATGCTTCC	2040
	GAAAGATTCAA	CTTCATCAGG	TTCAAGAGAA	TCAGTAAAGG	ATCCTTCTAT	GGAGGGAAAT	2100

	GTGTGGTTTC	CTAGCTCTAC	AGACATAACA	GCACAGCCCC	ATGTTGGATC	AGGCAGAGAG	2160
	AGCTTTCTCC	AGACTAATTA	CACTGAGATA	CGTGTGTATG	AATCTGAGAA	GACAAACCAAG	2220
	TCCTTTTCTG	CAGGCCCACT	GATGTACACG	GGTCCCTCAG	TTACAGATCT	GGAAATGCCA	2280
5	CATTATTCTA	CCTTTGCCCTA	CTTCCCAACT	GAGGTAACAC	CTCATGCTTT	TACCCCATCC	2340
	TCCAGACAAC	AGGATTGTGT	CTCCACGGCT	AACGTGGTAT	ACTCGCAGAC	AACCCAAACCG	2400
	GTATACAATG	CAGAGGCCAG	TAATAGTAGC	CATGAGTCTC	GTATTGGTCT	AGCTGAGGGG	2460
	TTGGAATCCG	AGAAGAAGGC	AGTTATACCC	CTTGTGATCG	TGTGAGCCCT	GACTTTTATC	2520
	TGTCTAGTGG	TTCTTGTGGG	TATTCTCATC	TACTGGAGGA	AATGCTTCCA	GACTGCACAC	2580
10	TTTTACTTAG	AGGACAGTAC	ATCCCTAGTA	GTTATATCCA	CACCTCCAAC	ACCTATCTTT	2640
	CCAATTTTCA	ATGATGTGGG	AGCAATTTCA	ATAAAGCACT	TTCCAAAGCA	TGTTGCAGAT	2700
	TTACATGCAA	GTAGTGGGTT	TACTGAAGAA	TTTGAGACAC	TGAAAGAGTT	TTACCAGGAA	2760
	GTGCAGAGCT	GTACTGTTGA	CTTAGGTATT	ACAGCAGACA	GCTCCAACCA	CCCAGACAAC	2820
	AAGCACAGA	ATCGATACAT	AAATATCGTT	GCCTATGATC	ATAGCAGGGT	TAAGTAGCA	2880
	CAGCTTGTCT	AAAAGGATGG	CAAACTGACT	GATTATATCA	ATGCCAATTA	TGTTGATGGC	2940
15	TACAAACAGC	CAAAAGCTTA	TATTGCTGCC	CAAGGCCCCAC	TGAAATCCAC	AGCTGAAGAT	3000
	TTCTGGAGAA	TGATGTGGGA	CAATATGTG	GAAGTTATTG	TCATGATAAC	AAACCTCGTG	3060
	GAGAAAGGAA	GGAGAAATG	TGATCAGTAC	TGGCCTGCCG	ATGGGAGTGA	GGAGTACGGG	3120
	AACCTTCTGG	TCACTCAGAA	GAGTGTGCAA	GTGCTTGCCCT	ATTATACTGT	GAGGAATTTT	3180
	ACTCTAAGAA	ACACAAAAT	AAAAAAGGCG	TCCCAGAAAG	GAAGACCCAG	TGGACGTGTG	3240
20	GTCAACAGT	ATCACTACAC	GCAGTGGCCT	GACATGGGAG	TACCAGAGTA	CTCCCTGCCA	3300
	GTGCTGACCT	TGATGGAGAA	GGCAGCCTAT	GCCAAGCGCC	ATGCAGTGGG	GCCTGTTGTC	3360
	GTCCACTGCA	GTGCTGGAGT	TGGAAGAAC	GGCACATATA	TTGTGCTAGA	CAGTATGTTG	3420
	CAGCAGATTC	AACACGAAGG	AACGTGCAAC	ATATTTGGCT	TCTTAAACCA	CATCCGTTCA	3480
	CAAGAATAAT	ATTGTGTACA	AACGTAGGAG	CAATATGTCT	TCATTATGA	TACACTGGTT	3540
25	GAGGCCATAC	TTAGTAAAGA	AACGTAGGAG	CTGGACAGTC	ATATTATGCT	CTATGTTAAT	3600
	GCACCTCTCA	TTCTCTGACC	ACGAGGCAAA	ACAAAGCTAG	AGAAACAATT	CCAGCTCCTG	3660
	AGCCAGTCAA	ATATACAGCA	GAGTGACTAT	TCTGCAGCCC	TAAAGCAATG	CAACAGGGAA	3720
	AAGAATCGAA	CTTCTCTAT	CATCCCTGTG	GAAAGATCAA	GGGTTGGCAT	TTCATCCCTG	3780
30	AGTGGAGAA	GCACAGACTA	CATCAATGCC	TCCTATATCA	TGGGCTATTA	CCAGAGCAAT	3840
	GAATTCATCA	TTACCCAGCA	CCCTCTCCTT	CATACCATCA	AGGATTTCTG	GAGGATGATA	3900
	TGGGACCAT	ATGCCCAACT	GGTGGTTATG	ATTCCTGATG	GCCAAACAT	GGCAGAAAGT	3960
	GAATTTGTTT	ACTGGCCAAA	TAAAGATGAG	CCTATAAATT	GTGAGAGCTT	TAAGGTCACT	4020
	CTTATGGCTG	AAGAACACAA	ATGCTATCT	AATGAGGAAA	AACCTATAAT	TCAGGACTTT	4080
35	ATCTTAGAAG	CTACACAGGA	TGATTATGTA	CTTGAAGTGA	GGCAGTTTCA	GTGCTCTAAA	4140
	TGGCCAAAT	CAGATAGCCC	CATTAGTAAA	ACTTTTGAAC	TTATAAGTGT	TATAAAGAAA	4200
	GAAGCTGCCA	ATAGGGATGG	GCTATGATT	GTTTATGATG	AGCATGGAGG	AGTGACGGCA	4260
	GGAACTTTCT	GTGCTCTGAC	AACCTTATG	CACCAACTAG	AAAAAGAAA	TTCCGTGGAT	4320
	GTTTACCAGG	TAGCCAAAGT	GATCAATCTG	ATGAGGCCAG	GAGTCTTTGC	TGACATTGAG	4380
40	CAGTATCAGT	TTCTCTACAA	AGTGATCCTC	AGCCTTGTGA	GCACAAGGCA	GGAGAGAAAT	4440
	CCATCCACCT	CTCTGGACAG	TAATGGTGCA	GCATTGCCTG	ATGGAATAT	AGCTGAGAGC	4500
	TTAGAGTCTT	TAGTTTAAAC	CAGAAAGGGG	TGGGGGGACT	CACATCTGAG	CATTGTTTTT	4560
	CTCTTCTCAA	AATTAGGCAG	GAAATCAGT	CTAGTCTGT	TATCTGTTGA	TTTCCCATCA	4620
	CCTGACAGTA	ACTTTCATGA	CATAGGATTC	TGCCGCCAAA	TTTATATCAT	TAACAATGTA	4680
45	TGCTTTTTTG	CAAGACTTGT	AATTTACTTA	TTATGTTTGA	ACTAAAAATGA	TTGAATTTTA	4740
	CAGTATTTCT	AAGAAATGGAA	TTGTGGTATT	TTTTTCTGTA	TTGATTTTAA	CAGAAATTTT	4800
	CAATTTATAG	AGGTTAGGAA	TTCCAAACTA	CAGAAATGT	TTGTTTTTAG	TGTCAAATTT	4860
	TTAGCTGTAT	TTGTAGCAAT	TATCAGGTTT	GCTAGAAATA	TAACTTTTAA	TACAGTAGCC	4920
	TGTAATAATA	ACACTCTTCC	ATATGATATT	CAACATTTTA	CAACTGCAGT	ATTACCTTAA	4980
50	AGTAGAAATA	ATCTGTTACT	TATTGTAAT	ACTGCCCTAG	TGCTCTCATG	GACCAAAATTT	5040
	ATATTTATAA	TTGTAGATTT	TTATATTTTA	CTACTGAGTC	AAGTTTTCTA	GTTCTGTGTA	5100
	ATTGTTTAGT	TTAATACAGT	AGTTTATTAG	CTGGTCTTAC	TCTACCAAGT	TCTCTGACAT	5160
	GTATTTGTTT	ACCTAAGTCA	TTAATTTTGT	TTGAGCATGT	AATTTTAACT	TTTGTGGAAA	5220
	ATAGAAATAC	CTTCAATTTT	AAGAAGTTT	TTATGAGAA	AACACCTTAC	CAACATTGTA	5280
55	TCAAATGGTT	TTTATCCAA	GAATTCGAAA	AATAAATATA	AATATTGCCA	TTAAAAAAA	5340
	AAAAAATAAA	AAAAAATAAA	AAAAAATA				

Seq ID NO: 575 Protein sequence:
Protein Accession #: Eos sequence

60	1	11	21	31	41	51	
	MRILKRFLAC	IQLLCVCRLD	WANGYYRQOR	KLVEEIGWSY	TGALNQKNWG	KKYPTCNSPK	60
	QSPINIDEDL	TQVNVNLKLL	KFGQWDKTSL	ENTPIHNTGK	TVEINLTNDY	RVSGGVSEMV	120
65	FKASKITPHW	GKCNMSDGS	EHSLEGQKFP	LEMQIYCFDA	DRFSSFEAV	KGKGLRLALS	180
	ILFEVGTEN	LDFAIIDGV	ESVSRFGKQA	ALDPFILLNL	LPNSTDKYYI	YNGSLTSPPC	240
	TDTVDWIVFK	DTVISISESL	AVFCEVLTMQ	QSGVVMMDY	LQNNFREQQY	KFSRQVFSY	300
	TGKEIEHEAV	CSSEPEENVQA	DPENYTSLLV	TWERPRVVD	TMIEKPAVLY	QQLDGEDQTK	360
70	HEFLTDGQD	LGAILNNLLP	NMSYVLQIVA	ICTNGLYGYK	SDQLIVDMPT	DNPELDLPE	420
	LIGTEBIIKE	EEBQKDIEEG	AIVNPGRDSA	TNQIRKKEBP	ISTTTHYNRI	GTKYNEAKTN	480
	RSPTRGSEFS	GKGDVPNTSL	NSTSPVTKL	ATEKDISLTS	QVTLELPHT	VEGTSASLND	540
	GSKTVLRSFH	MNLSGTAESL	NTVSITEYEE	ESLLTSFKLD	TGAEDSSGSS	PATSAIPFIS	600
	ENISQGYIFS	SENPEITTYD	VLIPESARNA	SEDSTSSGSE	ESLKDPMSMG	NVWFPSSTDI	660
75	TAQPDVGSGR	ESPLQNTYTE	IRVDESEKTT	KSFSAQPVMS	QGPSVTDLEM	PHYSTPAYFP	720
	TEVTPHAFPT	SSRQDLVST	VNVVYSQTTQ	PVYNAEASNS	SHERIGLAE	GLESEKKAVI	780
	PLVIVSALTF	ICLVVLVGIL	IYWRKCFQTA	HFYLEDSTSP	RVISTPPTPI	FPISDDVGA	840
	PIKHFPKHVA	DLHASSGFTE	EPETLKEFYQ	EVQSCITVDL	ITADSSNHDP	NKHKNNRYINI	900
	VAYDHSRYEKL	AQLAEKDGKL	TDYINANYVD	GYNRPKAYIA	AQGPLKSTAE	DFWRMIWEHN	960
80	VEVIVMITNL	VEKGRRCQDQ	YWPADGSEY	GNFLVTQKSV	QVLAYYTVRN	FTLRNTKIKK	1020
	GSQKGRPSGR	VVTQYHTQV	PDMGVPEYSL	PVLTFVRKAA	YAKRHAVGPV	VVHCSAGVGR	1080
	TGTIVLDSM	LQIQHEGTV	NIFGFLKHIR	SQRNLYVQTE	EQYVFIHDTL	VEAILSKETE	1140
	VLDSHIHAYV	NALLIPGPAG	KTKLEKQFQL	LSQSNIQQSD	YSALKQCNR	EKNRTSSII	1200
	VERSERGVSS	LSGEGTIDYN	ASYIMGYYS	NEFIITQHPL	LHTIKDFWRM	IWDHNAQLV	1260
	MLPDGQMAE	DEFPYWNKD	EPINCESFKV	TLMAEHEKCL	SNEEKLIQD	FILEATQDDY	1320
85	VLEVRFQCFP	KWPNFDPIS	KTFELISVIK	EAAANRDGPM	IVHDEHGGVT	AGTFCALTTL	1380
	MHOLEKENS	DVYQVAKMIN	LMRPGVFADI	EQYQFLYKVI	LSLVSTRQEB	NPSTSLDSNG	1440
	AALPDGNTAE	SLESIV					

Seq ID NO: 576 DNA sequence
Nucleic Acid Accession #: EOS sequence
Coding sequence: 148-4494

5	1	11	21	31	41	51	
	CACACATACG	CACGACGAT	CTCACTTCGA	TCTATACACT	GGAGGATTAA	AACAAACAAA	60
	CAAAAAAAC	ATTTCCTTCG	CTCCCCCTCC	CTCTCCACTC	TGAGAAGCAG	AGGAGCCGCA	120
10	CGGCGAGGGG	CCGCAGACCG	TCTGGAAATG	CGAATCTCAA	AGCGTTTCCT	CGCTTGCAAT	180
	CAGCTCCTCT	GTGTTTGCCG	CCTGGATTGG	GCTAATGGAT	ACTACAGACA	ACAGAGAAAA	240
	CTTGTGTAAG	AGATTGGCTG	GTCCTATACA	GGAGCACTGA	ATCAAAAAAA	TTGGGGAAAG	300
	AAATATCCAA	CACTGTAATAG	CCCAAAACAA	TCTCCTATCA	ATATTGATGA	AGATCTTACA	360
15	CAAGTAAATG	TGAATCTTAA	GAAACTTAAA	TTTCAGGGTT	GGGATAAAAC	ATCATTGGAA	420
	AACACATTCA	TTCATACAC	TGGGAAAAAC	GTGGAAATTA	ATCTCACTAA	TGACTACCGT	480
	GTCAGCGGAG	CAGATTTTCA	AATGGTGTTC	AAAGCAAGCA	AGATAACTTT	TCACTGGGGA	540
	AAATGCAATA	TGTCATCTGA	TGGATCAGAG	CATAGTTTAG	AAGGACAAAA	ATTTCCACTT	600
	GAGATGCAAA	TCTACTGCTT	TGATGCAGAC	CGATTTTCAA	GTTTTGAGGA	AGCAGTCAAA	660
20	GGAAAAAGGA	AGTAAAGAGC	TTTATCCATT	TTGTTTGAGG	TTGGGACAGA	AGAAAAATTG	720
	GATTTCAAAG	CGATTATTGA	TGGAGTCGAA	AGTGTTAGTC	GTTTTGGGAA	GCAGGCTGCT	780
	TTAGATCCAT	TCATATCTGT	GAACTTCTG	CCAAACTCAA	CTGACAAGTA	TTACATTTAC	840
	AATGGCTCAT	TGACATCTCC	TCCCTGCACA	GACACAGTTG	ACTGGATTGT	TTTAAAGAT	900
	ACAGTTAGCA	TCTCTGAAAG	CCAGTTGGCT	GTTTTTTGTG	AAGTTCTTAC	AATGCAACAA	960
25	TCTGTGTTAG	TCATGCTGAT	GGACTACTTA	CAAAACAATT	TTGAGAGCA	ACAGTACAA	1020
	TTCTCTAGAC	AGGTGTTTTT	CTCATACACT	GGAAAGGAAG	AGATTATGA	AGCAGTTTGT	1080
	AGTTCAGAAC	CAGAAAATGT	TCAGGCTGAC	CCAGAGAATT	ATACCAGCCT	TCTTGTACA	1140
	TGGGAAAGAC	CTCAGTCTGT	TTATGATACC	ATGATTGAGA	AGTTTGCAGT	TTTGTACCAG	1200
	CAGTTGGATG	GAGAGGACCA	AACCAAGCAT	GAATTTTGA	CAGATGGCTA	TCAAGACTTG	1260
30	GGTGCTATT	TCAATTAATTT	GCTACCCAAT	ATGAGTTATG	TTCTTCAGAT	AGTAGCCATA	1320
	TGCACTAATG	GCTTATATGG	AAAATACAGC	GACCAACTGA	TTGTCGACAT	GCCTACTGAT	1380
	AATCTGAAC	TTGATCTTTT	CCCTGAATTA	ATTGGAAGTG	AAGAAATAAT	CAAGGAGGAG	1440
	GAAGAGGGAA	AAGACATTGA	AGAAGGCGCT	ATTGTGAATC	CTGGTAGAGA	CAGTGCTACA	1500
	AACCAATCA	GGAAAAAGGA	ACCCAGATT	TCTACCAAA	CACACTACAA	TCGCATAGGG	1560
35	ACGAAATACA	ATGAAGCCAA	GACTAACCGA	TCCCCAACAA	GAGGAAGTGA	ATTCTCTGGA	1620
	AAGGGTGATG	TTCCCAATAC	ATCTTTAAAT	TCCACTTCCC	AACCAGTCAC	TAAATTAGCC	1680
	ACAGAAAAAG	ATATTCTCTT	GACTTCTCAG	ACTGTGACTG	AAGTGCACCC	TCACACTGTG	1740
	GAAGGTACTT	CAGCCTCTTT	AAATGATGGC	TCTAAAACCTG	TTCTTAGATC	TCCACATATG	1800
	AACCTTGTGG	GGACTGCAGA	ATCCTTAAAT	ACAGTTTCTA	TAACAGAAAT	TGAGGAGGAG	1860
40	AGTTTATTGA	CCAGTTTCAA	GCTTGATACT	GGAGCTGAAG	ATTCTTCAGG	CTCCAGTCCC	1920
	GCAACTTCTG	CTATCCCAT	CATCTCTGAG	AACATATCCC	AAGGGTATAT	ATTTCTCTCC	1980
	GAAACCCAG	AGACAATAAC	ATATGATGTC	CTTATACCAG	AATCTGCTAG	AAATGCTTCC	2040
	GAAGATTCAA	CTTCATCAGG	TTCAGAAGAA	TCATTAAGG	ATCCTTCTAT	GGAGGGAAAT	2100
	GTGTGGTTTC	CTAGCTCTAC	AGACATAACA	GCACAGCCCG	ATGTTGGATC	AGGCAGAGAG	2160
45	AGCTTTCTCC	AGACTAATTA	CACCTGAGATA	CGTGTGATG	AATCTGAGAA	GACAACCAAG	2220
	TCCTTTCTCG	CAGGCCAGT	GATGTACAG	GGTCCCTCAG	TTACAGATCT	GGAAATGCCA	2280
	CATTATTCTA	CTTTGCTCTA	TTCCCAACT	GAGGTAACAC	CTCATGCTTT	TACCCCATCC	2340
	TCCAGACAAC	AGGATTGGT	CTCCACGGTC	AACGTGGTAT	ACTCGCAGAC	AACCCAAACG	2400
	GTATACAATG	AGGCCAGTAA	TAGTAGCCAT	GAGTCTCGTA	TTGGTCTAGC	TGAGGGGTTG	2460
50	GAATCCGAGA	AGAAGGCAGT	TATACCCCTT	GTGATCGTGT	CAGCCCTGAC	TTTTATCTGT	2520
	CTAGTGGTTC	TTGTGGGTAT	TCTCATCTAC	TGGAGGAAAT	GCTTCCAGAC	TGCACACTTT	2580
	TACTTAGAGG	ACAGTACATC	CCCTAGAGTT	ATATCCACAC	CTCCAACACC	TATCTTTCCA	2640
	ATTTCAGATG	ATGTCGAGC	AATTCCAATA	AAGCACTTTC	CAAAGCATGT	TGCAGATTTA	2700
	CATGCAAGTA	GTGGGTTTAC	TGAAGAATT	GAGGAAGTGC	AGAGCTGTAC	TGTTGACTTA	2760
55	GGTATTACAG	CAGACAGCTC	CAACCAACCA	GACAACAAGC	ACAAGAATCG	ATACATAAAT	2820
	ATCGTTGCTT	ATGATCATAG	CAGGGTTAAG	CTAGCACAGC	TTGCTGAAAA	GGATGGCAAA	2880
	CTGACTGATT	ATATCAATGC	CAATATGTT	GATGGCTACA	ACAGACCAAA	AGCTTATATT	2940
	GCTGCCCAAG	GCCCACTGAA	ATCCACAGCT	GAAGATTTC	GGAGAATGAT	ATGGGAACAT	3000
	AATGTGGAAG	TTATTGTCAT	GATAACAAAC	CTCGTGGAGA	AAGGAAGGAG	AAAATGTGAT	3060
60	CAGTACTGGC	CTGCCGATGG	GAGTGAGGAG	TACGGGAACT	TTCTGTCTAC	TCAGAAGAGT	3120
	GTGCAAGTGC	TTGCCATTAT	TACTGTGAGG	AATTTTACTC	TAAGAAACAC	AAAAATAAAA	3180
	AAGGGCTCCC	AGAAAGGCAAG	ACCCAGTGGG	CGTGTGGTCA	CACAGTATCA	CTACACGCAG	3240
	TGGCCTGACA	TGGAGTATCC	AGAGTACTCC	CTGCCAGTGC	TGACCTTTGT	GAGAAAGGCA	3300
	GCCTATGCCA	AGGCCATCTG	AGTGGGGCCT	GTTGTCTGTC	ACTGCACTGC	TGGAGTTGGA	3360
65	AGAACAGGCA	CATATATTGT	GCTAGACAGT	ATGTTGCAGC	AGATTCAACA	CGAAGGAACT	3420
	GTCAACATAT	TTGGCTTCTT	AAAACACATC	CGTTCAACAA	GAAATATTAT	GGTACAAACT	3480
	GAGGAGCAAT	ATGCTTTCAT	TCATGATACA	CTGGTTGAGG	CCATACCTAG	TAAAGAAACT	3540
	GAGGTGCTGG	ACAGTCAATAT	TCATGCCTAT	GTTAATGCAC	TCTCTATTCC	TGGACCAGCA	3600
	GGCAAAACAA	AGCTAGAGAA	ACAATTCCAG	CTCCTGAGCC	AGTCAAAATAT	ACAGCAGAGT	3660
70	GACTATTCTG	CAGCCCTAAA	GCAATGCAAC	AGGGAAAAGA	ATCGAACTTC	TTCTATCATC	3720
	CCTGTGGAAA	GATCAAGGGT	TGGCATTTCA	TCCCTGAGTG	GAGAAGGCAC	AGACTACATC	3780
	AATGCCCTCT	ATATCATGGG	CTATTACCAG	AGCAATGAAT	TCATCATTTAC	CCAGCACCCCT	3840
	CTCCTTCATA	CCATCAAGGA	TTTCTGGAGG	ATGATATGGG	ACCATAATGC	CCAACCTGGT	3900
75	GTTATGATT	CTGATGGCCA	AAACATGGCA	GAAGATGAAT	TTGTTTACTG	GCCAAATAAA	3960
	GATGAGCCTA	TAAATTGTGA	GAGCTTTAAG	GTCACCTCTA	TGGCTGAAGA	ACACAAATGT	4020
	CTATCTAATG	AGGAAAAACT	TATAATTGAG	GACTTTATCT	TAGAAGCTAC	ACAGGATGAT	4080
	TATGTACTTG	AAGTGAGGCA	CTTTCAGTGT	CCTAAATGGC	CAAAATCCAGA	TAGCCCCATT	4140
	AGTAAACCTT	TTGAACCTTAT	AAGTGTATTA	AAAGAAGAAG	CTGCCAATAG	GGATGGGCTT	4200
	ATGATTGTTC	ATGATGAGCA	TGGAGGAGTG	ACGGCAGGAA	CTTCTGTGTC	TCTGACAACC	4260
80	CTTATGCACC	AACTAGAAAA	AGAAAAATCC	GTGGATGTTT	ACCAGGTAGC	CAAGATGATC	4320
	AATCTGATAG	GGCCAGGAGT	CTTGTCTGAC	ATTGAGCAGT	ATCAGTTTCT	CTACAAAAGTG	4380
	ATCCTCAGCC	TTGTGAGCAC	AAGGCAGGAA	GAGAATCCAT	CCACCTCTCT	GGACAGTAAT	4440
	GGTGACAGAT	TGCCGTATGG	AAATATAGCT	GAGAGCTTAG	AGTCTTTAGT	TTAACACAGA	4500
	AAGGGGTGGG	GGGACTCACA	CTGAGCATT	GTTTCTCTCT	TCCTAAAATT	AGGCAGGAAA	4560
	ATCAGTCTAG	TTCTGTATTC	TGTTGATTTC	CCATCACCTG	ACAGTAACCT	TCATGACATA	4620
85	GGATTCTGCC	GCCAAATTTA	TATCATTAAC	AATGTGTGCC	TTTTTGCAAG	ACTTGTAAAT	4680
	TACTTATTAT	GTTTGAACATA	AAATGATTGA	ATTTTACAGT	ATTTCTAAGA	ATGGAATTGT	4740
	GGTATTTTTT	TCTGTATTGA	TTTAAACAGA	AAATTTCAAT	TTATAGAGGT	TAGGAATTCC	4800

5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85

```

AAACTACAGA AAATGTTTGT TTTTAGTGTC AAATTTTGT CTGTATTGT AGCAATTATC 4860
AGGTTTGCTA GAAATATAAC TTTTAATACA GTAGCCTGTA AATAAACAC TCTTCCATAT 4920
GATATTCAAC ATTTTACAAC TGCAGTATTC ACCTAAAGTA GAAATAATCT GTTACTTATT 4980
GTAAATACTG CTTTGTGTC TCCATGGACC AAATTATAT TTATAATTGT AGATTTTAT 5040
ATTTTACTAC TGAGTCAAGT TTTCTAGTTC TGTGTAATG TTTAGTTAA TGACGTAGTT 5100
CATTAGCTGG TCTTACTCTA CCACTTTTCT GACATGTAT TGTGTACCT AAGTCATTAA 5160
CTTTGTTTCA GCATGTAATT TTAACTTTGT TGGAAATAG AAATACCTTC ATTTTGAAAG 5220
AAGTTTTTAT GAGAATAACA CCTTACCAAA CATTGTTCAA ATGGTTTTTA TCCAAGGAAT 5280
TGCAAAAATA AATATAAATA TTGCCATTAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 5340
AAA

```

Seq ID NO: 577 Protein sequence:
Protein Accession #: EOS sequence

1 11 21 31 41 51

```

MRILKRFLAC IQLLCVCRLD WANGYYRQOR KLVVEIGWSY TGALEKQNWG KKYPCTNSPK 60
QSPINIDEDL TQVNVNLKKL KFGQWDKTSL ENTFIHNTGK TVEINLTNDY RVSGGVSEMV 120
PKASKITPFH GKCNMSSDGS EHSLEGKQFP LEMQIYCFDA DRFSSFEBAV KKGKLRALS 180
ILFEVGTEN LDFKAIIDGV ESVSFRGKQA ALDPFILLNL LPNSTDYKI YNGSLTSPPC 240
TDTVDNIVFK DTVSISESQ L AVFCEVLTMO QSGYVLMMDY LQNNFREQQY KFSRQVFSSY 300
TGKEEHEAV CSSEPENVOA DPENYTSLLV TWERPRVVD TMIEKFAVLY QQLDGEDQTK 360
HEFLTDGYQD LGAILNLLP NMSYVLQIVA ICTNGLYGY SDQLIVDMPT DNPFLDLFPE 420
LIGTEEIIKE EEEGMDIEEG AIVNPGRDSA TNQIRKKEPQ ISTTHYNRI GTKYNEAKTN 480
RSPTRGSEFS GKGVDVNTSL NTSQPVTKL ATEKDLSLTS QTVTELPPT VEGTSASLND 540
GSKTVLRSPH MNLSSGTFESL NTVSITEYEE ESLLTSFKLD TGAEDSSGSS PATSAIPFIS 600
ENISQGYIFS SENPETITYD VLIPESARNA SEDSTSSGSE ESKDPSMEG NVWFPSSTDI 660
TAQPDVGSGR ESFLQNTYTE IRVDESEKTT KSFSAGPVMS QGPSVTDLEM PHYSTFAYFP 720
TEVTPHAFPT SSRQDVLST VNVVYSQTTQ PVYNEASNSS HESRIGLAEG LESEKKAVIP 780
LVIVSALTPI CLVVLVGLIL YWRKCFQTAH FYLEDSTSPR VISTPPTPIF PISDDVGAIP 840
IKHFPKHVAD LHASSGTFEE FEEVQSCSTD LGITADSSNH PDNKHKNRYI NIVAYDHSRV 900
KLAQLAEKDG KLTPIINANY VDGYNRPKAY IAAQGLKST AEDFWRMIWE HNVEVIVMIT 960
NLVEKGRRKC QWYFADGSE EYGNFLVTQK SVQVLAYYTV RNFTLRNTKI KKGSKGRPS 1020
GRVVTQYHT QDPMGVPEY SLPLVTFVRK AAYAKRHAVG PVVVCAGV GRTGYIYLD 1080
SMLQQIQHEG TVNIFGLPKH IRSQRNYLVQ TEEQVYFIHD TLVEALLSKE TEVLDSHIA 1140
YVNALLIPGP AGTKLEKQF QLLSQSNIQ SDYSAALKQC NREKNRTSSI IPVERSRVGI 1200
SSLSGEGTDY INASYIMGYV QSNEFIITQH PLLHTIKDFW RMIWDHNAQL VVMIPDGQNM 1260
AEDEFPVWPN KSEPINCESF KVTLMABEHK CLSNEEKLI QDFILEATQD DVLVLRHFQ 1320
CPKWPMPDSP ISKTFELISV IKEEAANRDG PMIVHDEHGG VTAGTFCAL TLMHQLKEN 1380
SDVYQVARM INLNRPGVFA DIEQYQFLYK VILSLVSTRQ EENPSTSLDS NGAALPDGNI 1440
AESLES LV

```

Seq ID NO: 578 DNA sequence
Nucleic Acid Accession #: EOS sequence
Coding sequence: 501-4514

1 11 21 31 41 51

```

CACACATACG CACGCACGAT CTCACCTCGA TCTATACACT GGAGGATTAA AACAAACAAA 60
CAAAAAAAC ATTTCCCTCG CTCCCCCTCC CTCTCCACTC TGAGAAGCAG AGGAGCCGCA 120
CGGCAGGGGG CGGCAGACCG TCTGGAATAG CGAATCCTAA AGCGTTTCCT CGCTTGCAAT 180
CAGCTCCTCT GGTGTTGCGG CCTGGATTGG GCTAATGGAT ACTACAGACA ACAGAGAAAA 240
CTTGTGTAAG AGATTGCGTG GTCCATATACA GGAGCACTGA ATCAAAAAAT TGGGGAAAGA 300
AATATCCAAC ATGTAATAGC CCAAAACAAT CTCCTATCAA TATTGATGAA GATCTTACAC 360
AAGTAAATG AGTCTTAAG AACTTAAAT TTCAGGGTTG GGATAAAACA TCATTGGAAA 420
ACACATTCAT TCATAACACT GGGAAACAG TGGAAATTA TCTCACTAAT GACTACCGTG 480
TCAGCGGAGG AGTTTCAGAA ATGGTGTTTA AAGCAAGCAA GATAACTTTT CACTGGGGAA 540
AATGCAATAT GTCATCTGAT GGATCAGAGC ATAGTTTAGA AGGACAAAAA TTCCACTTG 600
AGATGCAAA CTACTGCTTT GATGCGGACC GATTTTCAAG TTTTGAGGAA GCAGTCAAAG 660
GAAAAGGGAA GTTAAGAGCT TTATCCATT TGTTTGAGGT TGGGACAGAA GAAAATTTGG 720
ATTTCAAAGC GATTATTGAT GGAGTCGAAA GTGTAGTCG TTTTGGAAG CAGGCTGCTT 780
TAGATCCATT CATACTTTTG AACCTTCTGC CAACTCAAC TGACAAGTAT TACATTTACA 840
ATGGCTCATT GACATCTCCT CCTGACACAG ACACAGTTGA CTGGATTGTT TTTAAAGATA 900
CAGTTAGCAT CTCTGAAAGC CAGTTGGCTG TTTTGTGTA AGTCTTACA ATGCAACAAT 960
CTGGTTATGT CATGCTGATG GACTACTTAC AAAACAATTT TCGAGAGCAA CAGTACAAGT 1020
TCTCTAGACA GGTGTTTTC TCATACACTG GAAAGGAAGA GATTCATGAA GCAGTTTGT 1080
GTTCAGAAC AGAAAAATGTT CAGGCTGACC CAGAGAATTA TACCAGCCTT CTGTGTACAT 1140
GGGAAAGACC TCGAGTCGTT TATGATACCA TGATTGAGAA GTTTCGAGTT TTGTACCAGC 1200
AGTTGGATGG AGAGGACCAA ACCAAGCATG AATTTTGTAG AGATGGCTAT CAAGACTTGG 1260
GTGCTATTCT CAATAATTG CTACCCAATA TGAGTTATGT TCTTCAGATA GTAGCCATAT 1320
GCATAATGG CTTATATGGA AATACAGCG ACCAAGTATG TGTGACATG CCTACTGATA 1380
ATCCTGAAT TGATCTTTTC CCTGAAATTA TTGGAAGTGA AGAAATAATC AAGGAGGAGG 1440
AAGAGGGAAA AGACATTGAA GAAGGCGCTA TTGTGAATCC TGGTAGAGAC AGTGCTACAA 1500
ACCAATACAG GAAAAAGGAA CCCAGATT CTACCAACAC AACTACAAT CGCATAGGGA 1560
CGAAATACAA TGAAGCCAAG ACTAACCGAT CCCCACAG AGGAAGTGAA TTCTCTGGAA 1620
AGGGTGATGT TCCCAATACA TCTTTAAAT CCACCTCCCA ACCAGTCACT AAATTAGCCA 1680
CAGAAAAAGA TATTCTCTTG ACTCTCAGA CTGTGACTGA ACTGCCACT CACACTGTGG 1740
AAGTACTTTC AGCCTCTTTA AATGATGGCT CTAAGACTGT TCTTAGATCT CCACATATGA 1800
ACTTGTGCGG AGCTGACGAA TCCTTAAATA CAGTTTCTAT AACAGAATAT GAGGAGGAGA 1860
GTTTATTGAC CAGTTTCAAG CTGTGACTG GAGCTGAAGA TTCTTCAGGC TCCAGTCCCG 1920
CAACTTCTGC TATCCCATTC ATCTCTGAGA ACATATCCCA AGGGTATATA TTTTCTCCG 1980
AAAACCCAG GACATAACAA TATGATGTCC TTATACCAGA ATCTGCTAGA AATGCTTCCG 2040
AAGATTCAAC TTCAATCAGG TCAGAGAAT CACTAAAGGA TCCTTCTATG GAGGGAAATG 2100
TGTGTTTCC TAGCTCTACA GACATAACAG CACAGCCCGA TGTGATGATCA GGCAGAGAGA 2160
GCTTCTCCA GACTAATTAC ACTGAGATAC GTGTGATGA ATCTGAGAAG ACAACCAAGT 2220
CCTTTCTGCG AGGCCAGTG ATGTCACAGG GTCCCTCAGT TACAGATCTG GAAATGCCAC 2280

```

	ATTATTCTAC	CTTTGCTTAC	TTCCCAACTG	AGGTAACACC	TCATGCTTTT	ACCCCATCCT	2340
	CCAGACAACA	GGATTTGGTC	TCCACGGTCA	ACGTGGGTATA	CTCGCAGACA	ACCCAACCGG	2400
	TATACAATGA	GGCCAGTAAT	AGTAGCCATG	AGTCTCGTAT	TGGTCTAGCT	GAGGGGTGG	2460
5	AATCCGAGAA	GAAGGCAATT	ATACCCCTTG	TGATCGTGTC	AGCCCTGACT	TTTATCTGTC	2520
	TAGTGGTCT	TGTGGGTATT	CTCATCTACT	GGAGGAAATG	CTTCCAGACT	GCACACTTTT	2580
	ACTTAGAGGA	CAGTACATCC	CCTAGAGTTA	TATCCACACC	TCCAACACCT	ATCTTTCCAA	2640
	TTTCAGATGA	TGTCGGAGCA	ATTCCAATAA	AGCACTTTCC	AAAGCATGTT	GCAGATTTAC	2700
	ATGCAAGTAG	TGGGTTTACT	GAAGAAATTG	AGACACTGAA	AGAGTTTAC	CAGGAAGTGC	2760
10	AGAGCTGTAC	TGTTGACTTA	GGTATTACAG	CAGACAGCTC	CAACCAACCA	GACAACAAGC	2820
	ACAAGAAATCG	ATACATAAAT	ATCGTTGCCT	ATGATCATAG	CAGGGTTAAG	CTAGCACAGC	2880
	TGCTGAAAA	GGATGGCAAA	CTGACTGATT	ATATCAATGC	CAATTATGTT	GATGGCTACA	2940
	ACAGACCAAA	AGCTTATATT	GCTGCCCAAG	GCCCACTGAA	ATCCACAGCT	GAAGATTCTT	3000
	GGAGAAATGAT	ATGGGAACAT	AATGTGGAAG	TTATTGTCTAT	GATAACAAAC	CTCGTGGAGA	3060
	AAGGAAGGAG	AAAAATGTGAT	CAGTACTGGC	CTGCCGATGG	GAGTGAGGAG	TACGGGAACCT	3120
15	TTCTGGTCAC	TCAGAAAGAGT	GTGCAAGTGC	TGCGCTATTA	TACTGTGAGG	AATTTTACTC	3180
	TAGAAACACA	AAAAATAAAA	AGGGCTCCC	AGAAAGGAAG	ACCCAGTGGG	CGTGTGGTCA	3240
	CACAGTATCA	CTACACGCAG	TGGCCTGACA	TGGGAGTACC	AGAGTACTCC	CTGCCAGTGC	3300
	TGACCTTTGT	GAGAAAGGCA	GCCTATGCCA	AGCGCCATGC	AGTGGGGCCT	GTTGTCTGTC	3360
	ACTGCAAGTG	TGGAGTTGGA	AGAACAGGCA	CATATATTGT	GCTAGACAGT	ATGTTGCGAG	3420
20	AGATTCAACA	CGAAGGAACT	GTCAACATAT	TGGCTTCTT	AAAACACATC	CGTTCACAAA	3480
	GAATTTATTT	TGTACAAACT	GAGGAGCAAT	ATGTCTTCAT	TCATGATACA	CTGGTTGAGG	3540
	CCATACTTAG	TAAAGAAACT	GAGGTGCTGG	ACAGTCATAT	TCATGCCCTAT	GTTAATGCAC	3600
	TCCTCATTCC	TGGACCAAGCA	GGCAAAACAA	AGCTAGAGAA	ACAATTCAG	CTCCTGAGCC	3660
25	AGTCAAAATAT	ACAGCAGAGT	GACTATTCTG	CAGCCCTAAA	GCAATGCAAC	AGGGAAAAGA	3720
	ATCGAACTTC	TTCTATCATC	CCTGTGGAAA	GATCAAGGGT	TGGCATTTC	TCCCTGAGTG	3780
	GAGAAGGCAC	AGACTCAATC	AATGCCCTCT	ATATCATGGG	CTATTACCAG	AGCAATGAAT	3840
	TCATCATTAC	CCAGCACCTCT	CTCCTTCATA	CCATCAAGGA	TTTCTGGAGG	ATGATATGGG	3900
	ACCATAATGC	CCAACTGGTG	GTTATGATTG	CTGATGGCCA	AAACATGGCA	GAAGATGAAT	3960
30	TGTTTACTGC	GCCAAATAAA	GATGAGCCTA	TAAATTGTGA	GAGCTTTAAG	GTCACCTTAA	4020
	TGGCTGAAGA	ACACAAATGT	CTATCTAATG	AGGAAAAACT	TATAAATCAG	GACTTTATCT	4080
	TAGAAGCTAC	ACAGGATGAT	TATGTACTTG	AAGTGAGGCA	CTTTCAGTGT	CCTAAATGGC	4140
	CAATCCAGA	TAGCCCCATT	AGTAAACTTT	TGAACTTAT	AAGTGTGTATA	AAAGAAGAAG	4200
	CTGCCAAATAG	GGATGGGCGT	ATGATTGTTT	ATGATGAGCA	TGGAGGAGTG	ACGGCAGGAA	4260
35	CTTCTGTCGC	CTCAGCAACC	CTTATGCACC	AACTAGAAAA	AGAAAAATTC	GTGGATGTTT	4320
	ACCAGGTAGC	CAAGATGATC	AATCTGATGA	GGCCAGGAGT	CTTGTCTGAC	ATTGAGCAGT	4380
	ATCAGTTTCT	CTACAAAGTG	ATCTCAGCG	TGTGAGCAG	AAGGCAGGAA	GAGAATCCAT	4440
	CCACCTCTCT	GGACAGTAAT	GGTGACGAT	TGCGTATGG	AAATATAGCT	GAGAGCTTAG	4500
	AGTCTTTAGT	TTAACACAGA	AAGGGGTGGG	GGGACTCACA	TCTGAGCATT	GTTTCTCTCT	4560
40	TCCTAAAAAT	AGGCAGGAAA	ATCAGCTAG	TTCTGTTATC	TGTTGATTTC	CCATCACCTG	4620
	ACAGTAACTT	ACTGACATA	GGATTCTGCC	GCCAAATTTA	TATCATTAAC	AATGTGTGCC	4680
	TTTTTGCAAG	TCTGTATATT	TACTATTAT	GTTTGAACATA	AAATGATTGA	ATTTTACAGT	4740
	ATTTCTAAGA	ATGGAATTGT	GGTATTTTTT	TCTGTATTGA	TTTTAACAGA	AAATTTCAT	4800
	TTATAGAGGT	TAGGAATTCC	AAACTACAGA	AAATGTTTGT	TTTTAGTGTC	AAATTTTTAG	4860
45	CTGTATTGTT	AGCAATTATC	AGGTTTGCTA	GAAATATAAC	TTTTAATACA	GTAGCCTGTA	4920
	AATAAAACAC	TCTTCCATAT	GATATTCAAC	ATTTTACAAC	TGCAGTATTC	ACCTAAAGTA	4980
	GAAATAAATC	GTTACTTATT	GTAAATACTG	CCCTAGTGTC	TCCATGGAGC	AAATTTATAT	5040
	TTATAATTGT	AGATTTTTAT	ATTTTACTAC	TGAGTCAAGT	TTTCTAGTTC	TGTGTAATG	5100
	TTTAGTTTAA	TGACGTAGTT	CATTAGCTGG	TCTTACTCTA	CCAGTTTCTT	GACATTGTAT	5160
50	TGTGTTACCT	AAGTCATTAA	CTTTGTTTCA	GCATGTAATT	TTAACTTTTG	TGGAAAAATAG	5220
	AAATACCTTC	ATTTTGAAAG	AGGTTTTTAT	GAGAATAACA	CCTTACCAAA	CATTGTTCAA	5280
	ATGGGTTTTA	TCCAAGGAAT	TGCAAAAAATA	AATATAAATA	TTGCCATTAA	AAAAAAAATA	5340
	AAAAAAAATA	AAAAAAAATA	AAA				

Seq ID NO: 579 Protein sequence:
Protein Accession #: EOS sequence

	1	11	21	31	41	51	
60	MVFKASKITF	HWGKCNMSSD	GSEHSLEGQK	FPLEMQIYCF	DADRFSSFEE	AVKGGKGLRA	60
	LSILFEVQTE	ENLDFKALID	GVEVSRRFGK	QAALDPFILL	NLLPNSDQKY	YIYNGSLTSP	120
	PCTDITVDIV	FKDTVSISSE	QLAVFCEVLT	MQQSGYVMLM	DYLQNNFREQ	QYKFSRQVPS	180
	SYTGKEEIEH	AVCSSEPENV	QADPENYTSL	LVTWERPRVV	YDTMIEKFAV	LVQQLDGEDQ	240
	TRHEFLTDTG	QDLGAILNNL	LPNMSYVLQI	VAICTNGLYG	KYSDQLIVDM	PTDNPELDF	300
65	PELIGTEBII	KEEEEGKDIE	EGAIVNPGRD	SATNQIRKKE	PQISTTTTHYN	RIGTKYNEAK	360
	TNRSPTRGSE	PSGKQDVPT	SLNSTSQPV	KLATEKDIDL	TSQTVTELPP	HTVEGTSASL	420
	NDGSKTVLRS	PHMNLSTAE	SLNTVSITEY	EEESLLTBFK	LDTGAEDSSG	SSPATSAIPP	480
	ISENISQGYI	FSSNPETIT	YDVLIPESAR	NASEDSTSSG	SEESLKDPSM	EGNVWFPSST	540
	DITAQPDVGS	GRESFLQNTY	TEIRVDESEK	TKSFSAGPV	MSQGPSVTDL	EMPHYSTPAY	600
70	FPTEVTPHAF	TPSSRQQLDV	STVNVVYSQT	TQFVYNEASN	SSHESRIGLA	EGLESEKKAV	660
	IPLVIVSALT	FICLVVLVGI	LIYWRKCFQT	AHFVLEDSTS	FRVISTPPTP	IFPISDDVGA	720
	IPIKHPPKHV	ADLHASSGFT	EEFETLKRFY	QEVQSTVDL	GITADSSNHP	DNKHKNRYIN	780
	IVAYDHSRVK	LAQLAEKDGK	LTDYINANYV	DGYNRPKAYI	AAQGPLKSTA	EDFWRMIWEH	840
	NVEIVMITN	LVEKGRRKCD	QYWPADGSEE	YGNFLVTQKS	VQVLAYYTVR	NFTLRNTRIK	900
75	KGSQKGRPSG	RVVTQVHYTQ	WPDMGVPEYS	LPVLTFFVRKA	AYAKRHAVGP	VVHCSAGVG	960
	RTGYIYVLDS	MLQIQHEGT	VNIFGFLKHI	RSQRNYLVQT	EEQYVFIHDT	LVEAILSKET	1020
	EVLDSHIHAY	VNALLIPGPA	GKTKLEKQFO	LLSQSNIQQS	DYSAALKQCN	REKNRTSSII	1080
	PVERSRVGIS	SLSGEGTDYI	NASYIMGYQ	SNEFIITQHP	LLHTIKDFWR	MIWDHNAQLV	1140
	VIMPDGQDMA	EDFVYWPNK	DEPINCESFK	VTLMABEHKC	LSNEEKLIQ	DFILEATQDD	1200
80	YVLEVRHFQC	PKWNPDPSKI	SKTFELISVI	KEEAANRDGP	MIHDEHGGV	TAGTFCALTT	1260
	LMHQLEKENS	VDVYQVAKMI	NLMRPGVPAD	IEQYQFLYKV	ILSLVSTRQE	ENPSTSLDSN	1320
	GAALPDGNIA	ESLESVL					

Seq ID NO: 580 DNA sequence
Nucleic Acid Accession #: EOS sequence
Coding sequence: 148-4632

	1	11	21	31	41	51
--	---	----	----	----	----	----

	CACACATACG	CACGCACGAT	CTCACTTCGA	TCTATACACT	GGAGGATTAA	AACAAACAAA	60
	CAAAAAAAC	ATTTCTTCG	CTCCCCCTCC	CTCTCCACTC	TGAGAAGCAG	AGGAGCCGCA	120
5	CGGCGAGGGG	CCGCAGACCG	TCCTGGAAATG	CGAATCCTAA	AACGTTTCCT	CGCTTGCAAT	180
	CAGCTCCTCT	GTGTTTGCCG	CCTGGATTGG	GCTAATGGAT	ACTACAGACA	ACAGAGAAAA	240
	CTTGTTGAAG	AGATTGGCTG	GTCTATACA	GGAGCACTGA	ATCAAAAAAA	TGGGGGAAAG	300
	AAATATCCAA	CATGTAATAG	CCCAAAACAA	TCTCCTATCA	ATATTGATGA	AGATCTTACA	360
	CAAGTAAATG	TGAATCTTAA	GAACCTTAAA	TTTCAGGGTT	GGGATAAAAC	ATCATTGGAA	420
10	AACACATTCA	TTCATAAAC	TGGGAAAAACA	GTGGAAATTA	ATCTCACTAA	TGACTACCGT	480
	GTACGCGGAG	GAGTTTCAGA	AATGGTGTGT	AAAGCAAGCA	AGATAACTTT	TCACTGGGGA	540
	AAATGCAATA	TGTCATCTGA	TGGATCAGAG	CATAGTTTAG	AAGGACAAAA	ATTTCCACTT	600
	GAGATGCAAA	TCTACTGCTT	TGATGCGGAC	CGATTTTCAA	GTITTTGAGGA	AGCAGTCAAA	660
	GGAAAAGGGA	AGTTAAGAGC	TTTATCCATT	TTGTTTGAGG	TTGGGACAGA	AGAAAATTTG	720
	GATTTCAAAG	CGATTATTTG	TGGAGTCGAA	AGTGTTAGTC	GTITTTGGGAA	GCAGGCTGCT	780
15	TTAGATCCAT	TCATACTGTT	GAACCTTCTG	CCAAACTCAA	CTGACAAGTA	TTACATTTAC	840
	AATGGCTCAT	TCCATCTCC	TCCCTGCACA	GACACAGTTG	ACTGGATTGT	TTTAAAGAT	900
	ACAGTTAGCA	TCTCTGAAG	CCAGTTGGCT	GTITTTTGTG	AAGTTCTTAC	AATGCAACAA	960
	TCTGGTTATG	TGATGCTGAT	GGACTACTTA	CAAAACAATT	TTCCAGAGCA	ACAGTACAAG	1020
20	TTCTCTAGAC	AGGTGTTTTC	CTCATACACT	GGAAAGGAAG	AGATTCTAGA	AGCAGTTTGT	1080
	AGTTCAGAAC	CAGAAAATGT	TCAGGCTGAC	CCAGAGAATT	ATACCAGCCT	TCTTGTTACA	1140
	TGGGAAAGAC	TCGAGTCTG	TTATGATACC	ATGATTGAGA	AGTTTGCAGT	TTTGTACCAT	1200
	CAGTTGGATG	GAGAGGACCA	AACCAAGCAT	GAATTTTGA	CAGATGGCTA	TCAAGACTTG	1260
	GGTGCTATTG	TCAATAATT	GCTACCCAAT	ATGAGTTATG	TTCTTCAGAT	AGTAGCCATA	1320
25	TGCACTAATG	GCATTATTTG	AAAATACAGC	GACCAACTGA	TTGTGACAT	GCCTACTGAT	1380
	AATCTGTAAC	TGATCTTTT	CCCTGAATTA	ATTGGAAGTG	AAGAAATAAT	CAAGGAGGAG	1440
	GAAGAGGGAA	TAGACATCTG	AGAAGGCGCT	ATTGTGATC	CTGGTAGAGA	CAGTGCATCA	1500
	AACCAATCA	GGAAAAAGGA	ACCCAGATT	TCTACCACAA	CACACTACAA	TCGCATAGGG	1560
	ACGAATACA	ATGAAGCCAA	GACTAACCGA	TCCCCAACAA	GAGGAAGTGA	ATTCTCTGGA	1620
30	AAGGTGATG	TTCCCAATAC	ATCTTTAAAT	TCCACTTCCC	AACCACTCAC	TAAATTAGCC	1680
	ACAGAAAAAG	ATATTTCTTT	GACTTCTCAG	ACTGTGACTG	AACCTGCCAC	TCACACTGTG	1740
	GAAGGTACTT	CAGCTCTTT	AAATGATGGC	TCTAAACTG	TTCTTAGATG	TCCACATATG	1800
	AACCTGTGCG	GGACTGCGA	ATCCTTAAAT	ACAGTTTCTA	TAACAGAATA	TGAGGAGGAG	1860
	AGTTTATTGA	CCAGTTTCAA	GCTTGATACT	GGAGCTGAAG	ATTCTTCAGG	CTCCAGTCCC	1920
35	GCAACTCTCG	CTATCCCAT	CATCTCTGAG	AACATATCCC	AAGGGTATAT	ATTTTCTCTC	1980
	GAAGAACCCAG	AGACAATAAC	ATATGATGTC	CTTATACAG	AATCTGCTAG	AAATGCTTCC	2040
	GAAGATTCAA	TTCTCATCAG	TTCAAGAGAA	TCACTAAAGG	ATCCTTCTAT	GGAGGGAAT	2100
	GTGTGGTTTC	CTAGCTCTAC	AGACATAACA	GCACAGCCCG	ATGTTGGATC	AGGCAGAGAG	2160
	AGCTTCTCCC	AGACTAATTA	CACAGAGATA	CGTGTGATG	AATCTGAGAA	GACAACCAAG	2220
40	TCCTTTCTCG	CAGGCCAGT	GATGTCACAG	GGTCCCTCAG	TTACAGATCT	GGAAATGCCA	2280
	CATTATTCTA	CTTTGCGCTA	CTTCCCAACT	GAGGTAAAC	CTCATGCTTT	TACCCCATCC	2340
	TCCAGACAAC	AGATTTTGGT	CTCCACGGTC	AACGTGGTAT	ACTCGCAGAC	AACCCAAACC	2400
	GTATACAATG	AGGCCAGTAA	TAGTAGCCAT	GAGTCTCGTA	TTGGTCTAGC	TGAGGGGTTG	2460
	GAATCCGAGA	AGAAGGCAGT	TATACCCCTT	GTGATCGTGT	CAGCCCTGAC	TTTTATCTGT	2520
45	CTAGTGGTTC	TTGTTGGTAT	TCTCATCTAC	TGGAGGAAAT	GCTTCCAGAC	TGCACACTTT	2580
	TACTTAGAGG	ACAGTACATC	CCCTAGAGTT	ATATCCACAC	CTCCAACACC	TATCTTTCCA	2640
	ATTTAGATG	ATGTCGAGC	AATTCCAATA	AAGCACTTTC	CAAAGCATGT	TGCAGATTTA	2700
	CATGCAAGTA	TGTGGTTTAC	TGAAGAATTT	GAGACACTGA	AAGAGTTTAA	CCAGGAAGTG	2760
	CAGAGCTGTA	CTGTTGAATT	AGGTATTACA	GCAGACAGCT	CCAACCAACC	AGACAACAAG	2820
50	CACAAGAATC	GATACATAAA	TATCGTTGCC	TATGATCATA	GCAGGGTTAA	GCTAGCACAG	2880
	CTTGCTGAAA	AGGATGGCAA	ACTGACTGAT	TATATCAATG	CCAATTATGT	TGATGGCTAC	2940
	AACAGACCAA	AAGCTTATAT	TGCTGCCCAA	GGCCCACTGA	AATCCACAGC	TGAAGATTTC	3000
	TGGAGAAATG	TATGGGAACA	TAATGTGGAA	GTATTGTGTA	TGATAACAAA	CCTCGTGGAG	3060
	AAAGGAAGGA	GAAATATGTA	TCAGTACTGG	CCTGCGGATG	GGAGTGAGGA	GTACGGGAAG	3120
55	TTTCTGGTCA	CTCAGAAGAG	TGTGCAAGTG	CTTGCTTATT	ATACTGTGAG	GAATTTTACT	3180
	CTAAGAAACA	CAAAAAATAA	AAAGGGCTCC	CAGAAAGGAA	GACCCAGTGG	ACGTGTGGTC	3240
	ACACAGTATC	ACTACAGCCA	GTGGCCTGAC	ATGGGAGTAC	CAGAGTACTC	CCTGCCAGTG	3300
	CTGACCTTTG	TGAGAAAGGC	AGCCTATGCC	AAGCGCCATG	CAGTGGGGCC	TGTTGTCTGC	3360
	CAGTCAAGTG	CTGGAGTTGG	AGAACAAGGC	ACATATATTG	TGCTAGACAG	TATGTTGACG	3420
60	CAGATTCAAC	ACGAAGGAAC	TGTCAACATA	TTTGGCTTCT	TAAACACAT	CCGTTCACAA	3480
	AGAAATATT	TGTTACAAAC	TGAGGAGCAA	TATGTTCTCA	TTTATGATAC	ACTGGTTGAG	3540
	GCCATACTTA	GTAAGAAAC	TGAGGTGCTG	GACAGTCAATA	TTTATGCCTA	TGTTAATGCA	3600
	CTCCTCATTC	CTGGACGAGC	AGGCAAAACA	AAGCTAGAGA	AACAATTCCA	GGGTCTCACT	3660
	CTGTCAACCA	GGCTGGAATG	CAGAGGCACA	ATCTCGGCTC	ACTGCAACCT	TCTCTCTCCT	3720
65	GGCTTAACCTG	ATCTCTCTAC	CTCAGCCTCC	CGAGTGGCTG	GGACTATACT	CCTGAGCCAG	3780
	TCAATATATC	AGCAGAGTGA	CTATTCTGCA	GCCCTAAAGC	AATGCAACAG	GGAAAAGAA	3840
	CGAATCTCTT	CTATCATCCC	TGTTGAAAGA	TCAAGGGTTG	GCATTTCACT	CCTGAGTGGA	3900
	GAAGGCACAG	ACTACATCAA	TGCTCTCTAT	ATCATGGGCT	ATTACAGAG	CAATGAATTC	3960
	ATCATTACCC	AGCACCTCT	CCTTCATACC	ATCAAGGATT	TCTGGAGGAT	GATATGGGAC	4020
70	CATAATGCC	AATGTTGGT	TATGATTCTT	GATGGCCAAA	ACATGGCAGA	AGATGAATTT	4080
	GTTTACTGGC	CAAAATAAGA	TGAGCCTATA	AATGTGAGA	GCTTTAAGGT	CACTCTTATG	4140
	GCTGAAGAAC	ACAAATGTCT	ATCTAATGAG	GAAAAACCTA	TAATTCAGGA	CTTTATCTTA	4200
	GAAGCTACAC	AGGATGATTA	TGTACTTGAA	GTGAGGCACT	TTTCAATGTC	TAAATGGCCA	4260
	AATCCAGATA	GCCCCATTAG	TAAAACTTTT	GAACCTTATA	GTGTTATAAA	AGAAGAAAGT	4320
75	GCATATAGGG	ATGGGCTCT	GATTGTTTCT	GATGAGCATG	GAGGAGTGAC	GGCAGGAACT	4380
	TTCTGTGCTC	TGACAAACCT	TATGCCCAA	CTAGAAAAAG	AAAATTCCGT	GGATGTTTAC	4440
	CAGGTAGCCA	AGATGATCAA	TCTGATGAGG	CCAGGAGTCT	TTGCTGACAT	TGAGCAGTAT	4500
	CAGTTTCTCT	ACAAAGTGAT	CCTCAGCCTT	GTGGGCACAA	GGCAGGAAGA	GAATCCATCC	4560
	ACCTCTCTGG	ACAGTAAATG	TGCAGCAATT	CCTGATGGAA	ATATAGCTGA	GAGCTTAGAG	4620
80	TCTTTAGTTT	AACACAGAAA	GGGGTGGGGG	GACTCACATC	TGAGCATTTG	TTTCTCTTTC	4680
	CTAAAATTAG	GCAGGAAATG	CAGTCTAGTT	CTGTTATCTG	TTGATTTCCC	ATCACCTGAC	4740
	AGTAACCTTC	ATGACATAGG	ATTCTGCCGC	CAAAATTTATA	TCATTAAACA	TGTGTGCCTT	4800
	TTTGCAAGAC	TTGTAATTTA	CTTATTATGT	TTGAACTAAA	ATGATTGAAT	TTTACAGTAT	4860
	TTCTAAGAA	GGAAATGTGG	TATTTTTTTC	TGTATTGATT	TTAACAAGAA	ATTTCAATTT	4920
85	ATAGAGGTTA	GGAAATCCAA	ACTACAGAAA	ATGTTTGTGT	TTAGTGTCAA	ATTTTGTAGT	4980
	GTATTGTAG	CAATTATCTG	GTTTGCTAGA	AATATAACTT	TTAATACAGT	AGCCTGTAAA	5040
	TAAAAACATC	TTCCATATGA	TATTCACAT	TTTCAACTG	CAGTATTCAC	CTAAAGTAGA	5100
	AATAATCTGT	TACTATTGTT	AAATACTGCC	CTAGTGTCTC	CATGGACCAA	ATTTATATTT	5160

5
 10
 15
 20
 25
 30
 35
 40
 45
 50
 55
 60
 65
 70
 75
 80
 85

ATAATTGTAG ATTTTATAT TTTACTACTG AGTCAAGTTT TCTAGTCTCG TGTAATTGTT 5220
 TAGTTAATG ACGTAGTTCA TTAGCTGGTC TTACTCTACC AGTTTCTCGA CATTGTATTG 5280
 TGTACCTTAA GTCAATTAAC TTGTTTCAGC ATGTAATTTT AACTTTTGTG GAAATAGAAA 5340
 ATACCTTCAT TTTGAAAGAA GTTTTATGTA GAATAACACC TTACCAACA TGTGTTCAAT 5400
 GGTTTTTATC CAAGGAATTG CAAAATAAAA TATAAATATT GCCATTAAAA AAAAAAATAA 5460
 AAAAAAAAAA AAAAAAAAAA A

Seq ID NO: 581 Protein sequence:
 Protein Accession #: EOS sequence

1 11 21 31 41 51
 MRILKRFLAC IQLLCVCRLD WANGYYRQQR KLVEEIGWSY TGALEQKQNG KKYPCTNSPK 60
 QSPINIDEDL TVQNVNKKKL KFGGWDKTSL ENTFIHNTGK TVEINLTNDY RVSGGVSEMV 120
 FKASKITHFW GKCNMSDGS EHSLEGQKFP LEMQIYCFDA DRFSSFEAV KGKGLRLALS 180
 ILFEVGTEN LDFKAIIDGV ESVSRFGKQA ALDPFILLNL LPNSTDKYYI YNGSLTSPPC 240
 TDTVDVIVFK DTVSISESQL AVFCEVLTMQ QSGYVLMMDY LQNNFREQQY KPSRVQVSSY 300
 TGKEIEHEAV CSSEPEENVQA DPENYTSLLV TWERPRVVDY TMIEKFAVLY QQLDGEDQTK 360
 HEFLTGDYQD LGAILNNLLP NMSYVLQIVA ICTNGLYKGY SDQLIVDMPT DNPELDLFPK 420
 LIGTEEIIKE EEEGKDIEEG AIVNPGRDSA TNQIRKKEPY ISTTHYNNRI GTKYNEAKTN 480
 RSPTRGSEFS GKGDVPNTSL NSTSQPVTKL ATEKDISLTS QTVELPPTPH VEGTSASLND 540
 GSKTVLRSPH MNLSTGTAESL NTVSITYEY ESLTTSFKLD TGAEDSSGSS PATSAIPFIS 600
 ENISQGYIFS SENPETITYD VLIPESARNA SEDSTSSGSE ESLKDPMEG NVWFPSSDI 660
 TAQPDVGSGR ESFLQNTYTE IRVDESEKTT KSFSGAPVMS QGPSVTDLEM PHYSTFAYFP 720
 TEVTHAATP SSRQDLVST VNVVYSQTQ PVYNEASNS HESRIGLAEG LESEKKAVIP 780
 LVIVSALTPI CLVVLVGILI YWRKCPQTAH FYLEDSTSPR VISTPPTPI PISDDVGAIP 840
 LKHFPKHVAD LHASSGFTTE FETLKEFYQE VQSCVDLGI TADSSNHPDN KHKRYINIV 900
 AYDHSRVKLA QLAEKDKKLT DYINANYVDG YNRPKAYIAA QGPLKSTAE FWRMIWEHNV 960
 EVIVMITHLV KEGRRKCDQY WADGSESEY NFLVTQKSVQ VLAYYTVRNP TLRNTKIKKG 1020
 SQKGRPSGRV VTQVHYTQWP DMGVPEYSLP VLTFRVKAAY AKRHAVGPVV VHCSAGVGRT 1080
 GTYIVLDSML QQIQHEGTVN IFGFLKHIRS QRNYLVQTEE QYVFIHDTLV EALLSKETE 1140
 LDSHIHAYVN ALLIPGPAGK TKLEKQFQGL TSPRLRCRG TISAHCNLPL PGLTDPPTSA 1200
 SRVAGTILLS QSIHQSDYS AALKQCNREK NRTSSIIPE RSRVGISLS GEGTDYINAS 1260
 YIMGYQNE FIITQHPLH TIKDFWRMIW DHNAQLVMI PDQONMAE DE FVYWPKNKDE 1320
 INCESPKVTL MAEHEKCLSN EEKLIQDFI LEATQDDYVL EVRHFGCPKW PNPDSPIST 1380
 FELISVIKEE AANRDGPVIV HDEHGGVTAG TFCALTLMH QLEKENSVDV YQVAKMINLM 1440
 RFGVFADIEQ YQFLYKIVLS LVGTRQEENP STSLDSNGAA LPDGNIAESL ESLV

Seq ID NO: 582 DNA sequence
 Nucleic Acid Accession #: NM_002851.1
 Coding sequence: 148..7092

1 11 21 31 41 51
 CACACATACG CACGCACGAT CTCACCTCGA TCTATACACT GGAGGATTAA AACAAACAAA 60
 CAAAAAAAC ATTTCTCTCG CTCCTCCCTCC CTCTCCACTC TGAGAAGCAG AGGAGCCGCA 120
 CGGCGAGGGG CCGCAGACCG TCTGGAAATG CGAATCTCAA AGCGTTTCCT CGCTTGCATT 180
 CAGCTCCTCT GTGTTTCCCG CCTGGAATGG GCTAATGGAT ACTACAGACA ACAGAGAAAA 240
 CTGTGTTGAG AGATTGCTCG GTCCCTATACA GGAGCAGCTGA ATCAAAAAAA TTGGGGAAAG 300
 AAATATCAAA CATGTAATAG CCCAAACAAA TCTCTATCA ATATTGATGA AGATCTTACA 360
 CAAGTAAATG TGAATCTTAA GAAACTTAAA TTTGAGGTTT GGGATAAAAC ATCATTGGAA 420
 AACACATTCA TTCATAACAC TGGGAAAACA GTGGAAATTA ATCTCACTAA TGACTACCGT 480
 GTACGCGGAG GAGTTTTCAGA AATGGTGTTT AAAGCAAGCA AGATAACTTT TCACTGGGGA 540
 AAATGCAATA TGTCTCTGTA TGGATCAGAG CATAGTTTAG AAGGACAAA ATTTCCACTT 600
 GGATGCAAAA TCTACTGCTT TGATGCGGAC CGATTTTCAA GTTTTGAGGA AGCAGTCAAA 660
 GGAAAGGGA AGTTAAGAGC TTTATCCATT TTGTTGAGG TTGGGACAGA AGAAAATTG 720
 GATTTCAAAG CGATTATTGA TGGAGTCGAA AGTGTTAGTC GTTTTGGA GAGGCTGCT 780
 TTGATCCAT TCTACTGTT GAACCTCTG CCAAACTCAA CTGACAGTA TTACTTTTAC 840
 AATGGCTCAT TGACATCTCC TCCTGCGACA GACACAGTTG ACTGGATTGT TTTTAAAGAT 900
 ACAGTTAGCA TCTCTGAAAG CCAGTTGGCT GTTTTGTG AAGTCTTAC AATGCAACAA 960
 TCTGTTATG TCTGCTGAT GGACTACTTA CAAACAAAT TCGAGAGCA ACAGTACAAG 1020
 TTCTCTAGAC AGGTGTTTTT CTCATACACT GGAAGGAAG AGATTCTGA AGCAGTTTGT 1080
 AGTTCAGAAC CAGAAAATGT TCAGGCTGAC CCAGAGAATT ATACCAGCT TCTTGTTACA 1140
 TGGGAAAGAC CTGAGTCGT TTATGATACC ATGATTGAGA AGTTTGCAGT TTTGTACCAG 1200
 CAGTTGGATG GAGAGGACCA AACCAAGCAT GAATTTTGA CAGATGGCTA TCAAGACTTG 1260
 GGTGCTATTC TCAATAATTT GCTACCCAAT ATGAGTTATG TTCTTCAGAT AGTAGCCATA 1320
 TGCATAATG GCTTATATG AAAATACAGC GACCAACTGA TTGTCCAGAT GCCTACTGAT 1380
 AATCCTGAAC TTGATCTTTT CCTGGAATTA ATTGGAAGT AAGAAATAAT CAAGGAGGAG 1440
 GAAGAGGGAA AAGACATTGA AGAAGCGCT ATTGTGAATC CTGGTAGAGA CAGTGCTACA 1500
 AACCAATCA GGAAGGGA ACCTCAGATT TCTACCAACA CACTACACA TCGCATAGG 1560
 ACGAAATACA ATGAAGCAA GACTAACCGA TCCCAACAA GAGGAAGTGA ATTCTCTGGA 1620
 AAGGTGATG TTCCAATAC ATCTTTAAAT TCCACTTCCC AACCACTCAC TAAATTAGCC 1680
 ACAGAAAAAG ATATTTCTCT GACTTCTCAG ACTGTGACTG AACTGCCACC TCACACTGTG 1740
 GAAGGTACTT CAGCCTCTTT AATGATGGC TCTAAAACCTG TTCTTAGATC TCCACATATG 1800
 AACTTGTGCG GAGCTGCGA ATCTTAAAT ACAGTTTCTA TAACAGAATA TGAGGAGGAG 1860
 AGTTTATTGA CAGTTTCAA GCTTGATACT GGAGCTGAAG ATTCTTCAGG CTCCAGTCCC 1920
 GCACTCTCTG CATCTCCATT CATCTCTGAG AACATATCCC AAGGGTATAT ATTTCTCTCC 1980
 GAAAACCCAG AGACAATAAC ATATGATGTC CTTATACCAG AATCTGCTAG AAATGCTTCC 2040
 GAAGATTCAA CTTCATCAGG TTCAGAAAG TCACTAAAGG ATCTCTCTAT GGAGGAAAT 2100
 GTGTGTTCTG CTAGCTCTAC AGACATAACA GCACAGCCCG ATGTTGGATC AGGCAGAGAG 2160
 AGCTTTCTCC AGACTAATTA CACTGAGATA CGTGTGATG AATCTGAGAA GACAACCAAG 2220
 TCTTTTCTG CAGGCCAGT GATGTACAG GGTCCCTCAG TTACAGATCT GGAATAGCCA 2280
 CATTATTCTA CCTTGCCTA CTTCCTCACT GAGGTAAAC CTCTGCTTT TACCCATCC 2340
 TCCAGACAAC AGGATTTGGT CTCCACGGT AACGTGGTAT ACTCGCAGAC AACCCAACCG 2400
 GTATACAAAG GTGAGACACC TCTTCAACCT TCCTACAGTA GTGAAGTCTT TCCTCTAGTC 2460
 ACCCTTTTGT TGCTTGACAA TCAGATCTCT AACACTACCC CTGCTGCTTC AAGTAGTGAT 2520

	TCGGCCTTGC	ATGCTACGCC	TGTATTTCCT	AGTGTGATG	TGTCATTGGA	ATCCATCCTG	2580
	TCTTCCTATG	ATGGTGCACC	TTTGCTTCCA	TTTTCCTCTG	CTTCCTTCAG	TAGTGAATTG	2640
	TTTCGCCATC	TGCATACAGT	TTCTCAAATC	CTTCACAAAG	TTACTTCAGT	TACCGAGAGT	2700
5	GATAAGGTGC	CTTGTGCATG	TTCTCTGCCA	GTGGCTGGGG	GTGATTGTCT	ATTAGAGCCC	2760
	AGCCTTGCTC	AGTATTCTGA	TGTGCTGTCC	ACTACTCATG	CTGCTTCAGA	GACGCTGGAA	2820
	TTTGTAGTGG	AATCTGGTGT	TCTTTATAAA	ACGCTTATGT	TTTCTCAAGT	TGAACCACCC	2880
	AGCAGTGATG	CCATGATGCA	TGCACGTTCT	TCAGGGCCTG	AACCTTCTTA	TGCCTTGTCT	2940
	GATAATGAGG	GCTCCCAACA	CATCTTCACT	GTTTCTTACA	GTTCTGCAAT	ACCTGTGCAT	3000
10	GATTCTGTGG	GTGTAACCTT	TCAGGGTTCC	TTATTAGCGG	GCCTAGCCA	TATACCAATA	3060
	CCTAAGTCTT	CGTTAATAAC	CCCAACTGCA	TCATTACTGC	AGCCTACTCA	TGCCCTCTCT	3120
	GGTGATGGGG	AATGGTCTGG	AGCCTCTTCT	GATAGTGAAT	TTCTTTTACC	TGACACAGAT	3180
	GGGCTGACAG	CCCTTAACAT	TTCTTCACTT	GTTTCTGTAG	CTGAATTTAC	ATATACAAAC	3240
	TCTGTGTTTG	GTGATGATAA	TAAGGCGCTT	TCTAAAAGTG	AAATAATATA	TGGAAATGAG	3300
	ACTGAACCTG	GAATTCCTTC	TTTCAATGAG	ATGGTTTACC	CTTCTGAAAG	CACAGTCATG	3360
15	CCCAACATGT	ATGATAATGT	AAATAAGTTG	AATGCGTCTT	TACAAGAAAC	CTCTGTTTCC	3420
	ATTCTTAGCA	CCAAAGGCTG	TTTCCAGGG	TCCCTTGCTC	ATACCAACCAC	TAAGGTTTTT	3480
	GATCATGAGA	TTAGTCAAGT	TCCAGAAAAT	AACCTTTTCA	TTCAACCTAC	ACATACTGTC	3540
	TCTCAAGCAT	CTGGTGACAC	TTGCCTTAAA	CCTGTGCTTA	GTGCAAACTC	AGAGCCAGCA	3600
20	TCCTCTGACC	CTGCTTCTAG	TGAAATGTTA	TCTCCTTCAA	CTCAGCTCTT	ATTTTATGAG	3660
	ACCTCAGCTT	CTTTTAGTAC	TGAAGTATTG	CTACAACCTT	CCTTTTCAAG	TTCTGATGTT	3720
	GACACCTTGC	TAAACAGCTG	TCTTCCAGCT	GTGCCAGATG	ATCCAATATT	GGTTGAAACC	3780
	CCCAAGTTTG	ATAAAATTAG	TTCTACAATG	TGCACTCTCA	TTGTATCAAA	TTCTGCTTCA	3840
	AGTGAACAAA	TGCTGCACTC	TACATCTGTA	CCAGTTTTTG	ATGTGTGCTC	TACTTCTCAT	3900
25	ATGCACCTCT	CTTCACTCTA	AGGTTTGACC	ATTTCTTATG	CAAGTGAGAA	ATATGAACCA	3960
	GGTTTGTATA	AAAGTGAAAG	TTCCCAACAA	GTGGTACCTT	CTTTGTACAG	TAATGATGAG	4020
	TGTTTCCAAA	CGGCCAATTT	GGAGATTAA	CAGGCCCATC	CCCAAAAGG	AAGGCATGTA	4080
	TTTGCTACAC	CTGTTTTATC	AATTGATGAA	CCATTAAATA	CACATAATAA	TAAGCTTATA	4140
	CATTCCGATG	AAATTTTAA	CTCCACCAAA	AGTTCTGTTA	CTGGTAAGGT	ATTTGCTGGT	4200
30	ATTCCAACAG	TGCTTCTCTA	TACATTTGTA	TCTACTGATC	ATTCTGTCTC	TATAGGAAAT	4260
	GGGCATGTTT	CCATTACAGC	TGTTTCTCCC	CACAGAGATG	GTCTGTGAAC	CTCAACAAAG	4320
	TTGCTGTTTC	CTCTAAGGCT	AACTTCTGAG	CTGAGTCATA	GTGCCAAATC	TGATGCCGGT	4380
	TTAGTGGGTG	GTGGTGAAGA	TGGTGACACT	GATGATGATG	GTGATGATGA	TGATGACAGA	4440
	GATAGTGATG	GCTTATCCAT	TCATAAGTGT	ATGTCATGCT	CATCCTATAG	AGAATCAACG	4500
35	GAAAAGGTAA	TGAATGATTC	AGACACCCAC	GAAAACAGTC	TTATGGATCA	GAATAATCCA	4560
	ATCTCATACT	CACATCTGTA	GAATTCGTGA	GAAGATAATA	GAGTCACAAG	TGATCTCTCA	4620
	GACAGTCAAA	CTGGTAGTGA	CAGAACTCCT	GGTAAATCAC	CATCAGCAAA	TGGGCTATCC	4680
	CAAAAGCACA	ATGATGGAAG	AGAGGAAAT	GACATTGAGA	CTGGTAGTGC	TCTGCTTCTC	4740
	CTCAGCCCTG	AATCTAAAGC	ATGGGCAGTT	CTGACAAGTG	ATGAAGAAAG	TGGATCAGGG	4800
40	CAAGGTACCT	CAGATAGCCT	TAATGAGAAT	GAGACTTCCA	CAGATTTCAG	TTTTGCAGAC	4860
	ACTAATGAAA	AAGATGCTGA	TGGGATCCCT	GCAGCAGGTG	ACTCAGAAAT	AACTCCTGGA	4920
	TTCCACAGTG	CCCCAACATC	ATCTGTTACT	AGCGAGAACT	CAGAAGTGTG	CCACGTTTCA	4980
	GAGGCAGAGG	CCAGTAATAG	TAGCCATGAG	TCTCGTATTG	GTCTAGCTGA	GGGGTTGGAA	5040
	TCCGAGAAGA	AGGCAGTTAT	ACCCCTTGTG	ATCGTGTGAG	CCCTGACTTT	TATCTGCTTA	5100
45	GTGGTTCTTG	TGGGTATTCT	CATCTACTGG	AGGAAATGCT	TCCAGACTGC	ACACTTTTAC	5160
	TTAGAGGACA	GTACATCCCC	TAGAGTTATA	TCCACACCTC	CAACACCTAT	CTTTCCAATT	5220
	TCAGATGATG	TCCGAAGCAAT	CACCTTCCAA	AGCATGTTGC	AGATTATACAT	AGATTATACAT	5280
	GCAAGTAGTG	GGTTTACTGA	AGAAATTGAG	ACACTGAAAG	AGTTTACCA	GGAAAGTGAG	5340
	AGCTGTACTG	TTGACTTAGG	TATTACAGCA	GACAGCTCCA	ACCAACCCAG	CAACAGCAC	5400
50	AAGAATCGAT	ACATAAATAT	CGTTGCCTAT	GATCATAGCA	GGGTTAAGCT	AGCACAGCTT	5460
	GCTGAAAAGG	ATGGCAAAAT	GACTGATTAT	ATCAATGCCA	ATTATGTTGA	TGGCTACAA	5520
	AGACCAAAAG	CTTATATTGC	TGCCCAAGGC	CCACTGAAAT	CCACAGCTGA	AGATTCTGG	5580
	AGAATGATAT	GGGAACATAA	TGTGGAAGTT	ATTGTCTATG	TAACAAACCT	CGTGAGAGAA	5640
	GGAGGAGGAA	AATGTGATCA	GTACTGGCCT	GCCGATGGGA	GTGAGGAGTA	CGGGAACCTT	5700
55	CTGGTCACTC	AGAAGAGTGT	GCAAGTGCTT	GCCTATTATA	CTGTGAGGAA	TTTTACTCTA	5760
	AGAAACACAA	AAATAAAAAA	GGGCTCCCAG	AAAGGAAGAC	CCAGTGGAGC	TGTGGTCACA	5820
	CAGTATCACT	ACACGCACTG	GCCTGACATG	GGAGTACCAG	AGTACTCCCT	GCCAGTGCTG	5880
	ACCTTTGTGA	GAAAGGCAGC	CTATGCCAAG	CGCCATGCAG	TGGGGCCTGT	TGTCGTCCAC	5940
	TGCAATGCTG	GAGTTGGAAG	AACAGGCACA	TATATTGTGC	TAGACAGTAT	GTTCAGCAGC	6000
60	ATTCAACACG	AAGGAAGTGT	CAACATATTT	GGCTTCTTAA	AACACATCCG	TTCAACAAAG	6060
	AATTATTGTT	TACAACTCTA	GGAGCAATAT	GTCTTCATTC	ATGATACACT	GGTTGAGGCC	6120
	ATACTTAGTA	AAGAACTCTA	GGTGCTGGAC	AGTCATATTC	ATGCCATATG	TAATGCACCT	6180
	CTCATTCTCT	GAGCAGCAGG	CAAAACAAAG	CTAGAGAAAC	AATTCACAGT	CCTGAGCCAG	6240
	TCAAAATATC	AGCAGAGTGA	CTATTCTGCA	GCCCTAAAGC	AATGCAACAG	GGAAAAGAA	6300
65	CGAACTTCTT	CTATCATCCC	TGTGGAAGAA	TCAAGGGTTG	GCATTTCATC	CCTGAGTGGA	6360
	GAAGGCACAG	ACTACATCAA	TGCCCTCTAT	ATACAGGCTT	ATTACAGAG	CAATGAATTC	6420
	ATCATTACCC	AGCACCTCTT	CCTTCATACC	ATCAAGGATT	TCTGAGGAT	GATATGGGAC	6480
	CATAATGCCC	AACCTGGTGT	TATGATTCCT	GATGGCCAAA	ACATGGCAGA	AGATGAATTT	6540
	GTTTACTGGC	CAAAATAAGA	TGAGCCCTATA	AATTGTGAGA	GCTTTAAGGT	CACCTTATAG	6600
70	GCTGAAGAAC	ACAAATGTCT	ATCTAATGAG	GAAAACTTAA	TAATTACAGG	CTTTACTCTA	6660
	GAAGCTACAC	AGGATGATTA	TGTACTTGAA	GTGAGGCAC	TTCACTGTCC	TAAATGGCCA	6720
	AATCCAGATA	GCCCCATTAG	TAAAACTTTT	GAACCTTATA	GTGTTATAAA	AGAAGAAGCT	6780
	GCCAAATAGG	ATGGGCCATC	GATTGTTTCT	GATGAGCATG	GAGGAGTGAC	GGCAGGAAGT	6840
	TTCTGTGCTC	TGACAACCTT	TATGCACCAA	CTAGAAAAAG	AAAATTCCTG	GGATGTTTAC	6900
75	CAGGTAGCCA	AGATGATCAA	TCTGATGAGG	CCAGGAGTCT	TTGCTGACAT	TGAGCAGTAT	6960
	CAGTTTCTCT	ACAAAGTGAT	CCTCAGCCTT	GTGAGCACAA	GGCAGGAAGA	GAATCCATCC	7020
	ACCTCTCTGG	ACAGTAATGG	TGCAGCATTG	CCTGATGGAA	ATATAGCTGA	GAGCTTAGAG	7080
	TCTTTAGTTT	AACACAGAAA	GGGGTGGGGG	GACTCACATC	TGAGCATTTG	TTTCTCTTTC	7140
	CTAAATTAGG	CAGGAAAAAT	CAGTCTAGTT	CTGTTATCTG	TGATTTTCCC	ATCACCTGAC	7200
80	AGTAATTTTC	ATGACATAGG	ATTCTGCCGC	CAAAATTATA	TCATTACAAA	TGTGTGCCCT	7260
	TTTGCAAGAC	TTGTAATTTA	CTTATTATGT	TTGAACATAA	ATGATTGAAT	TTTACAGTAT	7320
	TTCTAAGGAT	GGAATTGTGG	TATTTTTTTC	TGTATTGATT	TTAACAGAAA	ATTTCAATTT	7380
	ATAGAGGTTA	GGAATTCCAA	ACTACAGAAA	ATGTTTGTIT	TAGTGTGCAA	ATTTTATGAT	7440
	GTATTGTAG	CAGATTCTAG	GTTTGCTAGA	AATATAACTT	TTAATACAGT	AGCCTGTAAA	7500
	TAAACACTCT	TTCATATGTA	TATTCAACAT	TTTCAAACTG	CAGTATTTCAC	CTAAAGTAGA	7560
85	AATAATCTGT	TACTTTTGTG	AAATACTGCC	CTAGTGTCTC	CATGGACCAA	ATTTATATTT	7620
	ATAATTGTAG	ATTTTATATAT	TTTACTACTG	AGTCAAGTTT	TCTAGTTCTG	TGTAATTGTT	7680
	TAGTTTAAATG	ACGTAGTTTCA	TTAGCTGGTC	TTACTCTACC	AGTTTCTCTA	CATTGTATTG	7740

TGTTACCTAA GTCATTAAC TTTGTTTCAGC ATGTAATTTT AACTTTTGTG GAAAAATAGAA 7800
 ATACCTTCAT TTTGAAAGAA GTTTTATGA GAATAACACC TTACCAACA TTGTTCAAAT 7860
 GGTGTTTATC CAAGGAATTG CAAAAATAAA TATAAATATT GCCATTAATAA AAAAAAATAA 7920
 AAAAAAAAAA AAAAAAAAAA A

Seq ID NO: 583 Protein sequence
 Protein Accession #: NP_002842.1

1 11 21 31 41 51
 10 MRILKRFLAC IQLLCVCRLD WANGYYRQOR KLVEEIGWSY TGALEQKNWG KKYPTCNSPK 60
 QSPINIDEDL TQVNVNKKL KFQGWDTSL ENTFIHNTGK TVEINLTNDY RVSGGVSEMV 120
 FKASKITFWH GKCNMSSDGS EHSLEGQKFP LEMQIYCFDA DRFSSFEAV KGKGLRLALS 180
 15 ILFEVGTBEN LDFKAIIDGV BSVSRFGKQA ALDPPFILLNL LPNSTDKYYI YNGSLTSPPC 240
 TDTVDWIVFK DTVSISESQL AVFCEVLTMO QSGYVMLMDY LQNNFREQQY KFSRQVFSSY 300
 TGKEEIHFAV CSSEFENVQA DPENYTSLLV TWERPRVVDY TMIEKFAVLY QQLDGEDQTK 360
 HEFLTDGYQD LGAILNLLP NMSYVLQIVA ICTNGLYGYK SDQLIVDMPT DNPEDLDFPE 420
 LIGTEEIIKE EEEGKDIEEG AIVNPGRDSA TNQIRKKEPQ ISTTTHYNRI GTKYNEAKTN 480
 20 RSPTRGSEFB KGKGVNPTSL NSTSQPVTKL ATEKDISLTS QVTVELPPTH VEGTSASLND 540
 GKSTVLRSFH MNLGTAESL NTVSITEYEE ESLLTSFKLD TGAEDSSGSS PATSAIPFIS 600
 ENISQGYIFS CSSEFENVQA VLPESARNA SEDSTSSGSE ESKLDPMEG NVWPPSSTDI 660
 TAQPDVGSGR ESFLQTNYTE IRVDESEKTT KSFSAGPVMS QGFSVTDLME PHYSTFAYFP 720
 TSVTPHAFPT SSRQQLVST VNVVYSQTQ PVYNGETPLQ PSYSSEVFPV VTPLLLDNQI 780
 25 LNTTPAASS DSALHATPVF PSVDVSFESI LSSYDGAPLL PFSSASFSE LFRHLHTVSQ 840
 ILFQVTSATB SDKVLPHASL PVAGGDLLE PSLAQYSDVL STTHAASETL EFGSESGVLY 900
 KTLMFQVPEP PSSDAMMHAR SSGPEPSYAL SDNEGSQHIF TVSYSSAIPV HDSVGVTYQG 960
 SLFSGESHIP IPKSLITPT ASLLQPTHAL SGDGEWSGAS SDSEFLLPDT DGLTALNISS 1020
 PVSVAEFTYT TSVFGDDNKA LSKSEIYGN ETELQIPSFN BMVVPSESTV MPNMYDNVVK 1080
 30 LNASLQETSV SISSTKGMFP GSLAHTTKV FDHEISQVPE NNFVQVPTH VSQASGDTSL 1140
 KPVLSANSEP ASSDPASSEM LSPSTQLLFY ETSASFSTEV LLQPSFQASD VDTLLKTVLP 1200
 AVPSDFILVE TPYVDKISST MLHLIVNSA SSENMLHSTS VPFVDVSPTS HMHSASLQLQ 1260
 TISYASEKYE PVLLKSESSH QVPSLYSND ELFQTANLEI NQAHPPKGRH VFATPVLSID 1320
 EPLNTLINKL IHSDEILTST KSSVTGKVFV GIPTVASDTF VSTDHSEVPIG NGHVAITAVS 1380
 35 PHRDGSVTST KLLFPKATS ELHSAKSDA GLVGGGEDGD TDDGDDDDDD RDSGLSLHK 1440
 CMSCSSYRES QEKVMNDSDT HENSLMDQNV PISYLSSENS EEDNRVTSVS SDSQTGMDRS 1500
 PGKSPSANGL SQKHNDGKEE NDIQTGSALL PLSPESKAWA VLTSDEESGS GQTSDSLNE 1560
 NETSTDFSPA DTNEKDADGI LAAGDSEITP GFQPSPTSSV TSENSEVFHV SEAEASNSH 1620
 ESRIGLAEGE ESEKKAIVPL VIVSALTFIC LVVLVGLIY WRKCFQTAHF YLEDSTSPRV 1680
 40 ISTPPTPIFP ISDDVGAIFI KHFPHKVDL HASSGFTEEF ETLKEFYQEV QSCVTDLGIT 1740
 ADSNNHNDK HKNRYINIVA YDHSRVKLAQ LAEKDGKLT YINANYVDGY NRPKAYIAAQ 1800
 GPLKSTAEDF WRMWIHNVE VIVMITNLVE KGRKCDQYV PADGSEEGN FLVTQKSVQV 1860
 LAYVTVRNET LRNTKIKKGS QKGRPSGRV TQVHYTQWPD MGVPYSLPV LTFVRKAAYA 1920
 KRHAVGPVVV HCSAGVGRTG TYIVLDSMLQ QIQHEGTVNI FGFLKHRSQ RNYLVQTEQE 1980
 45 YVFIHDTLVE ALLSKETEVL DSHIHAYVNA LLIPGPAGKT KLEKQFQLLS QSNIQSDYS 2040
 AALKQCNREK NRTSSIIIVE RSRVGISLS GEGTDYINAS YIMGYQNSNE FIITQHPLH 2100
 TIKDFWRMIV DHNAQLVMI PDGQNMAGE FVYWPKNDEP INCSPKVTI MAEHEKCLSN 2160
 EEKLIQDFI LEATQDDVVL EVRHFQCPKW PNPDSPIST FELISVIEKE AANRDGPMIV 2220
 HDEHGGVTAQ TFCALTTLMH QLEKENSVDV YQVAKMINLM RGPVFADIEQ YQFLYKVLIS 2280
 LVSTRQEENP STSLDSNGAA LPDGNIAESL ESLV

Seq ID NO: 584 DNA sequence
 Nucleic Acid Accession #: NM_005688.1
 Coding sequence: 126..4439

1 11 21 31 41 51
 55 CCGGGCAGGT GGCTCATGCT CGGGAGCGTG GTTGAGCGGC TGGCGCGGTT GTCTGGAGC 60
 AGGGGCGCAG GAATTCCTGAT GTGAACTAA CAGTCTGTGA GCCCTGGAAC CTCGCTCAG 120
 60 AGAAGATGAA GGATATCGAC ATAGGAAAG AGTATATCAT CCCAGTCTCT GGGTATAGAA 180
 GTGTGAGGGA GAGAACACGC ACTTCTGGGA CGCACAGAGA CCGTGAAGAT TCCAAGTTCA 240
 GGAGAACTCG ACCGTGGGAA TGCCAAGATG CCTTGGAAAC AGCAGCCCGA CGCAGGGGCC 300
 TCTCTCTTGA TGCTCTCATG CATCTCTCAG TCAGAACTCT GGATGAGGAG CATCCCAAGG 360
 GAAAGTACGA TCATGGCTTG AGTGCTCTGA AGCCCATCCG GACTACTTCC AAACACCAGC 420
 65 ACCCAGTGGA CAATGCTGGG CTTTTTCTCT GTATGACTTT TCGTGGCTT TCTTCTCTGG 480
 CCGGTGTGGC CCACAAGAAG GGGGAGCTCT CAATGGAAGA CGTGTGGTCT CTGTCCAAGC 540
 ACGAGTCTTC TGACGTGAAC TGCAGAAGAC TAGAGAGACT GTGGCAAGAA GAGCTGAATG 600
 AAGTTGGGCC AGACGCTGCT TCCCTGCGAA GGGTGTGTG GATCTTCTGC CGCACCAGGC 660
 TCATCTGTGC TCATCTGTGC CTGATGATCA CGCAGCTGGC TGGCTTCAGT GGACCAGCTC 720
 70 TCATGGTGAA ACACCTCTTG GAGTATACCC AGGCAACAGA GTCTAACCTG CAGTACAGCT 780
 TGTGTGTAGT GCTGGGCTCT CTCCTGACCG AAATCGTGGC GTCTTGGTGC CTTGCACTGA 840
 CTTGGGCATT GAATTACCGA ACCGGTGTCC GCTTGGCGGG GGCCATCTCA ACCATGGCAT 900
 TTAAGAAGAT CCTTAAGTTA AAGAACATTA AAGAGAAATC CCTGGGTGAG CTCATCAACA 960
 75 TTTGCTCCAA CGATGGCGAG AGAATGTTTG AGGCAGCAGC CGTTGGCAGC CTGCTGGCTG 1020
 GAGGACCCGT TGTGCTCATC TTAGGCATGA TTTATAATGT AATTATCTG GGACCAACAG 1080
 GCTTCTCTGG ATCAGCTGTT TTTATCTCTT TTTACCCAGC AATGATGTTT GCATCAGCGC 1140
 TCACAGCATA TTTAGGAGA AAATGCGTGG CCGCCACGGA TGAACGTGTC CAGAAAGATGA 1200
 ATGAAGTTCT TACTTACATT AAATTTATCA AAATGTATGC CTGGGTCAAA GCATTTTCTC 1260
 AGAGTGTTC AAAAAATCCG GAGGAGGAGC GTCGGATATT GGAATAAGCC GGGTACTTCC 1320
 80 AGGGTATCAC TGTGGGTGTG GCTCCCATG TGGTGGTGAT TGCCAGCGTG GTGACCTTCT 1380
 CTGTTTCATAT GACCTCTGGC TTCGATCTGA CAGCAGCACA GGCTTTCACA GTGGTGACAG 1440
 CTCTCAATTC CATGACTTTT GCTTTGAAAG TAACACCGTT TTCAGTAAAG TCCTCTCTAG 1500
 AAGCCTCAGT GGCTGTGAG AGATTTAAGA GTTTGTTTCT AATGGAAGAG GTTCACATGA 1560
 TAAAGAACAA ACCAGTCCAG CCTCACATCA AGATAGAGAT GAAAAATGCC ACCTTGGCAT 1620
 85 GGGACTCCTC CCACCTCAGT ATCCAGAACT CGCCCAAGCT GACCCCAAAA ATGAAAAAAG 1680
 ACAAGAGGGC TTCCAGGGGC AAGAAAGAGA AGGTGAGGCA GCTGCAGCGC ACTGAGCATC 1740
 AGCGGCTGCT GGCAGAGCAG AAAGGCCACC TCCTCTCTGA CAGTGACGAG CGGCCAGTC 1800
 CCGAAGAGGA AGAAGGCAAG CACATCCACC TGGGCCACCT GCGCTTACAG AGGACACTGC 1860

	ACAGCATCGA	TCTGGAGATC	CAAGAGGGTA	AATCGGTTGG	AATCTGCGGC	AGTGTGGGAA	1920
	GTGGAAAAAC	CTCTCTCATT	TCAGCCATTT	TAGGCCAGAT	GACGCTTCTA	GAGGGCAGCA	1980
5	TTGCAATCAG	TGGAACCTTC	GCTTATGTGG	CCCAGCAGGC	CTGGATCCTC	AATGTACTTC	2040
	TGAGAGACAA	CATCTCTGTT	GGGAAGGAAT	ATGATGAAGA	AAGATACAAC	TCTGTCTGA	2100
	ACAGCTGCTG	CCTGAGGGCT	GACCTGGCCA	TTCTTCCCAG	CAGCGACCTG	ACGGAGATTG	2160
	GAGAGCGAGG	AGCCAACCTG	AGCGGTGGGC	AGCGCCAGAG	GATCAGCCTT	GCCCGGGCCT	2220
	TGTATAGTGA	CAGGAGCATC	TACATCCTGG	ACGACCCCTT	CAGTGCCTTA	GATGCCCATG	2280
	TGGGCAACCA	CATCTTCAAT	AGTGCTATCC	GGAAACATCT	CAAGTCCAAG	ACAGTTCTGT	2340
10	TTGTTACCCA	CCAGTTACAG	TACCTGGTTG	ACTGTGATGA	AGTGATCTTC	ATGAAAGAGG	2400
	GCTGTATTAC	GGAAAGAGGC	ACCCATGAGG	AACCTGATGA	TTTAAATGGT	GACTATGCTA	2460
	CCATTTTAA	TAACCTGTGG	CTGGGAGAGA	CACCGCCAGT	TGAGATCAAT	TCAAAAAAGG	2520
	AAACCACTGG	TTACAGAAAG	AAGTCACAAG	ACAAGGGTCC	TAAACACGGA	TCAGTAAAGA	2580
	AGTAAAAAGC	AGTAAAGCCA	GAGGAAGGGC	AGCTTGTGCA	GCTGGAAGAG	AAAGGGCAGG	2640
15	GTTCAGTGCC	CTGAGTACAT	TATGGTGTCT	ACATCCAGGC	TGCTGGGGGC	CCCTTGGCAT	2700
	TCTCTGTTAT	TATGGCCCTT	TTTATGCTGA	ATGTAGGCAG	CACCGCCTTC	AGCACCTGGT	2760
	GGTTGAGTTA	CGAGGAAGCG	GGAAACCCAC	TGTGACTCGA	GGGAACGAGA	GGGAACGAGA	2820
	CCTCGGTGAG	TGACAGCATG	AAGGACAATC	CTCATATGCA	GTACTATGCC	AGCATCTACG	2880
	CCCTCTCCAT	GGCAGTCTAG	CTGATCTCTG	AAGCCATTGG	ACGAGTTGTC	TTTGTCAAGG	2940
20	GCACGCTCGG	AGCTTCTTCC	CGGCTGCATG	ACGAGCTTTT	CCGAAGGATC	CTTCGAAGCC	3000
	TATGAAGTT	TTTTGACACG	ACCCCCACAG	GGAGGATTCT	CAACAGGTTT	TCCAAAGACA	3060
	TGGATGAAGT	TGACCTGCGG	CTGCCGTTCC	AGGCGGAGAT	GTTTATCCAG	AACGTTATCC	3120
	TGGTGTCTTT	CTGTGTGGGA	ATGATCGCAG	GAGTCTTCCC	GTGGTTCCTT	GTGGCAGTGG	3180
	GGCCCTTGT	CATCTCTTTT	TCAGTCTGTC	ACATTTGCTC	CAGGGTCTCT	ATTCCGGAGC	3240
25	TGAAGCGTCT	GGACAATATC	ACGCAGTCAC	CTTCTCTCTC	CCACATCACG	TCCAGCATA	3300
	AGGGCCTTGC	CACCATCCAC	GCCTACAATA	AAGGGCAGGA	GTCTCTGCAC	AGATACCAGG	3360
	AGCTGCTGGA	TGACAAACAA	GCTCCTTTT	TTTTGTTTAC	GTGTGCGATG	CGGTGGCTGG	3420
	CTGTGCGGCT	GGACCTCATC	AGCATCGCCC	TCATCACCAC	CACGGGGCTG	ATGATCGTTC	3480
	TTATGCACGG	GCAGATTCCC	CCAGCCTATG	CGGGTCTCGC	CATCTCTTAT	GCTGTCCAGT	3540
30	TAACGGGGCT	GTTCAGTTAT	ACGGTCAGAC	TGGCATCTGA	GACAGAAGCT	CGATTCACTT	3600
	CGGTGGAGAG	GATCAATCAC	TACATTAAGA	CTCTGTCTCT	GGAAAGCACC	GCCAGAATTA	3660
	AGAACCAAGG	TCCCTCCCTC	GACTGGCCCC	AGGAGGGAGA	GGTGACCTTT	GAGAACGCGG	3720
	AGATGAGGTA	CCGAGAAATC	CTCCCTCTTG	TCCTAAAGAA	AGTATCCTTC	ACGATCAAAC	3780
	CTAAAGAGAA	GATTGGCATT	GTGGGGCGGA	CAGGATCAGG	GAAGTCTCTG	CTGGGGATGG	3840
35	CCCTCTTCCG	TCTGTGTGAG	TTATCTGGAG	GCTGCATCAA	GATTGATGGA	GTGAGAATCA	3900
	GTGATATTGG	CCTTCCGAC	CTCCGAAGCA	AACCTCTCTAT	CATTCTCTCA	GAGCCGGTGC	3960
	TGTTCAAGTG	CAGTGTGAGA	TCAAATTGGG	ACCCCTTCAA	CCAGTACACT	GAAGACCGAG	4020
	TTTGGGATGC	CCTGGAGAGG	ACACACATGA	AAGAATGTAT	TGCTCAGCTA	CCTCTGAAAC	4080
	TTGAATCTGA	AGTGTATGAG	AATGGGGATA	ACTTCTCAGT	GGGGGAACGG	CAGCTCTTGT	4140
40	GCATAGCTAG	AGCCCTGCTC	CGCCACTGTA	AGATTCTGAT	TTTAGATGAA	GCCACAGCTG	4200
	CCATGGACAC	AGAGACAGAC	TTATTTGATC	AAGAGACCAT	CCGAGAGACA	TTTGCAGACT	4260
	GTACCATGCT	GACCATTTGC	CATCGCCTGC	ACACGGTTCT	AGGCTCCGAT	AGGATTATGG	4320
	TGCTGGCCCA	GGGACAGGTG	GTGGAGTTTG	ACACCCCATC	GGTCTCTCTG	TCCAACGACA	4380
	TTTCCCGATT	CTATGCCATG	TTTGCTGCTG	CAGAGAACAA	GGTCTGCTGC	AAGGGCTGAC	4440
45	TCCTCCCTGT	TGACGAAGTC	TCCTTTCTTT	AGAGCATTGC	CATTCTCTGC	TTGGGGCGGG	4500
	CCCTCATCG	CGTCTCTGTA	CCGAAACCTT	GCCTTTCTCG	ATTTTATCTT	TCGCACAGCA	4560
	GTTCGGGATT	CGCTGTGTTG	TTTCACTTTT	AGGGAGAGTC	ATATTTTGAT	TATTGTATT	4620
	ATTCCATATT	CATGTAAACA	AAATTTAGTT	TTTGTCTCTA	ATTGCACTCT	AAAAGGTTCA	4680
	GGGAACCGTT	ATTATAATTG	TTTCAAGGCT	CTATAATGAA	GCTTTATACG	TGTAGCTATA	4740
50	TCATATATATA	ATTCTGTACA	TAGCCTATAT	TTACAGTGAA	AATGTAAGCT	GTTTATTTTA	4800
	TATTAATAATA	AGCATCTGTG	TAATAACAGT	GCATATTCTT	TTCTATCATT	TTTGTACAGT	4860
	TTGCTGTACT	AGAGATCTGG	TTTTGCTATT	AGACTGTAGG	AAGAGTAGCA	TTTCACTTCT	4920
	CTCTAGCTGG	TGTTTTCACG	GTGCCAGGTT	TTCTGGGTGT	CCAAAGGAAG	ACGTGTGGCA	4980
	ATAGTGGGCT	CTCCGACAGC	CCCTCTGCCC	GCCTCCCCAC	AGCCGCTCCA	GGGGTGGCTG	5040
55	GAGACGGGTG	GGCGGCTGGA	GACCATGCAG	AGCGCCGTGA	GTTCTCAGGG	CTCCTGCCTT	5100
	GTGCTCTGTT	GTCACTTACT	GTTTCTGTCA	GGAGAGCAGC	GGGGCGAAGC	CCAGGCCCCCT	5160
	TTTCACTCCC	TCCATCAAGA	ATGGGGATCA	CAGAGACATT	CCTCCGAGCC	GGGGAGTTTC	5220
	TTTCTCTGCT	TCTTCTTTTT	GCTGTTGTTT	CTAAACAAGA	ATCAGTCTAT	CCACAGAGAG	5280
	TCCCACTGCC	TCAGTTTCTT	ATGGCTGGCC	ACTGCACAGA	GCTCTCCAGC	TCCAAGACCT	5340
60	GTGGTTTCCA	AGCCCTGGAG	CCAACTGCTG	CTTTTGTAGG	TGGCACTTTT	TCATTGCGCT	5400
	ATTCCACACG	TCCACAGATT	CAGTGGCAGG	GCTCAGGATT	TCGTGGGTCT	GTTTTCTTCT	5460
	TCACGCGCAG	TGCTGCGACA	GTCTCTCTCT	CTCTCTCCCC	TCAAAGTCTG	CAACTTTAAG	5520
	CAGCTCTTGC	TAATCAGTGT	CTCACACTGG	CGTAGAAGTT	TTTGTACTGT	AAAGAGACCT	5580
	ACCTCAGGTT	GCTGTTTGTG	GTGTGTTTCC	GCAAACCCCT	TTTGTGCTGT	TTTGTGCTGT	5640
65	GGGGCTGGTA	GCTCAGGTGG	GCGTGGTCAC	TGCTGTCTAT	AGTTGAATGG	TCAGCGTTGC	5700
	ATGTCGTGAC	CAACTAGACA	TTCTGTGCGC	TTAGCATGTT	TGCTGAACAC	CTTGTGGAAG	5760
	AAAAAATCTG	AAAAATGTGA	TAAAAATTAT	TTGGATTTTG	TAAAAAATAA	AAAAAATAA	5820

Seq ID NO: 585 Protein sequence
Protein Accession #: NP_005679.1

	1	11	21	31	41	51	
75	MKDIDIGKEY	IIPSPGYRSV	RERTSTSGTH	RDREDSKFRF	TRPLECQDAL	ETAARAEGLS	60
	LDASMSQLR	ILDEEHPKKG	YHGLSALKP	IRTSKHQHP	VDNAGLFSCM	TFSWLSLAR	120
	VAHKGELSM	EDVWSLSKHE	SSDVNCRLE	RLWQELNEV	GPDAASLRV	VWIFCRTRLI	180
	LSIVCLMITQ	LAFSGPAPFM	VKHLLEYTQA	TESNLQYSL	LVLGLLLEI	VRWSLALTW	240
	ALNYRTGVR	LAGLITMAFK	KILKLNKE	KSLGELINIC	SNDGQRMFEA	AAVGSLLAG	300
	PVVAILGMY	NVILGPTGF	LGSVAVILFY	PAMMFASRLT	AYFRKRCVAA	TDERVQRMNE	360
80	VLTYIKFIKM	YAWVKAPSQS	VQKIREERR	ILEKAGYFQG	ITVGVAPIVV	VIASVVTFSV	420
	HMTLGFDLTA	AQAFVTVTF	NSMTFALKVT	PFSVKSLSEA	SVAVDRPKSL	FLMEVHMIK	480
	NKPASPHIK	EMKNATLAWD	SSHSIQNSP	KLTPKMKDK	RASRGKKEKV	RQLQRTHEQA	540
	VLAQKQHL	LDSDERPSP	EEGKHILG	HLRLQRTLHS	IDLEIQEKG	VGICGSVSGS	600
	KTSLISAILG	QMTLLEGSIA	ISGTFAYVAQ	QAWILNATLR	DNILEFGKEYD	EBRYNSVLNS	660
85	CCLRPLDAL	PSSDLTEIGE	RGANLSGGQR	QRISLARALY	SDRSIYILD	PLSALDAHVQ	720
	NHIFNSAIRK	HLKSKTVLFV	THQLQYLVDC	DEVIFMKEGC	ITERGTHEEL	MNLNGDYATI	780
	FNNLLGETP	PVEINSKKB	SGSQKKSQDK	GPKTGSVKKE	KAVKPEEQGL	VQLEBKQGS	840

VPWSVYGVYI QAAGGPLAPL VIMALFMLNV GSTAFSTWML SYWIKQGSQN TTVTRGNETS 900
 VSDSMKDNPH MQYVASYIAL SMAVMLILKA IRGVVFVKGT LRASSRLHDE LFRRLRSEPM 960
 KFFDTTPTGR ILNRFSDKMD EVDVRLPFQA EMFIQNVILV PFCVGMIAGV FWPLVAVGP 1020
 LVILFSVLHI VSRVLIRELK RLDNITQSPF LSHITSSIQG LATIHAYNKG QEFLHRYQEL 1080
 LDDNQAPFFL PTCAMRWLAV RLDLISIALI TTTGLMIVLM HGQIPPAYAG LAISYAVQLT 1140
 GLFQFTVRLA SETEARFTSV ERINHYIKTL SLEAPARIKN KAPSPDWQOE GEVTFENAEM 1200
 RYRENLPVLV KKVSTFIKPK EKIGIVGRTG SGKSSLGMAL FRLVELSGGC IKIDGVRI SD 1260
 IGLADLRSLK SIIPQEPVLF SGTVRSNLDP FNQYTEDQIW DALERTHMKC CIAQLPLKLE 1320
 SEVMENGDNF SVGERQLLCI ARALLRHCKI LILDEATAAM DTETDLIIQE TIREAFADCT 1380
 MLTIAHRLAT VLGSDRIMVL AQGVVEFDT PSVLLSNDSS RPYAMFAAAE NKVAVKGG

Seq ID NO: 586 DNA sequence
 Nucleic Acid Accession #: NM_001327.1
 Coding sequence: 89..631

1 11 21 31 41 51
 AGCAGGGGGC GCTGTGTGTA CCGAGAATAC GAGAATACCT CGTGGGCCCT GACCTTCTCT 60
 CTGAGAGCCG GGCAGAGGCT CCGAGGCCAT GCAGGCCGAA GGCAGGGGCA CAGGGGGTTC 120
 GACGGGCGAT GCTGATGGCC CAGGAGGCCC TGGCATTCTT GATGGCCAGG GGGGCAATGC 180
 TGGCGGCCCA GAGAGAGCGG GTGCCACGGG CGGCAGAGGT CCGCGGGGCG CAGGGGCAGC 240
 AAGGGCCTCG GGGCCGGGAG GAGGCGCCCC GCGGGGTCCG CATGGCGCGC CGGCTTCAGG 300
 GCTGAATGGA TGCTGCAGAT GCGGGGCCAG GGGGCGCGAG AGCCGCTCTG TTGAGTTCTA 360
 CCTCGCCATG CCTTTCGGCA CACCATGGA AGCAGAGCTG GCCCGCAGGA GCCTGGCCCA 420
 GGATGCCCA CCGCTTCCCG TGCCAGGGGT GCTTCTGAAG GAGTTCAGTG TGTCCGGCAA 480
 CATACTGACT CTCTGCAGTA CTGCTGCAGA CCACCGCAA CTGCAGCTCT CCATCAGCTC 540
 CTGTCTCCAG CAGCTTTCCC TGTTGATGTG GATCAGCGAG TGCTTTCTGC CCGTGTTTTT 600
 GGCTCAGCTC CCCTCAGGCG AGAGGCGCTA AGCCAGCCTT GCGCGCCCTT CCTAGGTCAT 660
 GGCTCTCTCC CTAGGGAATG GTCCAGCAC GAGTGGCCAG TTCATTGTGG GGGCCTGATT 720
 GTTTGTCTCT GGAGGAGGAC GGCTTACATG TTTGTTTCTG TAGAAAATAA AACTGAGCTA

Seq ID NO: 587 Protein sequence
 Protein Accession #: NP_001318.1

1 11 21 31 41 51
 MQAEGRGTTG STGDADGPGG PGIPDGPGGN AGGPGEAGAT GGRGPRGAGA ARASGPGGGA 60
 PRGPHGGAAS GLNGCCRCGA RGPESRLLEF YLAMPFATPM EABLARRSLA QDAPPLFVPG 120
 VLLKEFTVSG NLTIRLTAA DHRQLQLSIS SCLQLLSLLM WITQCFLPVF LAQPPSGQRR

Seq ID NO: 588 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 52..459

1 11 21 31 41 51
 CCTCGTGGGC CCTGACCTTC TCTCTGAGAG CCGGGCAGAG GCTCCGGAGC CATGCAGGCC 60
 GAAGGCCAGG GCACAGGGGG TCGACGGGC GATGCTGATG GCCCAGGAGG CCTTGGCATT 120
 CTGATGGGCC CAGGGGGCAA TGCTGGGGGC CCAGGAGAGG CGGGTGCCAC GGGCGGCAGA 180
 GGTCCCCGGG GCGCAGGGGC AGCAAGGGCC TCGGGGCCGA GAGGAGGCGC CCGCGGGGAT 240
 CGCATGGCG GTGCCGCTTC TGCGCAGGAT GGAAGGTGCC CCTGCGGGGC CAGGAGGGCG 300
 GACAGCCGCC TGCTTCAGTT CCGACTGACT GCTGCGAGCC ACCGCCAACT GCAGCTCTCC 360
 ATCAGTCTCT GTCTCCAGCA GTTTCCCTG TTGATGTGGA TCACGCACTG CTTTCTGCCC 420
 GTGTTTTTGG CTCAGGCTCC CTCAGGGCAG AGGCGCTAAG CCCAGCCTGG CGCCCTTCC 480
 TAGGTCATGC CTCCTCCCTC AGGGAATGGT CCCAGCACGA GTGGCCAGTT CATTGTGGGG 540
 GCCTGATTGT TTGTCGCTGG AGGAGGACGG CTTACATGTT TGTTCCTGTA GAAAATAAAG 600
 CTGAGCTA

Seq ID NO: 589 Protein sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 MQAEGGQTGG STGDADGPGG PGIPDGPGGN AGGPGEAGAT GGRGPRGAGA ARASGPGRGA 60
 PRGPHGGAAS AQDGRCPGCA RRPDSRLQLF RLTAADHRQL QLSISSCLQQ LSLLMWITQC 120
 FLFVFLAQAP SGQRR

Seq ID NO: 590 DNA sequence
 Nucleic Acid Accession #: NM_005562.1
 Coding sequence: 90..3671

1 11 21 31 41 51
 ACAGCGGAGC GCAGAGTGAG AACCACCAAC CGAGGCGCGG GGCAGCGACC CTGCAGCGG 60
 AGACAGAGAC TGAGCGGGCC GGCACCGCCA TGCCCTGCGT CTGGCTGGGC TGTGCTCTCT 120
 GCTTCTCGCT CCTCTGCCC GACGCCGGG CCACCTCCAG GAGGGAAGTC TGTGATTGCA 180
 ATGGGAAGTC CAGGCAGTGT ATCTTTGATC GGAACCTTCA CAGACAACT GGTAAATGGAT 240
 TCCGCTGCCT CACTGCAAT GACAACACTG ATGGCATTCA CTGCGAGAAG TGCAAGAATG 300
 GCTTTTACCG GCACAGAGAA AGGACCGCT GTTTGCCCTG CAATTGTAAC TCCAAGGTT 360
 CTCTTAGTGC TCGATGTGAC AACTCTGGAC GGTGAGCTG TAAACCAAGT GTGACAGGAG 420
 CCAGATGCGA CCGATGTCTG CCAGGCTTCC ACATGCTCAC GGATGCGGGG TGCACCAAG 480
 ACCAGAGACT GCTAGACTCC AAGTGTGACT GTGACCCAGC TGGCATCGCA GGGCCCTGTG 540
 ACGCGGGCCG GTGTGTCTCG AAGCCAGCTG TTAAGTGAGA ACGCTGTGAT AGGTGTGAT 600
 CAGGTTACTA TAATCTGATG GGGGGGAACC CTGAGGGCTG TACCCAGTGT TTCTGCTATG 660
 GGCATTGAGC CAGCTGCGCG AGCTCTGAG AATACAGTGT CCATAAGATC ACCTCTACCT 720
 TTCATCAAGA TGTGATGGC TGGAGGCTG TCCAACGAAA TGGGTCTCTT GCAAAGCTCC 780
 AATGGTCACA GCGCCATCAA GATGTGTTTA GCTCAGCCCA ACGACTAGAC CTGTCTATT 840

	TTGTGGCTCC	TGCCAAATTT	CTTGGGAATC	AACAGGTGAG	CTATGGGCAA	AGCCTGTCTCT	900
	TTGACTACCG	TGTGGACAGA	GGAGGCAGAC	ACCCATCTGC	CCATGATGTG	ATTCTGGAAG	960
	GTGCTGGTCT	ACGGATCACA	GCTCCCTTGA	TGCCACTTGG	CAAGACACTG	CCTTGTGGGC	1020
5	TCACCAAGAC	TTACACATTG	AGGTTAAATG	AGCATCCAAG	CAATAATTGG	AGCCCCCAGC	1080
	TGAGTTACTT	TGAGTATCGA	AGGTTACTGC	GGAAATCTCAC	AGCCCTCCCG	ATCCGAGCTA	1140
	CATATGGAGA	ATACAGTACT	GGGTACATTG	ACAATGTGAC	CCTGATTTC	GCCCCCGCTG	1200
	TCTCTGGAGC	CCCAGCACCC	TGGGTGGAAC	AGTGTATATG	TCCTGTTGGG	TACAAGGGGC	1260
	AATTCTGCCA	GGATTGTGCT	TCTGGCTACA	AGAGAGATTG	AGCGAGACTG	GGGCTTTTGG	1320
10	GCACCTGTAT	TCCTTGTAAAC	TGTCAAGGGG	GAGGGGCTCG	TGATCCAGAC	ACAGGAGATT	1380
	GTTATTCAGG	GGATGAGAAT	CCTGACATTG	AGTGTGCTGA	CTGCCCAATT	GGTTTCTACA	1440
	ACGATCGCGA	CGACCCCGCG	AGCTGCAAGC	CATGTCCCTG	TCATAACGGG	TTCAGCTGCT	1500
	CAGTGATGCC	GGAGACGGAG	GAGGTGGTGT	GCAATAACTG	CCCTCCCGGG	GTACCCGGTG	1560
	CCCGCTGTGA	GCTCTGTGCT	GATGGCTACT	TTGGGGACCC	CTTTGGTGAA	CATGGCCAG	1620
	TGAGGCCTTG	TCAAGTGTGT	CAATGCAACA	ACAAATGTGA	CCCCAGTGCC	TCTGGGAATT	1680
15	GTGACCGGCT	GACAGGCAGG	TGTTGAAAGT	GTATCCACAA	CACAGCCGGC	ATCTACTCGG	1740
	ACCAAGTGCAA	AGCAGGCTAC	TTCGGGGACC	CATTGGCTCC	CAACCCAGCA	GACAAGTGTC	1800
	GAGCTTGCAA	CTGTAACCCC	ATGGGCTCAG	AGCCTGTAGG	ATGTGGAAGT	GATGGCACCT	1860
	GTGTTTGCAA	GCCAGGATTT	GGTGGCCCCA	ACTGTGAGCA	TGGAGCATTG	AGCTGTCCAG	1920
20	CTTGCTATAA	CCAGTTGGAAG	ATTCAGATGG	ATCAGTTTAT	GCAGCAGCTT	CAGAGAATGG	1980
	AGGCCCTGAT	TTCAAAGGCT	CAGGGTGGTG	ATGGAGTAGT	ACCTGATACA	GAGCTGGAAG	2040
	CGAGGATGCT	CAGGCTGAG	CAGGCCCTTC	AGGACATTCT	GAGAGATGCC	CAGATTTCAG	2100
	AAGGTGCTAG	CAGATCCCTT	GGTCTCCAGT	TGGCCAAGGT	GAGGAGCCAA	GAGAACAGCT	2160
	ACCAGAGCCG	CCTGGATGAC	CTCAAGATGA	CTGTGGAAGG	AGTTCGGGCT	CTGGGAAGTC	2220
25	AGTACCAGAA	CCGAGTTGGG	GATACTCACA	GGCTCATCAC	TCAGATGCAG	CTGAGCCTGG	2280
	CAGAAAGTAG	AGCTTCTCTG	GGAAACACTA	ACATTCTCTG	CTCAGACCAC	TACGTGGGGC	2340
	CAAAATGGCTT	TAAAGCTAGT	GCTCAGGAGG	CCACAGATT	AGCAGAAAGC	CACGTTGAGT	2400
	CAGCCAGTAA	CATGGAGCAA	CTGACAAGGG	AACTGAGGA	CTATTCCAAA	CAAGCCCTCT	2460
	CACCTGGTCG	CAAGGCCCTG	CATGAAGGAG	TCCGAAGCGG	AAGCGGTAGC	CCGGAAGGTC	2520
30	CTGTGGTGCA	AGGAGTTGTC	GAATAATTGG	AGAAATCCAA	GTCCCTGGCC	CAGCAGTTGA	2580
	CAGGGAGGCG	CACCTCAAGC	GAATTTGAAG	CAGATAGGTC	TTATCAGCAC	AGTCTCCGCC	2640
	TCCTGGATTG	AGTGTCTCGG	CTTCAGGGAG	TCAGTGATCA	GTCTTTTCAG	GTGGAAGATC	2700
	CAAAGAGGAT	CAACAAAAA	GCGGATTAC	TCTCAACGCT	GGTAACCCAG	CATATGGATG	2760
	AGTTCAGCG	TACACAAAG	AATCTGGGAA	ACTGGAAGA	AGAAGCACAG	CAGCTCTTAC	2820
35	AGAAATGAAA	AAGTGGGAGA	GAGAAATCAG	ATCAGCTGCT	TTCCTGGTCC	AATCTTGCTA	2880
	AAAGCAGAGC	ACAAGAAACA	CTGAGTATGG	GCAATGCCAC	TTTTTATGAA	GTGAGAGCA	2940
	TCCTTAAAAA	CCTCAGAGAG	TTTGACCTGC	AGGTGGACAA	CAGAAAGCA	GAAGCTGAAG	3000
	AAGCCATGAA	GAGACTCTCC	TACATCAGCC	AGAAGGTTTC	AGATGCCAGT	GACAAGACCC	3060
	AGCAAGCAGA	AAGAGCCCTG	GGGAGCGCTG	CTGCTGATGC	ACAGAGGGCA	AAGAATGGGG	3120
40	CCGGGAGGCG	CTGGGAAATC	TCCAGTGAGA	TTGAACAGGA	GATTGGGAGT	CTGAACCTGG	3180
	AAGCCAAATG	GACAGCAGAT	GGAGCCTTGG	CCATGGAAAA	GGGACTGGCC	TCTCTGAAAG	3240
	GTGAGATGAG	GGAAATGAG	GGAGAGCTGG	AAAGGAAGGA	GCTGGAGTTT	GACACGAATA	3300
	TGGATGCACT	ACAGATGCTG	ATTACAGAAG	CCCAGAAGGT	TGATACCCAG	GCCAAAGAAC	3360
	CTGGGGTTAC	AATCCAAGAC	ACACTCAACA	CATTAGACGG	CCTCTGTCAT	CTGATGGACC	3420
45	AGCCTCTCAG	TGTAGATGAA	GAGGGGCTGG	TCTTACTGGA	GCAGAAGCTT	TCCCGAGCCA	3480
	AGACCCAGAT	CAACAGCCAA	CTGCGGCCCA	TGATGTGAGA	GCTGGAAAGG	AGGGCACGTC	3540
	AGCAGAGGGG	CCACCTCCAT	TTGCTGGAGA	CAAGCATAGA	TGGGATTCTG	GCTGATGTGA	3600
	AGAACTTGGA	GAACATTAGG	GACAACCTGC	CCCCAGGCTG	CTACAATACC	CAGGCTCTTG	3660
	AGCAACAGTG	AAGCTGCCAT	AAATATTCTT	CAACTGAGGT	TCTTGGGATA	CAGATCTCAG	3720
50	GGCTCGGGAG	CCATGTCATG	TGAGTGGGTG	GGATGGGGAC	ATTTGAACAT	GTTTAATGGG	3780
	TATGCTCAGG	TCAACTGACC	TGACCCCAT	CCTGATCCCA	TGGCCAGGTC	GTGTCTTAT	3840
	TGCACCATAC	TCTTGTCTTC	CTGATGCTGG	GCAATGAGGC	AGATAGCATT	GGGTGTGAGA	3900
	ATGATCAAGG	ATCTGGACCC	CAAGAATAG	ACTGGATGGA	AAGACAAACT	GCACAGGCAG	3960
	ATGTTTGCCT	CATAATAGTG	GTAAGTGGAG	TCCTGGAATT	TGGACAAGTG	CTGTTGGGAT	4020
55	ATAGTCAACT	TATTCTTTGA	GTAATGTGAC	TAAAGGAAAA	AACTTTGACT	TTGCCCAGGC	4080
	ATGAAATTC	TCCTAATGTC	AGAACAGAGT	GCAACCCAGT	CACACTGTGG	CCAGTAAAT	4140
	ACTATTGCCT	CATATTGTCC	TCTGCAAGCT	TCTTGTCTGAT	CAGAGTTCTC	CCTACTTACA	4200
	ACCCAGGGTG	TGAACATGTT	CTCCATTTC	AAGCTGGAAG	AAGTGAGCAG	TGTTGGAGTG	4260
	AGGACCTGTA	AGGCAGGGCC	ATTGAGGCT	ATGGTGCTTG	CTGGTGCTTG	CCACCTTCAA	4320
60	GTCTGGACC	TGGGCATGAC	ATCCTTTCTT	TTAATGATGC	CATGGCAACT	TAGAGATTGC	4380
	ATTTTATTA	AAGCATTTCC	TACCAGCAAA	GCAAAATGTT	GGAAAGTATT	TACTTTTTCG	4440
	GTTCAGAAAT	GATAGAAAG	TGTGGCTTGG	GCATTGAAAG	AGGTAAATTT	CTCTAGATT	4500
	ATTAGTCTTA	ATTCATCTCT	ACTTTTCGAA	CACCAAAAAAT	GATGCGCATC	AATGTATTTT	4560
	ATCTTATTTT	CTCAATCTCC	TCTCTCTTTC	CTCCACCCAT	AATAAGAGAA	TGTTCTTACT	4620
65	CACACTTCAG	CTGGGTCCAC	TCCATCCCTC	CATTCTCCTT	TCCATCCATC	TTTCCATCCA	4680
	TTACCTCCAT	CCATCCTTCC	AACATATATT	TATTGAGTAC	CTACTGTGTC	CCAGGGGCTG	4740
	GTGGGACAGT	GGTGACATAG	TCTCTGCCCT	CATAGAGTTG	ATTGTCTAGT	GAGGAAGACA	4800
	AGCATTTTAA	AAAAATAAAT	TAAACTTTAC	AAACTTTGTT	TGTCACAACT	GGTGTATTAT	4860
	GCAATAACCG	CTTGGTTTGC	AACCTCTTTG	CTCAACAGAA	CATATGTTGC	AAGACCCCTC	4920
70	CATGGGGGCA	CTTGAGTTT	GGCAAGGCTG	ACAGAGCTCT	GGGTGTGTC	CATTCTTTG	4980
	CATTCCAGCT	GTCACCTCTG	GCCTTTCTAC	AACTGATTGC	AACAGACTGT	TGAGTTATGA	5040
	TAAACACAGT	GGGAATTGCT	GGAGGAACCA	GAGGCACCTC	CACCTTGGCT	GGGAAGACTA	5100
	TGGTGCTGCC	TGCTTCTGCT	ATTTCTCTTG	ATTTCTCTGA	AAGTGTTTTT	AAATAAGAA	5160
	CAATTGTTAG	ATGCC					

Seq ID NO: 591 Protein sequence
Protein Accession #: NP_005553.1

	1	11	21	31	41	51	
80	MPALWLGCCL	CPSLLLPAA	ATSRREVCD	NGKSRCIFD	RELHRQTNG	FRCLNCNDNT	60
	DGIHCEKCKN	GFYRHRERDR	CLPCNCNSK	SLSARCDNSG	RCSEKPGVTG	ARCDRCPLGF	120
	HMLTDAGCTQ	DQRLDLSKCD	CDPAGIAGPC	DAGRCVCKPA	VTGERCDRCR	SGYINLDGGN	180
	PEGCTQCFCY	GHSASCRSSA	EYSVHKITST	FHQDVGWKA	VQRNGSPAKL	QWSQRHQDVF	240
85	SSAQRDLDPV	FVAPAKFLGN	QOVSYGQSL	FDYRVDGRGR	HPSAHDVILE	GAGLRITAPL	300
	MPLGKTLPCG	LTKTYTFRLN	EHPNNWSPQ	LSYFEYRRL	RNLTLALRIRA	TYGEYSTGYI	360
	DNVTLLISAR	VSGAPAPWE	QCICPVGYKG	QFCQDCASGY	KRDSARLGP	GTICPCNCOG	420
	GGACDPDTGD	CYSGDENPDI	ECADCPIGFY	NDPHDPRSC	PCPCNNGPSC	SVMPEETEVEV	480

CNHCPPGVTV ARCELCAADY FGDFFGEHGP VRPCQPCQCN NNVDPSASGN CDRLTGRCLK 540
 CIHNTAGIYC DQCKAGYFGD PLAPNPADKC RACNCNPMGS EPVGCERSDGT CVCKPGFGGP 600
 NCEHGAFCSP ACYNQVQIQM DQFMQQLQRM EALISKAQGG DGVVPDTELE GRMQQAQAL 660
 QDLRDAQIS EGASRSLGLQ LAKVRSQENS YQSRLLDLKM TVERVRALGS QYQNRVRDTH 720
 RLITQMQLSL AESEASLGNT NIPASDHYVG FNGFKSLAQE ATRLAESHVE SASNMEQLTR 780
 ETEDYSKQAL SLVVRKALHEG VSGSGSPDG AVVQGLVEKL EKTSLAQQL TREATQAEIE 840
 ADRSYQHSRL LLDVSRLQG VSDQSFOVEE AKRIKQKADS LSTLVTRHMD EFKRTQKNLG 900
 NWKEEAQQLL QNGKSGREKS DQLLSRANLA KSRAQEALSM GNATPYEVES ILKNLREFDL 960
 QVDNRKAEE EAMKRLSYIS QKVSADSDKT QQAERALGSA AADAQRAKNG AGEALEISSE 1020
 IEQEIGSLNL EANVTADGAL AMEKGLASLK SEMREVEGEL ERKELEFDTN MDAVQMVITE 1080
 AQKVDTRAKN AGVTIQDTLN TLDGLLHMD QPLSVDEEGL VLEQKLSRA KTQINSQRLP 1140
 MMSELBERAR QQRGHLHLE TSIDGILADV KNLENIRDNL PPGCYNTQAL EQQ

Seq ID NO: 592 DNA sequence
 Nucleic Acid Accession #: AF101051.1
 Coding sequence: 221.856

1 11 21 31 41 51
 | | | | |
 20 GAGCAACCTC AGCTTCTAGT ATCCAGACTC CAGCGCGGCC CCGGGCGCGG ACCCCAACCC 60
 CGACCCAGAG CTTTCTCCAGC GGCGGCGCAG CGAGCAGGGC TCCCGCGCTT AACTTCTCC 120
 GCGGGGCCCA GCCACCTTGG GGAGTCCGGG TTGCCACCTI GCAAACTCTC CGCCTTCTGC 180
 ACCTGCCACC CTGAGGCCAG CGCGGGCGCC CGAGCGAGTC ATGGCCAAAG CGGGGCTGCA 240
 25 GCTGTGTTGGG TPCATTCTCG CCTTCTTGGG ATGGATCGGC GCCATCGTCA GCACTGCCCT 300
 GCGCCAGTGG AGGATTACTT CCTATGCCGG CGACAACATC GTGACCGCCC AGGCCATGTA 360
 CGAGGGGCTG TGGATGTCCT GCGTGTGCGA GAGCACCAGG CAGATCCAGT GCAAAAGTCTT 420
 TGAATCTCTG CTGAATCTGA GCAGCACATT GCAAGCAACC CGTGCTTGA TGGTGGTTGG 480
 CATCCTCCTG GGAGTGATAG CAATCTTTGT GGCCACCGTT GGCATGAAGT GTATGAAGTG 540
 CTTGGAAGAC GATGAGGTGC AGAAGATGAG GATGGCTGTC ATTGGGGGTG CGATATTTCT 600
 30 TCTTGCAAGT CTGGCTATT TTAGTGGCAC AGCATGGTAT GGCAATAGAA TCGTTCAAGA 660
 ATTCTATGAC CCTATGACCC CAGTCAATGC CAGGTACGAA TTTGGTCAGG CTCTCTTCA 720
 TGGCTGGGCT GCTGCTTCT TCTGCTTCT GGGAGGTGCC CTACTTTGCT GTTCTGTCC 780
 CCGAAAAACA ACCTCTTACC CAACACCAAG GCCCTATCCA AAACCTGCAC CTTCCAGCGG 840
 35 GAAAGACTAC GTGTGACACA GAGGCAAAAG GAGAAATATCA TTTGAAACA AACCGAAAAAT 900
 GGACATTGAG ATACTATCAT TAACATTAGG ACCTTAGAAT TTTGGGTATT GTAATCTGAA 960
 GTATGGTATT ACAGAAACAA CAAACAAACA AAAAAACCAT GTGTAAATAT ACTCAGTGT 1020
 AAACATGGCT TAATCTTATT TTATCTTCTT TCCTCAATAT AGGAGGGAAG ATTTTACCAT 1080
 TTGTATTACT GCTTCCCAT TGAATATCAT ACTCAAATGG GGGAAAGGGT GCTCCTTAAA 1140
 40 TATATATAGA TATGATATATA TACATGTTTT TCTATTAAAA ATAGACAGTA AAATACTATT 1200
 CTATATATGT TGATAGTTCG ATACTTAAAA TATCTCTAAA ATAGGTAAAT GTATTTAATT 1260
 CCATATATGT GAAGATGTAT ATTGGTATAT TTTCTTTTTC GTCCCTTAT ACATATGTAA 1320
 CAGTCAAATA TCATTACTC TTCTTCATTA GCTTTGGGTG CCTTTGCCAC AAGACCTAGC 1380
 CTAATTTACC AAGGATGAAT TCTTTCAATT CTTCAATGCT GCCCTTTTCA TATACTTATT 1440
 45 TTATTTTFTA CATATACTCT ATAGCACTTG CATCGTTATT AAGCCCTTAT TTGTTTTGTG 1500
 TTTTATGGT CTCTACTCTC TGAATCTAAC ACATTTTCA GCCTACATTT TAGTTTCTAA 1560
 AGCCAAAGAG AATTATTTAT AAATCAGAAC TTTGGAGGCA AATCTTTCTG CATGACCAA 1620
 GTGATAAATT CCGTTTGACC TTCCACACA ATCCCTGTAC TCTGACCAT AGCACTCTTG 1680
 50 TTTGCTTTGA AATATTTGT CCAATTGAGT AGCTGCATGC TGTTCGCCCA GGTGTGTAA 1740
 CACAACCTTA TTGATTGAAT TTTTAAGCTA CTTATTCTA GTTTTATATC CCCCTAAACT 1800
 ACCTTTTGT TCCCACTCC TTAATTGTAT TGTTTTCCCA AGTGTAAATA TCATGCGTTT 1860
 TATATCTTCC TAATAAGGTG TGGTCTGTT GTCTGAACAA AGTGCTAGAC TTTCTGGAGT 1920
 GATAATCTGG TGACAAATAT TCTCTCTGTA GCTGTAAACA AGTCACTTAA TCTTTCTACC 1980
 55 TCTTTTCTT ATCTGCCAAA TTGAGATAAT GATACITTA CAGTTAGAAG AGGTAGTGTG 2040
 AATATTAATT AGTTTATATT ACTCTCATTC TTTGAACATG AACTATGCCT ATGTAGTGTG 2100
 TTTATTTGCT CAGCTGGCTG AGACACTGAA GAAGTCACTG AACAAAACCT ACACACGTAC 2160
 CTTCACTGTA TCACTGCTCT TCCTCTCTCT ACCAGTCTAT TTCCACTGAA CAARAACCTAC 2220
 ACACATACCT TCATGTGGTT CAGTGCCTTC CTCTCTCTAC CAGTCTATT CCACCTGAACA 2280
 60 AAACCTACGC ACATACCTTC ATGTGGCTCA GTGCCCTTCT CTCTCTACCA GTCTATTTC 2340
 ATTCTTTAG CTGTGTCTGA CATGTTTGTG CTCTGTCCA TTTTAAACA TGCTCTTACT 2400
 TTTCCAGTCT GTACAGAATG CTAITTTCACT TGAGCAAGAT GATGTATGGA AAGGGTGTG 2460
 GCACTGTGTG CTGGAGACCT GGATTTGAGT CTTGGTGCTA TCAATCACCG TCTGTGTTG 2520
 AGCAAGGACT TTGGCTGCTG TAAGCTTATT GCTTCATCTG TAAGCGGTGG TTTGTAATTC 2580
 CTGATCTTCC CACCTCACAG TGATGTTGTG GGGATCCAGT GAGATAGAAT ACATGTAAGT 2640
 65 GTGGTTTGT AATTTGAAA GTGCTATACT AAGGGAAGA ATTGAGGAAT TAATGCATA 2700
 CGTTTGGTG TTGCTTTTCA AATGTTTGA AATAAAAAAA TGTTAAGAAA TGGTTTCTT 2760
 GCCTTAACCA GTCTCTCAAG TGATGAGACA GTGAAGTAAA ATTGAGTGCA CTAACCGAAT 2820
 AAGATTCTGA GGAAGTCTTA TCTTCTGAG TGAGTATGGC CCAATGCTTT CTGTGGCTAA 2880
 ACAGATGTAA TGGGAAGAAA TAAAGCCCTA CGTGTGGTA AATCCAACAG CAAGGGAGAT 2940
 70 TTTTGAATCA TAATACTCA TAAGGTGCTA TCTGTTCACT GATGCCCTCA GAGCTCTTGC 3000
 TGTTAGCTGG CAGCTGACGC TGCTAGGATA GTTAGTTTGG AATGTTACT TCATAATAAA 3060
 CTACACAAGG AAAGTCAGCC ACCGTGTCTT ATGAGGAATT GGACCTAATA AATTTTAGTG 3120
 TGCTTCCAA ACCTGAGAAT ATATGCTTTT GGAAGTTAAA ATTTAAATGG CTTTGGCCAC 3180
 ATACATAGAT CTTCTAGATG TGTGAGTGA ATTCCATGTG GATATCAGTT ACCAAACATT 3240
 75 AAAAAAAAT TTTATGGCCC AAAATGACCA ACGAAATTGT TACAATAGAA TTTATCCAAT 3300
 TTTGATCTTT TTATATTCTT CTACCACACC TGGAAACAGA CCAATAGACA TTTTGGGGTT 3360
 TTATAATGGG AATTGTATA AAGCATTACT CTTTTTCAAT AAATTTGTTT TTAATTTAAA 3420
 AAAAGGAAAA AAAAAAAA AAA

Seq ID NO: 593 Protein sequence
 Protein Accession #: AAD16433.1

1 11 21 31 41 51
 | | | | |
 85 MANAGLQLLG FILAFLGWIG AIVSTALPQW RIYSYAGDNI VTAQAMYEGL WMSCVSQSTG 60
 IQICKVFDL LNLSSLTQAT RALMVVGILL GVIAIFVATV GMKCMKLED DEVQMRMAV 120
 IGGAILFLAG LAILVATAWY GNRIVQEPYD PMTPVNARYE FGQALPTGWA AASLCLLGG 180
 LLCCSCPRKT TSYPTPRYP KPARSSGKDY V

Seq ID NO: 594 DNA sequence
Nucleic Acid Accession #: NM_006180.1
Coding sequence: 352..2820

```

5      1      11      21      31      41      51
|      |      |      |      |      |
CCCCCATTCG CATCTAACAA GGAATCTGCG CCCAGAGAG TCCCGGACGC CGCCGGTCCG 60
TGCCCGGCGC GCCGGGCCAT GCAGCGACGG CCGCGCGGGA GCTCCGAGCA GCGGTAGCGC 120
CCCCCTGTAA AGCGGTTGCG TATGCCGGGA CCAGTGTGAA CCCTGCCGCC TGCCGGAAAC 180
CTCTTCGCTC CGGACCAGCT CAGCCTCTGA TAAGCTGGAC TCGGCACGCC CGCAACAAGC 240
ACCGAGGAGT TAAGAGAGCC GCAAGCGCAG GGAAGGCCCTC CCCGCACGGG TGGGGGAAAG 300
CGGCCGGTGC AGCGCGGGGA CAGGCACTCG GGCTGGCACT GGCTGCTAGG GATGTCGTCC 360
TGGATAAGAT GCGATGGAGA CGCCATGGCG CGGCTCTGGG GCTTCTGCTG GCTGGTTGTG 420
GGCTCTGGA GGGCGCTTT CGCCTGTCCC ACGTCTGCA AATGCACTGC CTCTCGGATC 480
TGGTGACGG CGCCTCTTCC TGGCATCGTG GCATTTCCGA GATTGGAGCC TAACAGTGTA 540
GATCCTGAGA ACATCACCGA AATTTTCATC GCAAACCAGA AAAGGTTAGA AATCATCAAC 600
GAAGATGATG TTGAAGCTTA TGTGGGACTG AGAAATCTGA CAATTGTGGA TTCTGGATTA 660
AAATTTGTGG CTGTAAGTAA ATTTCTGAAA AACAGCAACC TGCAGCACAT CAATTTTACC 720
CGAAACAAC TGACGAGTTT GTCTAGGAAA CATTTCCGTC ACCTTGACTT GTCTGAACTG 780
ATCCTGGTGG AGGCTCTCTT TACATGCTCC TGTGACATTA TGTGGATCAA GACTCTCCAA 840
GAGGCTAAAT CCAGTCCAGA CACTCAGGAT TTGTACTGCC TGAATGAAAG CAGCAAGAAT 900
ATTCCTCTGG CAAAGCTGCA GATACCCAAT TGTGGTTTGC CATCTGCAAA TCTGGCCGCA 960
CCTAACTCTA CTGTGGAGA AGGAAAGTCT ATCATTATAT CCTGTAGTGT GGCAGGTGAT 1020
CGGTTCTCTA ATATGATATG GATGTTGGT AACCTGGTTT CCAAACATAT GAATGAAACA 1080
AGCCACACAG AGGCTCTCTT AAGGATAACT AACATTTTCC CCGATGACAT TGGGAAGCAG 1140
ATCTCTTGTG TGGCGGAAAA TCTTGTAGGA GAAGATCAAG ATTCTGTCAA CCTCACTGTG 1200
CATTTTGCAC CAACTATCAC ATTTCTCGAA TCTCCAACCT CAGACCACCA CTGGTGCATT 1260
CCATTCACTG TCGAAGGCAA CCGCAACCAA CGCCTTCAGT GGTCTATATA CGGGGCAATA 1320
TTGAATGAGT CCAATACATC CTGTACTAAA ATACATGTTA CCAATCACAC GGAGTACCAC 1380
GGCTGGCTCC AGCTGGATTA TCCCACTCAC ATGAACAATG GGGACTACAC TCTAATAGCC 1440
AAGAATGAGT ATGGGAAGGA TGAGAAACAG ATTTCTGCTC ACTTCATGGG CTGGCCTGGA 1500
ATTGACGATG GTGCAAAACC AAATTATCCT GATGTAATTT ATGAAGATTA TGGAACTGCA 1560
GCGAATGACA TCGGGAGCAC CACGAACAGA AGTAATGAAA TCCCTTCAC AGACGTCAC 1620
GATAAACCAG GTCCGGGAACA TCTCTCGGTC TATGCTGTGG TGGTGATTGC GTCTGTGGTG 1680
GGATTTTGGC TTTTGTGTAAT GCTGTTTCTG CTTAAGTTGG CAAGACACTC CAAGTTTGGT 1740
ATGAAGGCC CAGCCTCCGT TATCAGCAAT GATGATGACT CTGCCAGCCC ACTCCATCAC 1800
ATCTCCAATG GGAGTAACAT TCCATCTTCT TCGGAAGGTG GCCCAGATGC TGTCAATTAT 1860
GGAATGACCA AGATCCCTGT CATTGAAAAT CCCAGTACT TTGGCATCAC CAACAGTCAG 1920
CTCAAGCCAG ACACATTTGT TCAGCACATC AAGCGACATA ACATTTGTCT GAAAGGGGAG 1980
CTAGGCGAAG AACTGCTTGG AAAAGTGTTC CTAGCTGAAT GCTATAACCT CTGTCTGTAG 2040
CAGGACAGA TCTTGGTGGC AGTGAAGACC CTGAAGGATG CCAATGACAA TGCAACGAAG 2100
GACTTCCACC GTGAGGCCGA GCTCCTGACC AACCTCCAGC ATGAGCACAT CGTCAAGTTC 2160
TATGGCGTCT GCGTGGAGGG CGACCCCTCT ATCATGGTCT TTGAGTACAT GAAGCATGGG 2220
GACCTCAACA AGTTCTCTAG GGCACACGGC CCTGATGCCG TGCTGATGGC TGAGGGCAAC 2280
CGGCCACGG AACTGAGGCA GTGCGAGATG CTGCATATAG CCCAGCAGAT CGCCGCGGGC 2340
ATGGTCTACC TGGCGTCCCA GCACCTCTGT CACCGCGATT TGGCCACGAG GAACTGCCTG 2400
GTCGGGGAGA ACTTGCTGGT GAAAATCGGG GACTTTGGGA TGTCCCGGGA CGTGATACAG 2460
ACTGACTACT ACAGGGTCGG TGGCCACACA ATGCTGCCCA TTCGCTGGAT GCCTCCAGAG 2520
AGCATCATGT ACAGGAAAT CACGACGGAA AGCGACGTCT GGAGCGCTGG GGTGCTGTGG 2580
TGGGAGATTT TCACCTATGG CAACACGCCC TGGTACCAGC TGTCAACAAA TGAGGTGATA 2640
GAGTGTATCA CTCAGGGCCG AGTCTCTGAG CGACCCCGCA CGTGCCCGCA GGAGGTGTAT 2700
GAGCTGATGC TGGGGTGTCT GCAGCGAGAG CCCACATGA GGAAGAACAT CAAGGGCATC 2760
CATACCTCTC TCCAGAACTT GGCACAGGCA TCTCCGCTCT ACCTGGACAT TCTAGGCTAG 2820
GGCCCTTTTC CCCAGACGCA TCCTTCCCAA CGTACTCCTC AGAGCGGGCTG AGAGGATGAA 2880
CATCTTTTAA CTGCGCTGG AGGCCACCAA GCTGCTCTCC TTAATCTGTA CAGTATTAAC 2940
ATCAAGAGCT CCGAGAAGCT CTCGAGGGAA GCAGTGTGTA CTCTCTCATC CATAGACACA 3000
GTATTGACTT CTTTGTGCA TATCTCTTCT CTCTCTTCCC ATCTCCCTTG GTTGTCTCTT 3060
TTTCTTTTTT TAAATTTTCT TTTTCTTCTT TTTTTCGTC TTCCCTGCTT CACGATCTCT 3120
ACCTTTTCTT TTGAATCAAT CTGGCTTCTG CATTACTATT AACTCTGCAT AGACAAAGGC 3180
CTTAAACAAC GTAATTTTGT ATATCAGCAG ACACTCCAGT TTGCCACCA CAATTAACAA 3240
TGCTTGTGTT TATTCCTGCC TTTGATGTGG ATGAAAAAAA GGGAAAAACA ATATTTCACT 3300
TAAACTTTGT CACTTCTGCT GTACAGATAT CGAGAGTTTC TATGGATTCA CTTCTATTTA 3360
TTTATTATTA TTAAGTTTCT TATTGTTTCT GGATGGCTTA AGCCTGTGTA TAAAAAGAA 3420
AACTTGTGTT CAATCTGTGA AGCCTTTATC TATGGGAGAT TAAACCAGA GAGAAAGAG 3480
ATTTATTATG AACCGCAATA TGGGAGGAAC AAAGACAACC ACTGGGATCA CTGGTGTCA 3540
GTCCCTACTT AGGAAATACT CAGCAACTGT TAGCTGGGAA GAATGTATTG GGCACCTTCC 3600
CTGAGGACCT TTTCTGAGGA GTAAAAAGAC TACTGGCCTC TGTGCCATGG ATGATTCTTT 3660
TCCCATCACC AGAAATGATA GCGTGCAGTA GAGAGCAAAG ATGGCTTT

```

Seq ID NO: 595 Protein sequence
Protein Accession #: NP_006171.1

```

75      1      11      21      31      41      51
|      |      |      |      |      |
MSSWIRWHGP AMARLWGFCW LVVGFWRAAF ACPTSCCKSA SRIWCSDFSP GIVAFPRLEP 60
NSVDPENITE IFIANQKRL E IINEDDVEAY VGLRNLITVD SGLKFVAHKA FLKNSNLQHI 120
NFTRNKLTSL SRKHFRLDL SELILVGNPF TSCSDIMWIK TLQEAKESSPD TDLYCLNES 180
SKNIPLANLQ IPNCLPSAN LAAPNLVVEE GKSITLSCSV AGDPVPNNMYV DVGNLVSXHM 240
NETSHSQSL RITNISSDDS GKQISCAVEN LVGEDQDSVN LTVHFAPTIT FLESPTSDDH 300
WCIPFTVKGN PKPALQWYN GAILNESKYI CTKIHVTNHT EYHGLQLDN PTHMNGDYT 360
LIAKNEYGKH EQISAHFVG WPGIDDGANP NYPDVIYEDY GTAANDIGDT TNSRNEIPST 420
DVTDKTGREH LSVYAVVIA SVVGFCLLVM LFLKLARHS KFGMKGPASV ISNDDDSASP 480
LHHISNGSNT PSSSEGGPDL VIIGMTKIPV IENPOYFGIT NSQLKPDFTFV QHKRHNIVL 540
85      KRELGEAGFQ KVFLAECYNL CPEQDKILVA VKTLKADSDN ARKDFHREAE LLTNLQHEHI 600
VRFYGVCEG DPLIMVFYEM KHGDLNKLFLR AHGPDVAVLMA EGNPFTELTO SQMLHIAQOI 660
AAGMVYLASQ HFVHRDLATR NCLVGENLLV KIGDFGMSRD VYSTDYRVG GHMTLPIRMW 720

```


PPESIMYRKP TTBSDVWBLG VVLWEIFTYG KQFWYQLSNN EVIECITQGR VLQRPRTCPQ 780
 EVYELMLGCW QREPHMRKNI KGIHTLLQNL AKASPVYLDI LG

Seq ID NO: 596 DNA sequence
 Nucleic Acid Accession #: AF410899
 Coding sequence: 483..2999

	1	11	21	31	41	51	
10	GGGAGCAGGA	GCCTCGCTGG	CTGCTTCGCT	CGCGCTCTAC	GCGCTCAGTC	CCCGGCGGTA	60
	GCAGAGCCCT	GGACCCAGCG	GCCGCGGGCG	GGCGTGAGGC	GCCGAGAGCC	GGCCTCGAGG	120
	TGCATACCGG	ACCCCATCTC	GCATCTAACA	AGGAATCTGC	GCCCCAGAGA	GTCCCGGACG	180
	CCGCGCGTGC	GTGCCCGGCG	CGCCGGGCCA	TGCAGCGACG	GCGCCGCGCG	AGCTCCGAGC	240
15	AGCGGTAGCG	CCCCCTGTGA	AAGCGGTTGG	CTATGCCGGG	ACCACTGTGA	ACCCTGCCGC	300
	CTGCCGGAAC	ACTCTTCGCT	COGACCAAGC	TCAGCTCTGT	ATAAGCTGGA	CTCGGCACCG	360
	CCGCAACAAG	CACCGAGGAG	TAAAGAGAGC	CGCAAGCGCA	GGGAAGGCGT	CCCCGCACCG	420
	GTGGGGGAAA	GCGGCGCGTG	CAGCGCGGGG	ACAGGCACTC	GGGCTGGCAC	TGGCTGCTAG	480
	GGATGTCGTC	CTGGATAAGG	TGGCATGGAC	CCGCCATGGC	GCGGCTCTGG	GGCTTCTGCT	540
20	GGCTGGTTGT	GGGCTTCTGG	AGGGCCGCTT	TGCGCTGTCC	CACGTCCTGC	AAATGCAGTG	600
	CCCTCTCGAT	CTGGTGCAGC	GACCCCTTCT	CTGGCATCGT	GGCATTTCGG	AGATTGGAGC	660
	CTAACAGTGA	GGATGCTAGG	AACATCACCG	AAATTTTCAT	CGCAAAACCAG	AAAAGGTTAG	720
	AAATCATCAA	CGAAGATGAT	GTTGAAGCTT	ATGTGGGACT	GAGAAATCTG	ACAATTGTGG	780
	ATTCTGGATT	AAAAATTTGT	GCTCATAAAG	CATTTCTGAA	AAACAGCAAC	CTGCAGCACA	840
25	TCAATTTTAC	CGAAACAAAA	CTGACGAGTT	TGTCTAGGAA	ACATTTCGGT	CACCTTGACT	900
	TGCTGAAGAT	GATCCTGGTG	GGCAATCCAT	TTACATGCTC	CTGTGACATT	ATGTGGATCA	960
	AGACTCTCCA	GATCTCTTGT	TCCAGTCCAG	ACACTCAGGA	TTTGTACTGC	CTGAATGAAA	1020
	GCAGCAAGAA	TATCCCCCTG	GCAAACTCTG	AGATACCCAA	TTTGTGTTTG	CCATCTGCAA	1080
	ATCTGGCGCG	ACCTAACCTC	ACTGTGGAGG	AAGGAAAGTC	TATCACATTA	TCCTGTAGTG	1140
30	TGGCAGGTGA	TCCGTTTCCT	AATATGTATT	GGGATGTTGG	TAACTTGTTT	TCCAAACATA	1200
	TGAATGAAAC	AAGCCACACA	CAGGGCTCCT	TAAGGATAAC	TAAACATTCA	TCCGATGACA	1260
	GTGGGAAGCA	GATCTCTTGT	GTGGCGGAAA	ATCTTGTAGG	AGAAGATCAA	GATTCTGTGA	1320
	ACCTCACTGT	GCATTTTGCA	CCAACTATCA	CATTTCTCGA	ATCTCCAACC	TCAGACCACC	1380
	ACTGGTGCAI	TCCATTCACT	GTGAAAGGCA	ACCCCAAACC	AGCGCTTCAG	TGGTTCTATA	1440
35	ACGGGGCAAT	ATTGAATGAG	TCCAAATACA	TCTGTACTAA	AATACATGTT	ACCAATCACA	1500
	CGGAGTACCA	CGGCTGCCTC	CAGCTGGATA	ATCCCACTCA	CATGAACAAT	GGGGACTACA	1560
	CTCTAATAGC	CAAGAAATGAG	TATGGGAAGG	ATGAGAAACA	GATTTCGTCT	CACCTTCATG	1620
	GCTGGCCTCG	AATTGACGAT	GGTGCAAAAC	CAAATATATC	TGATGTAATT	TATGAAGATT	1680
	ATGGAAGTGC	AGCGAATGAC	ATCGGGGACA	CCACGAACAG	AAGTAATGAA	ATCCCTTCCA	1740
40	CAGACGTAC	TGATAAAACC	GGTCGGGAAC	ATCTCTCGGT	CTATGCTGTG	GTGGTGATTG	1800
	CGTCTGTGGT	GGGATTTTGC	CTTTTGTGTA	TGCTGTTTCT	GCTTAAAGTG	GCAAGACACT	1860
	CCAGATTGG	GATCTCTGAT	TTCTCATGGT	TTGGATTGAG	GAAAGTAAAA	TCAAGACAAG	1920
	GTGTGGCCCC	AGGCTCCGTT	ATCAGCAATG	ATGATGACTC	TGCCAGCCCA	CTCCATCACA	1980
	TCTCCAATGG	GAGTAACACT	CCATCTTCTT	CGGAAGGTGG	CCCAGATGCT	GTCAATTATT	2040
45	GAATGACCAA	GATCCCTGTC	ATTGAAAATC	CCCAGTACTT	TGGCATCACC	AACAGTCAGC	2100
	TCAGGACGAA	CACATTTGTT	CAGCACATCA	AGCGACATAA	CATTGTTCTG	AAAAGGGAGC	2160
	TAGGCGAAGG	AGCCCTTTGG	AAAGTGTTC	TAGCTGAATG	CTATAACCTC	TGCTCTGAGC	2220
	AGGACAGAT	CTTGTGTGCA	GTGAAGACCC	TGAAGGATGC	CAGTGACAA	GACGCAAGG	2280
	ACTTCCACCG	TGAGGCCGAG	CTCTGACCA	ACCTCCAGCA	TGAGCACATC	GTCAAGTTCT	2340
50	ATGGCGTCTG	CGTGGAGGGC	GACCCCTCA	TCATGGTCTT	TGAGTACATG	AAGCATGGGG	2400
	ACCTCAACAA	GTTTCTCAGG	GCACACGGCC	CTGATGCCGT	GCTGATGGCT	GAGGGCAACC	2460
	CGCCACGGA	ACTGACGAG	TGCGAGATGC	TGCATATAGC	CCAGCAGATC	GCCGCGGGCA	2520
	TGGTCTACCT	GGCGTCCGAG	CACCTTCGTG	ACCGCGATT	GGCCACCAAG	AACCTGCTGG	2580
	TCGGGGAGAA	CTTGTCTGGT	AAAATCGGGG	ACITTTGGAT	GTCCCGGGAC	GTGTACAGCA	2640
55	CTGACTACTA	CAGGGTCCGT	GGCCACACAA	TGCTGCCCAT	TCGCTGGATG	CCTCCAGAGA	2700
	GCATCTATGA	CAGGAAATTC	ACGACGAAAA	GCGACGCTCT	GAGCCTGGGG	GTGCTGTTGT	2760
	GGGAGATTTT	CACCTATGGC	AAACAGCCCT	GGTACCAGCT	GTCAAAACAT	GAGGTGATAG	2820
	AGTGTATCAC	TCAGGGCCGA	GTCTCTGAGC	GACCCCGCAC	GTGCCCCCAG	GAGGTGTATG	2880
	AGCTGATGCT	GGGGTCTGGG	CAGCGAGAGC	CCCAATGAG	GAAAGAACAT	AAGGGCATCC	2940
60	ATACCCCTCT	TCAGAACTTG	GCCAAAGCAT	CTCCGGTCTA	CCTGACATT	CTAGGCTAGG	3000
	GCCTTTTCC	CCAGACCGAT	CCTTCCCAAC	GTACTCTCTA	GACGGGCTGA	GAGGATGAAC	3060
	ATCTTTTAA	TGCCGCTGGA	GGCCACCAAG	CTGCTCTCCT	TCACCTGAC	AGTATTAAAC	3120
	TCAAAGACTC	CAGAAAGCTC	TCGAGGGAAG	CAGTGTGTAC	TTCTTATACC	ATAGACACAG	3180
	TATTGACTCT	TTTTTGGCAT	TATCTCTTTC	TCTCTTTCCA	TCTCCCTTGG	TTGTTCTTTT	3240
65	TTCTTTTTTT	AAATTTTCTT	TTTCTTCTT	TTTTTCTGCT	TCCCTGCTTC	ACGATTCTTA	3300
	CCCTTTCTTT	TGAATCAATC	TGGCTTCTGC	ATTACTATTA	ACTCTGCATA	GACAAAGGCC	3360
	TTAACAAACG	TAATTTGTTA	TATCAGCAGA	CACCTCAGTT	TGCCCAACAC	AACTAACAT	3420
	GCCTTGTGTT	ATCTCTGCTT	TTGATGTGGA	TGAAAAAAG	GGAAAAACAA	TATTTCACCT	3480
	AAACTTTTGT	ACTCTGCTGT	TACAGATATC	GAGAGTTTCT	ATGGATTAC	TTCTATTAT	3540
70	TTATTATTAT	TACTGTTCTT	ATTGTTTTTG	GATGGCTTAA	GCCTGTGTAT	AAAAAGAAA	3600
	ACTTGTGTTT	AATCTGTGAA	GCCTTTATCT	ATGGGAGATT	AAAAACAGAG	AGAAAGAGA	3660
	TTTATTATGA	ACCGCAATAT	GGGAGGAACA	AAGACAACCA	CTGGGATCAG	CTGGTGTGAC	3720
	TCCTTACTTA	GGAAATACTC	AGCAACTGTT	AGCTGGGAAG	AATGTATTGG	GCACCTTCCC	3780
	CTGAGGACCT	TTCTGAGGAG	TAAAAAGACT	ACTGGCCTCT	GTGCCATGGA	TGATTCTTTT	3840
75	CCCATCACCA	GAAATGATAG	CGTGCAAGTAG	AGAGCAAAGA	TGGCTTCCGT	GAGACACAAG	3900
	ATGGCGCATA	GTGTGCTCGG	ACACAGTTTT	GTCTTCTGTG	GTGTGTATGA	TAGCACTGGT	3960
	TTGTTTCTCA	AGCGCTATCC	ACAGAACTTT	TGTCAACTTC	AGTTGAAAAG	AGGTGGATTG	4020
	ATGTCAGAG	CTCATTTCCG	GGTCAGGTGG	GAAAGCC			

Seq ID NO: 597 Protein sequence
 Protein Accession #: AAL67965.1

	1	11	21	31	41	51	
85	MSSWIRWHGP	AMARLWGFCE	LUVGFWRAAF	ACPTSCCKCSA	SRWCSDFSP	GIVAFPRLEP	60
	NSVDPENITE	IFIANQKRL	INEDDVEAY	VGLRNLITVD	SGLFKFAHKA	FLKNSNLQHI	120
	NPTRNKLTS	SRKHFRHL	SELILVGNPF	TCSCDIMWIK	TLQEAQSSPD	TQDLYCLNES	180
	SKNIPLANLQ	INCGLPSPN	LAAPNLTVET	GKSIITLSCSV	AGDPVPNMWY	DVGNLVSKHM	240

NETSHTQGSGL RITN1SSDDSGKQISCVAEN LVGEDQDSVN LTVHFAPTIT FLESPTSDHH 300
WCIPFTVKGK PKPALQWFYNGAILNESKYI CTKIHVTNHT EYHGCLQLDN PTHMNGDYT 360
LIAKNEYGKD EKQISAHFMG WFGIDDDGANP NYPDVIYEDY GTAANDIGDT TNRSNEIPST 420
5 DVTDKTGREH LSVYAVVVIA SVVGFCLLVM LFLKLARHS KFGMKDPSWF GFGKVKSRQG 480
VGPAVISND DDSASPLHHI SNGSNTFSSS EGGPDVAIIG MTKIPVIEHP QYFGITNSQL 540
KPDTFVQH1K RHNI1VKREL GEGAFGKVFL ABCYNLCPEQ DKILVAVKTL KDASDNARKD 600
FHREAE1LTN LQHEHIVKFY GVCVEGDPLI MVFEYMKHGD LNKFLRAHGP DAVLMAEGNP 660
PTELTQSQML HIAQ1IAAGM VYLASQHFVH RDLATRNCLV GENLLVKIGD FGMSRDVYST 720
10 DYYRVGGHTM LPIRWMPES IMYRKFTTES DVWSLGVVLW EIFTYKGQPW YQLSNNEVIE 780
CITQGRVLQR PRTCEQEVYE LMLGCWQREP HMRKNIKGIH TLLQNLAKAS PVYLDILG

Seq ID NO: 598 DNA sequence
Nucleic Acid Accession #: AB052906
Coding sequence: 74..814

1 11 21 31 41 51
| | | | | |
AAAACCTTGA GGTGATTCAT CTTCCAGGCT CTCCTTCCAT CAACTCTCTC CTCCCTAGCG 60
20 CTCTGGGTCC TTAATGGCAG CAGCCGCCGC TACCAAGATC CTTCTGTGCC TCCCGCTTCT 120
GCTCCTGCTG TCCGCTAGGT CCCGGGCTGG GCGAGCCGAC CCTCACTCTC TTGTGCTATGA 180
CATCACCGTC ATCCCTAAGT TCAGACCTGG ACCACGGTGG TGTGCGGTTC AAGGCCAGGT 240
GGATGAAAAG ACTTTTCTTC ACTATGACTG TGGCAACAAG ACAGTCACAC CTGTCAGTCC 300
CCTGGGGAAG AAACATAATG TCACAACGGC CTGGAAGACA CAGAACCAG TACTGAGAGA 360
25 GGTGGTGGAC ATACTTACAG AGCAACTGCG TGACATTCAG CTGGAGAATT ACACACCCAA 420
GGAACCCCTC ACCCTGACAG CCAGGATGTC TTGTGAGCAG AAAGCTGAAG GACACAGCAG 480
TGGATCTTGG CAGTTCAAGT TCGATGGGCA GATCTTCTCT CTCTTTGACT CAGAGAAGAG 540
AATGTGGACA ACGGTTATC CTGGAGCCAG AAAGATGAAA GAAAAGTGGG AGAATGACAA 600
GGTTGTGGCC ATGTCCTTCC ATTACTTCTC AATGGGAGAC TGTATAGGAT GGCTTGAGGA 660
30 TTCTTTGATG GGCATGGACA GCACCCCTGA GCCAAGTGCA GGAGCACCAC TCGCCATGTC 720
CTCAGGACCA ACCCAACTCA GGGCCACAGC CACCACCTC ATCCTTTGCT GCCTCTCTAT 780
CATCCTCCCC TGCTTCATCC TCCCTGGCAT CTGAGGAGAG TCCTTTAGAG TGACAGGTTA 840
AAGCTGATAC CAAAAGGCTC CTGTGAGCAC GGTCTTGATC AAACCTCGCC TTCTGTCTGG 900
CCAGCTGCCC ACGACCTACG GTGTATGTCC AGTGGCTCC AGCAGATCAT GATGACATCA 960
35 TGGACCCAAT AGCTCATTCA CTGCCTTGAT TCCTTTTGCC AACAATTTTA CCAGCAGTTA 1020
TACCTAACAT ATTATGCAAT TTTCTCTTGG TGCTACCTGA TGGAAATCCT GCACTTAAAG 1080
TTCTGGCTCA CTAAACAAGA TATATCATT TCTTTCTTCT CTTTGTGTTT GGAAATCAA 1140
GTACTTCTTT GAATGATGAT CTCTTCTTGG CAAATGATAT TGTCAAGTAA ATAATCACGT 1200
TAGACTTCAG ACCTCTGGGG ATTCTTTCOG TGTCTGAAA GAGAATTTT AAATTATTTA 1260
40 ATAAGAAAAA ATTTATATTA ATGATTGTTT CCTTTAGTAA TTTATTGTTT TGTACTGATA 1320
TTTAATAATA GAGTCTATT TCCAAAAA AAAAAAAAAA AA

Seq ID NO: 599 Protein sequence
Protein Accession #: BAB61048.1

1 11 21 31 41 51
| | | | | |
MAAAATKIL LCLPLLLLLS GWSRAGRADP HSLCYDITVI PKFRPGPRWC AVQGVDEKT 60
45 FLHYDCGNKT VTPVSP1GKK LNVTTAWKAQ NPVLREVVDI LTELRLDIQL ENYTPKEPLT 120
LQARMSCEBQ AEGHSSGSWQ FSPDQIPLL FDSEKRMWTT VHPGARKMKE KWENDKVAM 180
50 SFHYFSMGDC IGWLEDFLMG MDSTLEPSAG APLAMSSGTT QLRATATTLI LCCLLIILPC 240
FILFPI

Seq ID NO: 600 DNA sequence
Nucleic Acid Accession #: NM_001898.1
Coding sequence: 57..482

1 11 21 31 41 51
| | | | | |
GGCTCTCACC CTCCTCTCCT GCAGCTCCAG CTTTGTGCTC TGCCCTCTGAG GAGACCATGG 60
60 CCCAGTATCT GAGTACCCTG CTGCTCCTGC TGGCCACCTC AGCTGTGGCC CTGGCCTGGA 120
CCCCAAGGA GGAGGATAGG ATAATCCCGG GTGGCATCTA TAACGAGAC CTCAATGATG 180
AGTGGGTACA GCGTGCCCTT CACTTCGCCA TCAGCGAGTA TAACAAGGCC ACCAAGATG 240
ACTACTACAG ACGTCCGCTG CGGGTACTAA GAGCCAGGCA ACAGACCGTT GGGGGGGTGA 300
65 ATACTTCTT CGACGTAGAG GTGGGCCGCA CCATATGTAC CAAGTCCAGC CCCAACTTGG 360
ACACCTGTGC CTTCATGAA CAGCCAGAAC TGCAGAAGAA ACAGTTGTGC TCTTTCGAGA 420
TCTACGAAGT TCCCTGGGAG AACAGAAGGT CCCTGGTGAA ATCCAGGTGT CAAGAATCCT 480
AGGGATCTGT GCCAGGCCAT TCGCACCAGC CACCACCCAC TCCACCCCCC TGTAGTGCTC 540
CCACCCCTGC ACTGGTGGCC CCCACCTGC GGGAGGCCCT CCCATGTGCC TGCGCCAAGA 600
70 GACAGACAGA GAAGCTGCA GGAGTCCTTT GTTGCTCAGC AGGGCGCTCT GCCTCCCTC 660
CTTCTTCTT GCTTCTAATA GCCCTGTGAC ATGGTACACA CCCCCCACC TCCTGCAATT 720
AAACAGTAGC ATCGCC

Seq ID NO: 601 Protein sequence
Protein Accession #: NP_001889.1

1 11 21 31 41 51
| | | | | |
MAQYLSTLLL LLATLAVALA WSPKEEDRII FGGIYNADLN DEWVQRALHF AISBYNKATK 60
80 DDYRRPLRV LRARQQTGG VNYFFDVEVG RTICTKSQPN LDTCAFHEQP ELQKKQLCSF 120
EIYEVWENR RSLVSRQCE S

Seq ID NO: 602 DNA sequence
Nucleic Acid Accession #: NM_003976.2
Coding sequence: 299..961

1 11 21 31 41 51
| | | | | |

CTCTGAGCTT CTCTGAGCCT TGTTTGCTCA TCTGGA AAAA GGGGATTAAA CCATTACCT 60
CATGGAGTTG TGAAGAATA GCTGCAAGC ACCTAACACA TAGTAAGGTT CCCAGTGCAG 120
CTACTTCTGC TGGGTGAGT CTAGCTGTGT AGGCCCCCTG TTCTCACCT GGAGAAACTG 180
GGGTGGCAGG CCGGTCCCCC ACAAAGATA ACTCATCTCT TAATTGCAA GCTGCCTCAA 240
CAGGAGGGTG GGGGAACAGC TCAACAATGG CTGATGGGCG CTCTGGTGTG TGATAGAGAT 300
GGAACTTGGA CTTGAGAGCC TCTCCACGCT GTCCCACTGC CCCTGGCCTA GCGGCGAGCC 360
TGCCCTGTGG CCCACCTGG CCGCTCTGGC TCTGCTGAGC AGCGTCGAGC AGGCCTCCCT 420
GGGCTCCGCG CCCCCGAGCC CTGCCCCCGG CGAAGGCCCC CCGCTGTGCC TGGCGTCCCC 480
CGCCGCGCAC CTGCGGGGGG GACGCAAGC CCGCTGTGTC AGTGAAGAGC CCCGGCGGCC 540
GCGCGCGCAG CCTTCTGGGC CCGCGCCCCC GCGCCTGCA CCCCCTCTG CTCTTCCCCG 600
CGGGGGCGCG GCGCGCGGGG CTGGGGGGCC GGGCAGCGCG GCTCGGGCAG CCGGGGCGCG 660
GGGCTGCCCG CTGCGCTCGC AGCTGGTGCC GGTGCGCGCG CTGCGCTGGG GCCACCGCTC 720
CGACGAGCTG GTGCGTTTCC GCTTCTGCAG CCGCTCCTGC CCGCGCGCGC GCTCTCCACA 780
CGACCTCAGC CTGCGCGAGC TACTGGGCGC CCGGGCCCTG CGACCGCCCC CCGGCTCCCG 840
GCCCGTCAGC CAGCCCTGCT GCCGACCCAC GCGCTACGAA GCGGTCTCCT TCATGAGAGT 900
CAACAGCAGC TGGAGAAGC TGGACCGCCT CTCGCCACC GCCTGGCGCT GCCTGGGCTG 960
AGGGCTCGCT CCAGGGCTTT GCAGACTGGA CCCTTACCGG TGGCTCTTCC TGCTTGGGAC 1020
CCTCCCGCAG AGTCCCACTA GCCAGCGGCC TCAGCCAGGG ACGAAGGCCT CAAAGCTGAG 1080
AGGCCCTGAC CCGTGGGTGA TGGATATCAT CCGCGAACAG GTGAAGGAGC AACTGACTAG 1140
CAGCCCCAGA GCCCTCACCC TGCGGATCCC AGCCTAAAAG ACACAGAGAA CCTCAGCTAT 1200
GGAGCCCTTC GAGCGCCCTT CTCACAGACT CTGGCACTGG CCAGGCTCG AACCTGGGAC 1260
CCCTCCTCTG ATGAACACTA CAGTGGCTGA GGCATCAGCC CCGGCCCAGG CCTGTAGGG 1320
ACAGCATTTG AAGGACACAT ATTGCAGTTG CTTGGTTGAA AGTGCTGTG CTGGAACCTG 1380
CCTGTACTCA CTCATGGGAG CTGGCCCC

Seq ID NO: 603 Protein sequence
Protein Accession #: NP_003967.1

1 11 21 31 41 51
MELGLGGLST LSHCPWPRRQ PALWPTLAAL ALLSSVAEAS LGSAPRSPAP REGPPPVLAS 60
PAGHLPGGRT ARWCSSRRARR PPPQPSRPAP PPPAPPSALP RGGRARAGG PGSRARAAGA 120
RGCRRLRSQVL PVRALGLGHR SDELVRFRFC SGSCRRARSP HDLSLALSLG AGALRPPPGS 180
RPVSQPCCRP TRYEAVSFMD VNSTWRTVDR LSATACGCLG

Seq ID NO: 604 DNA sequence
Nucleic Acid Accession #: NM_057091.1
Coding sequence: 783..1445

1 11 21 31 41 51
ACTGGCCGCT GAGAGAAGAA TCGGGTGGAG CAGAGAGCAG CTGCTGCAGG GCAGACAGCC 60
GGACCCCCAA ATCTGCACGT ACCAGCAGTC AGCCGCCCCA CGCAGGGACC GGCTTACCCC 120
TCGCTCCCCG CCTCACTCA CTCTCTCCCG CCTCGGCCG GGCCTCCAGC CTCTCTACTT 180
CGCGTGTCTA CAAACTCAAC TCCCGGTTTC CGTGCCCTTC CACCGCTCGA GTTCTCTACT 240
TCTCATATCC GAGGGGCCCC TCCAGCATC TACCCCTTC CCAACCTCGG GGGACCTAGC 300
CAAGCTAGGG GGGACTGGAT CCGCAGGGTG GAGCAGCCAG GTGAGCCCGG AAAGGTGGGG 360
CGGGGCAAGG GCGCTCCAG CCCACCCCG GGATCTGGTG ACGCTGGGGC TGGAAATTGA 420
CACCGGACGG CTGCGGCGGC GGGCAGGAGG CTGCTGAGGG ATGGAGTTGG GCCCGGCCCC 480
CAGACAAGGC CCGGGGGCTC CGCCAGCAGC AGGTCCCTCG GGCCTCCAGC CTGCTGCCA 540
CCCGGGCCTG GAGCCCCACA CCCGAGGGTG CAGACTGGCT GCCAAGGCCA CACTTTTGGC 600
TAAAGAGGCG ACTGCCAGGT GTACAGTCTT GGGCATGCGC TGTTTGAGCT TCGGGGGAGA 660
GCCCGACACT GCTCCCGGGA AAGGTGCCTA GAAGAACAAG GTGCAGGACC CCGTGTCTGC 720
TCAACAGGAG GGTGGGGGAA CAGCTCAACA ATGGCTGATG GGCCTCTCTG GTGTTGATAG 780
AGATGGAAGT TGGACTTGGG GGCCTCTCCA CGCTGTCCCA CTGCCCCTGG CCTAGGCGGC 840
AGCCTGCCCC CTGGCCGCTC CTGGCCGCTC TGGCTCTGCT GAGCAGCGTC GCAGAGCCCT 900
CCCTGGGCTC CCGCGCCCGC AGCCCTGCCC CCGCGGAAGG CCCCCCGCCT GTCTTGGCGT 960
CCCCCGCGCG CCGCTTGGC GGGGAGCGCA CCGCCGCTG GTGCAGTGA AGAGCCCGGC 1020
GGCCCGCGCC GCAGCTTCT CCGCCCGCGC CCGCGCGGCC TGACCCCCCA TCTGCTCTTC 1080
CCCGCGGGGG CCGCGCGGCG CCGGCTGGGG GCCCGGGCAG CCGCGCTCGG GCAGCGGGGG 1140
CGCGGGGCTG CCGCTTGGC TCGCAGCTGG TGCCGCTGCG CCGCTCTGCG CTGGGCCACC 1200
GCTCGGACGA GCTGTGGGT TTCCGCTTCT GCAGCGGCTC CTGCGCGCGC GCGCGCTCTC 1260
CACACGACCT CAGCCTGGCC AGCCTACTGG CCGCGGGGGC CTTGCGACCG CCCCCGGGCT 1320
CCCGGCCCGT CAGCCAGCCC TGCTGCCGAC CCACGCGCTA CGAAGCGGTC TCCTTCATGG 1380
ACGTCAACAG CACCTGGAGA ACCGTGGACC GCCTCTCCGC CACCGCTGCG GGTGCTCTGG 1440
GCTGAGGGCT CGCTCCAGGG CTTTGCAGAC TGGACCTTA CCGGTGGCTC TTCTTGCCTG 1500
GGACCTCCC GCAGAGTCCC ACTAGCCAGC GGCTCAGCC AGGGACGAAG GCCTCAAAGC 1560
TGAGAGGCCC CTACCGGTGG GTGATGGATA TCATCCCCGA ACAGGTGAAG GGACAACTGA 1620
CTAGCAGCCC CAGAGCCCTC ACCCTGCGGA TCCCAGCCTA AAAGACACCA GAGACCTCAG 1680
CTATGAGGCC CTTGAGCCC ACTTCTCACA GACTCTGGCA CTGCGCAGGC CTCGAACCTG 1740
GGACCCCTCC TCTGATGAAC ACTACAGTGG CTGAGGCATC AGCCCCCGCC CAGGCCCTGT 1800
AGGGACAGCA TTTGAAGGAC ACATATTGCA GTTGCTTGGT TGAAGTGCC TGTGCTGGAA 1860
CTGGCCTGTA CTCATCATG GGAGCTGGCC CC

Seq ID NO: 605 Protein sequence
Protein Accession #: NP_003967.1

1 11 21 31 41 51
MELGLGGLST LSHCPWPRRQ PALWPTLAAL ALLSSVAEAS LGSAPRSPAP REGPPPVLAS 60
PAGHLPGGRT ARWCSSRRARR PPPQPSRPAP PPPAPPSALP RGGRARAGG PGSRARAAGA 120
RGCRRLRSQVL PVRALGLGHR SDELVRFRFC SGSCRRARSP HDLSLALSLG AGALRPPPGS 180
RPVSQPCCRP TRYEAVSFMD VNSTWRTVDR LSATACGCLG

Seq ID NO: 606 DNA sequence
Nucleic Acid Accession #: NM_057160.1

Coding sequence: 1..714

	1	11	21	31	41	51	
5	ATGCCCGGGC	TGATCTCAGC	CCGAGGACAG	CCCTCCTTGT	AGGTCCCTTC	TCCCCAAGCC	60
	CACCTGGGTG	CCCTCTTTCT	CCCTGAGGCT	CCACTTGGTC	TCTCCGCGCA	GCCTGCGCTG	120
	TGGCCCAACC	TGGCCGCTCT	GGCTCTGCTG	AGCAGCGTCG	CAGAGGCCTC	CCTGGGCTCC	180
	GGCCCCCGCA	GGCCCTGCCCC	CCGCGAAGGC	CCCCCGCCTG	TCCTGGCGTC	CCCCGCGGCG	240
10	CACCTGCGCG	GGGACGCGAC	GGCCCGCTGG	TGCAGTGGAA	GAGCCCGGCG	GCGCGCGCGG	300
	GAGCCTTCTC	GGCCCGCGCC	CCCGCGCGCT	GCACCCCAT	CTGCTCTTCC	CCGCGGGGCG	360
	CGCGCGGCGC	GGGCTGGGGG	CCCGGGCAGC	CGCGCTCGGG	CAGCGGGGCG	GCGGGGCTGC	420
	CGCTTGCCTG	CGCAGCTGGT	GCCGCTGCGC	CGCTCGGCC	TGGGCCACCG	CTCCGACGAG	480
	CTGGTGCCTT	TCCGCTTCTG	CAGCGGCTCC	TGCCCGCGCG	CGCGCTCTCC	ACACGACCTC	540
	AGCTTGGCCA	GCCTACTGGG	CGCGGGGGCC	CTGCGACCGC	CCCCGGGCTC	CCGCGCGCTC	600
15	AGCCAGCCCT	GCTGCCGACC	CACGCGCTAC	GAAGCGGTCT	CCTTCATGGA	CGTCAACAGC	660
	ACCTGGAGAA	CGTCTGACCG	CCTCTCGGCC	ACCGCTCGCG	GCTGCTGGGG	CTGAGGGCTC	720
	GCTCCAGGGC	TTTGCACT	GGACCTTAC	CGGTGGCTCT	TCCTGCCTGG	GACCTCTCCG	780
	CAGAGTCCCA	CTAGCCAGCG	GCCTCAGCCA	GGGACGAAGG	CCTCAAAGCT	GAGAGGCCCC	840
	TACCGTGGG	TGATGGATAT	CATCCCGAA	CAGGTGAAGG	GACAACTGAC	TAGCAGCCCC	900
20	AGAGCCCTCA	CCCTGCGGAT	CCCAGCCTAA	AAGACACCA	AGACCTCAGC	TATGGAGCCC	960
	TTGCGACCAA	CTTCTCAGC	ACTCTGGCAC	TGGCCAGGCC	TCGAACCTGG	GACCCCTCCT	1020
	CTGATGAACA	CTACAGTGGC	TGAGGCATCA	GCCCCCGCCC	AGGCCCTGTA	GGGACAGCAT	1080
	TTGAAGGACA	CATATTGCAG	TTGCTTGGTT	GAAAGTGCCT	GTGCTGGAAC	TGGCCTGTAC	1140
25	TCACCTCATG	GAGCTGGCCC	C				

Seq ID NO: 607 Protein sequence
Protein Accession #: NP_476501.1

	1	11	21	31	41	51	
30	MPGLISARGQ	PLLEVLPPQA	HLGALFLPEA	PLGLSAQPAL	WPTLAALALL	SSVAEASLGS	60
	APRSPAPRPG	PPFVLASAPG	HLPGGRTARW	CSGRARRPPF	QPSRPAPPPP	APPSALPRGG	120
	RAARAGGPGS	RARAAGARGC	RLRSQLVFVR	ALGLGHRSD	LVRFRFCSSG	CRRARSFHD	180
35	LSLASLLGAG	LRPPPGSRPV	SQPCRPTRY	EAVSFMDVNS	TWRTVDRLSA	TACGCLG	

Seq ID NO: 608 DNA sequence
Nucleic Acid Accession #: NM_057090.1
Coding sequence: 29..715

	1	11	21	31	41	51	
40	CTGATGGGCG	CTCCTGGTGT	TGATAGAGAT	GGAACCTTGA	CTTGGAGGCC	TCTCCACGCT	60
	GTCCCACTGC	CCCTGGCCTA	GGCGGCAGGC	TCCACTTGGT	CTCTCCGCGC	AGCCTGCCCT	120
	GTGGCCCAACC	TGGCCGCTCT	TGGCTCTGCT	GAGCAGCGTC	GCAGAGGCCT	CCCTGGGCTC	180
45	CGCGCCCGCG	AGCCCTTGCC	CCCGCGAAGG	CCCCCGCCT	GTCTGGGCT	CCCCGCGCGG	240
	CCACCTGCGG	GGGGGACGCA	CGGCGCGCTG	GTGCACTGGA	AGAGCCCGGC	GGCGCGCGCC	300
	GCAGCCTTCT	CGGCCCGCGC	CCCGCGCGCC	TGCACCCCA	TCTGCTCTTC	CCCGCGGGGG	360
	CCGCGCGGCG	CGGGCTGGGG	GCCCGGGCAG	CGCGCTCGG	GCAGCGGGGG	CGCGGGGCTG	420
	CCGCTTGCCT	TCGCACTGG	TGCGGGTGG	CGCGCTCGG	CTGGGCCACC	GCTCCGACGA	480
50	GCTGGTGCCT	TTCCGCTTCT	GCAGCGGCTC	CTGCCGCGC	GCGCGCTCTC	CACACGACCT	540
	CAGCCTGGCC	AGCCTACTGG	CGCGGGGGG	CCTGCGACCG	CCCCGGGCT	CCCGGCGCGT	600
	CAGCCAGCCC	TGCTGCCGAC	CCACGCGCTA	CGAAGCGGTC	TCCTTCATGG	ACGTCAACAG	660
	CACCTGGAGA	ACCTGGGACC	GCCTCTCGC	CACCGCCTGC	GGCTGCTTGG	GCTGAGGGCT	720
	CGCTCCAGGG	CTTTGCACT	TGGACCCCTA	CCGCTGGCTC	TTCTGCTTGG	GGACCTCTCC	780
55	GCAGAGTCCC	ACTAGCCAGC	GGCCTCAGCC	AGGGAACGAG	GCCTCAAAGC	TGAGAGGCCC	840
	CTACCGGTGG	GTGATGGATA	TCATCCCCGA	ACAGGTGAAG	GGACAACTGA	CTAGCAGCCC	900
	CAGAGCCCTC	ACCTTGCGGA	TCCAGCCTA	AAAGACACCA	GAGACCTCAG	CTATGGAGCC	960
	CTTGGAGCCC	ACTTCTCACA	GACTCTGGCA	CTGGCCAGGC	CTGAACTCTG	GGACCCCTCC	1020
	TCTGATGAAC	ACTACAGTGG	CTGAGGCATC	AGCCCCCGCC	CAGGCCCTGT	AGGGACAGCA	1080
60	TTGAAGGAC	ACATATTGCA	GTTGCTTGGT	TGAAAGTGCC	TGTGCTGGAA	CTGGCCTGTA	1140
	CTCACTCATG	GGAGCTGGCC	CC				

Seq ID NO: 609 Protein sequence
Protein Accession #: NP_476431.1

	1	11	21	31	41	51	
65	MELGLGGLST	LSHCPWPRRQ	APLGLSAQPA	LWPTLAALAL	LSSVAEASLG	SAPRSPAPRE	60
	GPPPVLASPA	GHLPGGRTAR	WCSGRARRPP	QPSRPAPPPP	PAPPSALPRG	GRAARAGGPG	120
70	SRARAAGARG	CRLRSQLVFV	RALGLGHRSD	ELVRFRFCSSG	SCRARSFHD	LSLASLLGAG	180
	ALRPPPGSRP	VSPCCRPTRY	YEAVSFMDVN	STWRTVDRLS	ATACGCLG		

Seq ID NO: 610 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..1746

	1	11	21	31	41	51	
80	ATGCCACTGA	AGCATTATCT	CCTTTTGCTG	GTGGGCTGCC	AAGCCTGGGG	TGCAGGGTTG	60
	GCCTACCATG	GCTGCCCTAG	CGAGTGTAAC	TGCTCCAGGG	CCTCCAGGT	GGAGTGCACC	120
	GGGGCACGCA	TTGTGGCGGT	GCCCAACCCT	CTGCCCTGGA	ACGCCATGAG	CCTGCAGATC	180
	CTCAACACGC	ACATCACTGA	ACTCAATGAG	TCCCGTTTCC	TCAATATCTC	AGCCCTCATC	240
	GCCTGAGGAA	TTGAGAAGAA	TGAGCTGTGG	CGCATCACGC	CTGGGGCTTC	CCGAACCTTG	300
	GGCTCGCTGC	GCTATCTCAG	CCTCGCCAAC	AAAGAGCTGC	AGGTTCTGCC	CATCGGCCTC	360
85	TTCCAGGGCC	TGAGCAGCCT	TGAGTCTCTC	CTTCTGTCCA	GTAACCAAGT	GTTGCAATATC	420
	CAGCCGGGCC	ACTTCTCCCA	GTGCAGCAAC	CTCAAGGAGC	TGCAGTTGCA	CGGCAACCAC	480
	CTGGAATACA	TCCCTGACGG	AGCCTTCGAC	CACCTGGTAG	GACTCACGAA	GCTCAATCTG	540

	GGCAAGAATA	GCCTCACCCA	CATCTCACCC	AGGGTCTTCC	AGCACCTGGG	CAATCTCCAG	600
	GTCTCTCCGC	TGTATGAGAA	CAGGCTCAGC	GATATCCCCA	TGGGCACCTT	TGATGGGCTT	660
	GTTAACCTGC	AGGAACTGGC	TCTACAGCAG	AACCAGATTG	GACTGTCTCT	CCCTGGTCTC	720
5	TTCCACAACA	ACCACAACCT	CCAGAGACTC	TACCTGTCCA	ACAACCACT	CTCCAGCTG	780
	CCACCCAGCA	TCTTCATGCA	GCTGCCCCAG	CTCAACCGTC	TACTCTCTT	TGGGAATTCC	840
	CTGAAGGAGC	TCTCTCTGGG	GATCTTGGG	CCCATGCCCA	ACCTGCCGGA	GCTTTGGCTC	900
	TATGACAACC	ACATCTCTTC	TCTACCCGAC	AATGTCTTCA	GCAACCTCCG	CCAGTTGCAG	960
	GTCTGATTTC	TTAGCCGCAA	TCAGATCAGC	TTTCTCTCCC	CGGGTGCCTT	CAACGGGCTA	1020
10	ACGGAGCTTC	GGGAGCTGTC	CCTCCACACC	AACGCACCTG	AGGACCTGGA	CGGGAATGTC	1080
	TTCCGCGATG	TGGCCAACTC	GCAGAACATC	TCCCTGCAGA	ACAATCGCCT	CAGACAGCTC	1140
	CCAGGGAATA	TCTTCCGCAA	CGTCAATGGC	CTCATGGCCA	TCCAGCTGCA	GAACAACCAG	1200
	CTGGAGAACT	TGCCCCCTCG	CATCTTCGAT	CACCTGGGGA	AATGTGTGTA	GCTGCGGCTG	1260
	TATGACAATC	CCTGGAGGTG	TGACTCAGAC	ATCCTTCCGC	TCCGCAACTG	GCTCTGCTC	1320
15	AACCAAGCTA	GGTAACTGAC	GGACACTGTA	CCTGTGTGTT	TCAGCCGAGC	CAATGTCCGA	1380
	GGCCAGTCCC	TCATTATCAT	CAATGTCAAC	GTGTCTGTTT	CAAGCGTCCA	TGTCCCTGAG	1440
	TGCTCTAGTT	ACCCAGAAAC	ACCATGGTAC	CCAGACACAC	CCAGTTACCC	TGACACCACA	1500
	TCCGTCTCTT	CTACCACTGA	GCTAACCAAG	CCTGTGGAAG	ACTACACTGA	TCTGACTACC	1560
	ATTACAGTCA	CTGATGACCG	CAGCGTTTGG	GGCATGACCC	AGGCCAGAG	CGGGCTGGCC	1620
20	ATTGCCGCGA	TGGTAATTGG	CATTGTGCGC	CTGGCGTGTG	CCCTGGCTGC	CTGCGTGGC	1680
	TGTTGTCTGT	GCAAGAAAGG	GAGCCAAAGT	GTCTGTATGC	AGATGAAGGC	ACCCAATGAG	1740
	TGTTAAAGAG	CTTGTGCGCA	CGAGGGCTGG	GGAAATGATG	GACTGGAGGA	CCTGGGAATT	1800
	TCATCTTTCT	GCCTCCACCC	CTGGGTCCAT	GGAGCTTTCC	CGTGATTGCT	CTTTCTGGCC	1860
	CTAGATAAAG	GTGTGCCTAC	CTCTTCTGTA	CTTGCCTGAT	TCTCCCTGAG	AGAAGCAGGT	1920
25	CGTGCCGCGA	CTTCTCTAAA	TCAGGAAGAT	AGATCCAAC	GGCCATGGCA	AAAGCCCTGG	1980
	GGATTTCCGA	TTCTATACCC	TGGGCTTCTT	TCAGAGGGGC	TCTTCTCTCA	AATCTCTCCC	2040
	ACCTGTCTCT	CAGAACAAGC	CTTCCCTGCG	CCCAGGCCCC	CTCCGGGCTT	CTGTAGACTG	2100
	AGTTAGTCCA	CAGCTGTCTC	ACTTCTGTGG	AATAGTTCTC	CGCTGAGATA	GCCCCCTCTG	2160
	CCTAAGTATT	ATGTAAGTTG	ATTTCCTTTC	TTTTGTTTCT	CTTGTGTTGT	CTATGGCTTG	2220
30	ACCCAGCATG	TCCCTCTAAA	TGAAAGTTCT	CCCCTTGATT	TTCTGCTCTG	GAAGGCAGGG	2280
	TGAGTTCTCT	CCTCAAGAAA	GACTTCAAAC	CATTAACTAG	GTCTTCTTAAG	AGCCGTCAAT	2340
	CAGCTGTGTT	TGGGAGTATG	TATGAAAGAG	AGAAGGAAAA	TCATGCCGCT	CAGTTCTCTG	2400
	AGACAGAAAG	GCCGTCTATC	GTGTCTCACT	TGTGATTTTT	ATCTGGAAAA	GGAAGAAACA	2460
	CCCCAGCACA	GCAAGCTCAG	CCTTTTAGAG	AAGGATATTT	CCAAACTGCA	AATTTGCTT	2520
35	TGAAAGTTT	AGCCCTTAA	GGAAATGAAAT	CATGTAGAA	TTTGGACTTC	TAAAACATT	2580
	AAAAACAGCT	TATTAATACG	GGATAGAGAA	AGAAATCTGG	TGCCCTGGGG	TCCCTGTGTT	2640
	CACCCCTAGA	GTTTGTCTTA	AAATTTTAA	TTGAAGCATG	TGAAGTGATC	STGCAGAAAA	2700
	GTGGGAACAT	GATAGTGTAT	GGCTTGTGTT	ATTTTCAACA	ACTGAACATA	CCTGTGTAAT	2760
	CAGCATCTAG	ACCCAGACCC	AGAGCATCAC	AAATATCCCC	CATCTGGGCT	TTTTCCGAGA	2820
40	GGAGATGGGG	GCTTCTGAAG	ATGGACTTAC	CTGGGACCTG	CCCCCATGTA	GCCAGGACGG	2880
	TCCCCCCACA	GTCCAGCTGT	GCAAGAGGCC	CGTGGCCAGG	GGTGGAGGAG	AATATGTGGG	2940
	TGTGGACAGG	TGAGGAGACT	GTGGCCTGAA	CAGGAGATTT	TATATATCT	GGAGACCTCG	3000
	AGAGACCCCT	AGACCTGGGG	CACCATGGCT	GGCCAGGTCA	GAAGCATCCT	GACTGCAGAG	3060
	GTCCGTGCAG	CCACACCTCT	TTCCCTGCCA	GCAAGTTGTC	TGCGGCTCAT	CGGAGGCCCC	3120
45	TCCGCTGGGA	GCCTTCTATG	GACGTGATAT	GCCTGTATCT	GTTTTAAATT	TTTATCTTCT	3180
	ACTTAGGGGA	AGTGAAATCG	CTCAGAGATG	AGATCCTTTA	ATTGAAACAG	AGGTGTAACG	3240
	GAATCTAGTG	TCTTTCTAAT	GTGGTAAAT	TCTCCATCAA	CATCACAGCT	AGCTGGCAGC	3300
	TGAATCTCAG	AATCTCACTT	ACACGAGGCG	ACACGGGGGT	ACACCGATGG	GTCACTCTGG	3360
	GTCTGGGGGG	TCCCTGGGAG	TCTCTCTGGG	TGTGGTCTGG	TTAGGAGTTG	AGTTGTTTGG	3420
50	TCAGGGGTTA	TTCTCTCTCT	CGAGTCACAG	TCACACGAAT	ACCTGCCTTC	TCTGGCTTTT	3480
	CTGCTATACA	CATATTACCA	TGGCGCTCAA	GAAGTTAGGC	TCATGGCAAC	GTGTGTCTTT	3540
	CTCTGGACAA	TGTTGCCAGT	TTACAGTGAA	ATGGAGAAAT	TCAGGTCTCC	ACGTCTGCCC	3600
	AGGAAAGAA	TTACAGCTGAC	TCCACGGGGA	TCTGGAATTC	CACGACCAAT	CCCGATCGGC	3660
	TCTTATTAGC	TCCCGCTTCC	ACAAGACACC	TGTGCTTTGG	AAATCCACCA	CCAATCCCGA	3720
55	TCCGCTCTTA	TTAGCTCCCC	GCTCCACAAG	ACACCTGTGA	TCTGGAATTC	TACCACCAAT	3780
	CCCGATCGGC	TCTTATTAGC	TCCCGCTTCC	ACAAGACACC	TGTGACATCC	TCCAGGGCCA	3840
	CAGGAGCAGG	TCTTATAGCT	TTTCCCTTTC	CAGTTCTCTG	ACAAAAAGTG	TCCAGAGGGC	3900
	TGTTTGCAAA	CACCTAGTGA	CTTGTAGCTT	TTTCAACCTC	TGTCCCAAGG	AATCTAGGAG	3960
	AGATGAGGCC	CGTCAGATGC	AAGAGATGTC	ATCCCCCAG	GGTCTCCAG	GCATTTCCAC	4020
60	ACTATTGGTG	GCACCTGGAG	GACATGCACC	AAGGCTTGCC	AGAGCCAACA	GGAAGTGAGC	4080
	CCAGAGCATG	GCACATGAGC	ATCACCCGCT	GATGGTGGCC	TGCTGTGCCT	GGTGCCAACA	4140
	GGGGCATCCC	GGCCCGTACC	CCTCCAGACA	GGAAAGCATG	GTTCGCCAC	AGACCTGTG	4200
	GGTGCTCCTG	TGAGTGGGCT	CCAGATGTCT	TTGTGCATAG	GCACAAGTGG	GCCAGGGCTG	4260
	GAGGGAGGTG	GGAAACCTCA	TCATCCGGTG	GGCCCTGCCA	ATCTTAACCC	AGAACCCCTA	4320
65	GGTATTCTTG	GCAGTAGCCA	TGACATTGGA	GCACCTTCTT	CTCCAGCCAG	AGGCTGACCT	4380
	GAGGGCCACT	GTCTTCAGAT	GACACCACCC	AGGAGCACCC	TAGGTGAGGG	GTGAGGGCCC	4440
	CCTTATGTGA	ACCTCTTGCC	TCTTCTTCTC	TCCCATCAGA	GTGGTTGGAT	GGAGCCATTG	4500
	GCCTCTTTTT	CTTACAGCGG	CCCTTCAACC	TCTCTGCACC	ATGTTGTCTG	GCTGAGGAGC	4560
	TACTAGAAAA	GCTGAGTGGG	GTCTCCTTTC	CAACAGGATG	ATGCATTGTC	TCAATTCTCA	4620
70	GGGCTGGAA	GAGCCGGCTG	GTCCCCCAGA	AAGCTGGAGT	GGGGTACAGA	GTTCAGTTTT	4680
	CCTCTCTGTT	TACAGCTCCT	TGACAGTCCC	ACGCCCATCT	GGAGTGGGAG	CTGGAGTTTA	4740
	GTGTTGGAGA	AGAAACAACA	AAAGCCAATT	AGAACCATA	TTTTTAAAAA	GTGCTTACTG	4800
	TGACACAGATA	CTCTTCAAGC	ACTGAGCGTG	GATTCTCTCT	CTAGCCCTCA	GCACCCCTGC	4860
	GGTAGGAGTG	CGCCCTCTAC	CCACTTGTGA	TGGGGTACAG	AGGCACCTGC	TCTTCTGCAT	4920
75	GGTGTTCAT	AGGCTGGGAT	TTTTATTAT	CTCTTCAAAC	TTGTACAAAG	AGCTCATGGC	4980
	TTGTCTTGGG	CTTTCGTGAT	TAAACCAAAG	GAAATGGAAG	CCATTCCTCT	GTGCTCTCC	5040
	TTAGTCTTGG	TCATCAGAAC	CTCACTTGGT	ACCATATAGA	TCAAAGCTT	TGTAACCACA	5100
	GGAAAAAATA	AACCTTCTCA	TCCCTTAAAG	AATAGAATAG	TTTGTCCCTC	TCATGGGAAT	5160
	TGGGCTGTAT	GTATATTTCT	CTTCTCCTT	AGAATTAGTA	GATACAAAG	TTCTACTTAG	5220
	AACCTTTCAT	GGACACAATT	TCCACAACCT	TTCAGATGCT	GATGTAGAGC	TATTGGGAAA	5280
80	GAACCTCCAA	ACTCAGGAAG	TTTGACAGAG	GCAGACAGCT	AGAGATAACT	CGGGACCCAG	5340
	AGTTGGTCTG	CAGATGTTAG	ATGTATCCTA	GCTTTTAGCC	ATAAACCACT	CAAGATTCTA	5400
	GCCCCAGAT	CCCAAGTCA	GAACCTGAAT	TGCGTTGTTG	GGAAAGCCAG	AGTGGCCTTG	5460
	GGAAAGGAGC	CATGGCTGTG	GTTCAGAGAG	GGTGGGCTGG	CAAGCCACTT	CCGGGGAAAA	5520
	CTCCTTCCCG	CCAGGTTTTC	TTCTTCTCTT	AAGGAGAGAT	TGTTCTCACC	AACCCGCTGC	5580
85	CTTCATGCTG	CCTTCAAAGC	TAGATCATGT	TTGCTTGTCT	TAGAGAATTA	CTGCAATATC	5640
	GCCCCAGTGC	TTGGCGATGC	ATTTACAGAT	TTCTAGGCCC	TCAGGCTTTT	GTAGAGTGTG	5700
	AGCCCTGGTG	GGCAGGGTTG	GGGGGTCTGT	CTTCTGCTGG	ATGCTGCTTG	TAATCCATT	5760

GGTGTACAGA ATCAACAATA AATAATATAC ATGTAT

Seq ID NO: 611 Protein sequence
Protein Accession #: BAB84587.1

1	11	21	31	41	51	
MPLKHYLLLL	VGCQAWGAGL	AYHGCPSECT	CSRASQVECT	GARIVAVPTP	LPWNAMSLQI	60
LNTHITELNE	SPFLNISALI	ALRIEKNELS	RITPGAFRNL	GSLRYLSLAN	NKLQVLPIGL	120
PQGLDSLESL	LLSSNQLLQI	QPAHFSQCSN	LKELQLHGMH	LEYIPDGAPD	HLVGLTKLNL	180
GKNSLTHISP	RVFQHLGNLQ	VLRLYENRLT	DIPMGTFDGL	VNLQELALQQ	NQIGLLSPGL	240
FHNHNLQRL	YLSNNHISQL	PPSIFMQLPQ	LNRLTLFGNS	LKELSLGIFG	PMPNRLRELWL	300
YDNHISLLPD	NVFSNLRQLQ	VLILSRNQIS	FISPGAFNGL	TELRELSLHT	NALQDLQDNV	360
FRMLANLQNI	SLQNNRLRQL	PGNIPANVNG	LMAIQLQNNQ	LENLPLGIFD	HLGKLCCELRL	420
YDNPWRCDS	ILPLRNWLLL	NQPRLGTDTV	PVCFSPANVR	GQSLIIINVN	VAVPSVHVPE	480
VPSYPETPWY	PDTSPYPDTT	SVSSTELTS	PVEDYDILT	IQVTDDRSVW	GMTQAQSGLA	540
IAAIVIGIVA	LACSLAACVG	CCCCKKRSQA	VLMQMKAPNE	C		

Seq ID NO: 612 DNA sequence
Nucleic Acid Accession #: XM_098151
Coding sequence: 1..447

1	11	21	31	41	51	
ATGATGCATT	TGCTCAATTC	TCAGGGCTGG	AATGAGCCCG	CTGGTCCCC	AGAAAGCTGG	60
AGTGGGGTAC	GAGGTTTCAGT	TTTCTCTCT	GTTTACAGCT	CCTTGACAGT	CCCACGCCCA	120
TCTGGAGTGG	GAGCTGGGAG	TCAGTGTGG	AGAAGAAACA	ACAAAAGCCA	ATTAGAACCA	180
CTATTTTAA	AAAGTGCTTA	CTGTGCACAG	ATACTCTTCA	AGCACTGGAC	GTGGATTCTC	240
TCTCTAGCCC	TCAGCACCCC	TGCGGTAGGA	GTGCGGCTC	TACCCACTTG	TGATGGGGTA	300
CAGAGGCACT	TGCTCTTCTG	CATGGTGTTC	AATAGGCTGG	GAGTTTTATT	TATCTCTTCA	360
AACCTTTGTAC	AAGAGCTCAT	GGCTTGTCTT	GGGCTTTCGT	CATTAAACCA	AAGGAAATGG	420
AAGCCATTCC	CCTGTTGCTC	TCCTTAG				

Seq ID NO: 613 Protein sequence
Protein Accession #: XP_098151

1	11	21	31	41	51	
MMHLLNSQGW	NEPAGPPPSW	SGVQSSVFLS	VYSSLTVP RP	SGVGAGSQCW	RRNNKSQLEP	60
LFLKSAYCAQ	ILFKHWITIL	SLALSTPAVG	VPPLPTCDGV	QRHLFLCMVF	NRLGVLPFIS	120
NFVQELMACL	GLSSLNQKRW	KPFPCSP				

Seq ID NO: 614 DNA sequence
Nucleic Acid Accession #: NM_002658.1
Coding sequence: 77..1372

1	11	21	31	41	51	
GTCCCGCAG	CGCCGTCGCG	CCCTCCTGCC	GCAGGCCACC	GAGGCCGCGG	CCGTCTAGCG	60
CCCGGACCTC	GCCACCATGA	GAGCCCTGCT	GGCGCGCCTG	CTTCTCTGCG	TCCTGGTCTG	120
GAGCGACTCC	AAAGGCAGCA	ATGAATTTCA	TCAAGTTCCA	TGGAAGTGTG	ACTGCTCTAA	180
TGGAGGAACA	TGTGTGTCCA	ACAAGTACTT	CTCCACATT	CAGTGGTGCA	ACTGCCCAAA	240
GAAATTCAG	GGGCAGCACT	GTGAATAGA	TAAGTCAAAA	ACCTGCTATG	AGGGGAATGG	300
TCACITTTAC	CGAGGAAAGG	CCAGCACTGA	CACCATGGGC	CGGCCCTGCC	TGCCCTGGAA	360
CTCTGCCACT	GTCCTTCAGC	AAAGCTACCA	TGCCACAGA	TCTGATGCTC	TTGAGCTGGG	420
CCTGGGGAAA	CATAATTACT	GCAGGAACCC	AGACAACCGG	AGGCGACCTT	GGTGCTATTG	480
GCAGGTGGCG	CTAAGCCGCG	TTGTCCAAGA	GTGCATGGTG	CATGACTGCG	CAGATGGAAA	540
AAAGCCCTCC	TCTCCTCCAG	AAGAATTAAA	ATTTCAGTGT	GGCCAAAAGA	CTCTGAGGCC	600
CCGCTTTAAG	ATTATTGGGG	GAGAATTCAC	CACCATCGAG	AACAGCCCTT	GGTTTGGCGC	660
CATCTACAGG	AGGCACCGGG	GGGGCTCTGT	CACCTACGTG	TGTGGAGGCA	GCCTCATCAG	720
CCCTTGCTGG	GTGATCAGCG	CCACACACTG	CTTCATTGAT	TACCCAAAGA	AGGAGGACTA	780
CATGCTCTAC	CTGGGTGCGT	CAAGGCTTAA	CTCCACACG	CAAGGGGAGA	TGAAGTTTGA	840
GGTGGAAGAC	CTCATCTTAC	ACRAGGACTA	CAGCGCTGAC	ACGCTTGCTC	ACCACAACGA	900
CATTGCCCTG	CTGAAGATCC	GTTCCAAGGA	GGGCAGGTGT	GCGCAGCCAT	CCCGGACTAT	960
ACAGACCATC	TGCCTGCCCT	CGATGTATAA	CGATCCCCAG	TTTGGCACAA	GCTGTGAGAT	1020
CACCTGGCTT	GGAAAAGAGA	ATTCTACCGA	CTATCTCTAT	CCGGAGCAGC	TGAAAATGAC	1080
TGTTGTGAAG	CTGATTTCCC	ACCGGGAGTG	TCAGCAGCCC	CACCTACTACG	GCTCTGAAAT	1140
CACCAACAAA	ATGCTATGTG	CTGCTGACCC	CCAATGGAAA	ACAGATTCCCT	GCCAGGGAGA	1200
CTCAGGGGGA	CCCTCTGCTT	GTTCCCTCCA	AGGCCGCGATG	ACTTTGACTG	GAATTGTGAG	1260
CTGGGGCCGT	GGATGTGCCC	TGAAGGACAA	GCCAGGCGTC	TACACGAGAG	TCTCACACTT	1320
CTTACCCTGG	ATCCGCACTG	ACACCAAGGA	AGAGAATGGC	CTGGCCCTCT	GAGGGTCCCC	1380
AGGGAGGAAA	CGGGCACCAC	CCGCTTTCTT	GCTGTTTGTC	ATTTTGTGAG	TAGAGTCATC	1440
TCCATCAGCT	GTAAGAAGAG	ACTGGGAAGA	TAGGCTCTGC	ACAGATGGAT	TTGCTGTGGG	1500
CACCAACAGG	GTGAACGACA	ATAGCTTTAC	CCTCAGGAT	AGGCCTGGGT	GCTGGCTGCC	1560
CAGACCCTCT	GGCCAGGATG	GAGGGTGGT	CCTGACTCAA	CATGTTACTG	ACCAGCAACT	1620
TGCTTTTTTC	TGGACTGAAG	CCTGCAGGAG	TTAAAAAGGG	CAGGGCATCT	CCTGTGCATG	1680
GGCTCGAAGG	GAGAGCCAGC	TCCCCCGACC	GGTGGGCATT	TGTGAGGCC	ATGGTTGAGA	1740
AATGAATAAT	TGCCCAATTA	GGAAGGTGAA	GCAGCTGAGG	TCTCTTGAGG	GAGCTTAGCC	1800
AATGTGGGAG	CAGCGTTTGG	GGGAGCAGAG	ACACTAACGA	CTTCAGGGCA	GGGCTCTGAT	1860
ATTCCATGAA	TGTATCAGGA	AATATATATG	TGTGTGATG	TTTGCACTAT	TGTTGTGTGG	1920
GCTGTGAGTG	TAAGTGTGAG	TAAGAGCTGG	TGTCTGATTG	TTAAGTCTAA	ATATTTCCTT	1980
AAACTGTGTG	GACTGTGATG	CCACACAGAG	TGGTCTTTCT	GGAGAGGTTA	TAGGTCACTC	2040
CTGGGGCCTC	TTGGGTCCCC	CACGTGACAG	TGCTGGGAAA	TGTACTTATT	CTGCAGCATC	2100
ACCTGTGACC	AGCACTGTCT	CAGTTTCACT	TTCCATAGAG	TGTCCTTTTC	TTGGCCAGTT	2160
ATCCCTTACC	TTTAGCCTAG	TTATCCAAT	CCTCACTGGG	TGGGGTGAGG	ACCACTCCTT	2220
ACACTGAATA	TTTATATTTC	ACTATTTTTA	TTTATATTTT	TGTAATTTTA	AATAAAAGTG	2280
ATCAATAAAA	TGTGATTTTT	CTGA				

Seq ID NO: 615 Protein sequence
Protein Accession #: NP_002649.1

5	1	11	21	31	41	51	
	MRALLARLLL	CVLVVSDSKG	SNELHQVPSN	CDCLNGGTCV	SNKYFSNIHW	CNCPKKFGGQ	60
	HCEIDKSKTC	YEGNGHFYRG	KASTDTMGRP	CLPWSNATVL	QQTYYAHRSD	ALQLGLGKHN	120
	YCRNPDNRNR	PWCYVQVGLK	PLVQECMVHD	CADGKKPSSP	PEELKFQCCQ	KTLPFRPKII	180
10	GGEFTTIENQ	PWFAAIYRRH	RGGSVTVVCG	GSLISPCWVI	SATHCFIDYP	KKEDYIVYLG	240
	RSRLNSNTQG	EMKFEVENLI	LHKDYSADTL	AHHNDIALLK	IRSKEGRCQA	PSRTIQITICL	300
	PSMYNDPQFG	TSCEITGFGK	ENSTDYLYPE	QLKMTVVKLI	SHRECQPHY	YGSEVTTKML	360
	CAADPQWKTD	SCQDSDGGGL	VCSLQGRMTL	TGIVSWGRGC	ALKDKPGVYT	RVSHFLPWIR	420
15	SHTKEENGLA	L					

Seq ID NO: 616 DNA sequence
Nucleic Acid Accession #: NM_024422.1
Coding sequence: 202..2907

20	1	11	21	31	41	51	
	CGCCAAAGGA	AAAGCCCCCT	GGATGAGAGG	CAGGCGCTTC	AGAGAAGCTA	AGAAAAGCAC	60
	CTCTCCGCGC	GCCCCACCTC	CTCCGCTCTG	CGCTCCTCCT	GAGCAGCGGG	CCCAGACTGC	120
	GCTCCGCGCG	CGGCCCTCGC	CCCGCGGAGC	CCTCCTACCC	CGGCCCGACG	CTCGGCCGCG	180
25	GACCTGCCCC	GAGCCCTCTC	CATGGAGGCA	GCCCCGCCCT	CCGGCTCCTG	GAACGGAGCC	240
	CTCTGCCGCG	TGCTCCTGCT	GACCTCGCG	ATCTTAATAT	TTGCCAGTGA	TGCCCTGCAA	300
	AATGTGACAT	TACATGTTCC	CTCCAAACTA	GATGCCGAGA	AACCTGTTGG	TAGAGTTAAC	360
	CTGAAAGAGT	GCTTTACAGC	TGCAAACTTA	ATTCAATCAA	GTGATCCTGA	CTTCCAAATT	420
	TTGGAGGATG	GTTTCAGTCT	TACAACAAAT	ACTATTCTAT	TGTCCTCGGA	GAAGAGAAAT	480
30	TTTACCATAT	TACTTTCCAA	CACCTGAGAA	CAAGAAAAGA	AGAAAATATT	TGTCTTTTGG	540
	GAGCATCAAA	CAAGGTCTCT	AAAGAAAAGA	CATACTAAAG	AAAAAGTTCT	AAGGCGCGCC	600
	AAGAGAAGAT	GGGCTCCAAT	TCCTTGTTCT	ATGCTAGAAA	ACTCCTTGGG	TCCTTTTCCA	660
	CTTTTCCTTC	AACAGGTCTA	ATCTGACACG	GCCCAAAACT	ATACCATATA	CTATTCCATA	720
	AGAGGTCTCT	GAGTGAACCA	AGAACCTCGG	AATTTATTTT	ATGTGGAGAG	AGACACTGGA	780
35	AACCTGTATT	GTACTCGTCC	TGTAGATCGT	GAGCAGTATG	AATCTTTTGA	GATAATTGCC	840
	TTTGCACAA	TCCAGATAGG	GTATACTCCA	GAACTTCCAC	TGCCCTTAAT	AATCAAAATA	900
	GAGGATGAAA	ATGATAACTA	CCCAATTTTT	ACAGAAGAAA	CTTATACTTT	TACATTTTTT	960
	GAAATATGCA	GAGTGGGCAC	TACTGTGGGA	CAAGTGTGTG	CTACTGACAA	AGATGAGCCT	1020
40	GACACGATGC	ACACACGCCCT	GAAGTACTCC	ATCATTGGGC	AGGTGCCACC	ATCACCCACC	1080
	CTATTTTCTA	TGCATCCAAC	TACAGGCGTG	ATCACCACAA	CATCATCTCA	GCTAGACAGA	1140
	GAGTTAATTG	ACAAGTACCA	GTGAAAAATA	AAAGTACAAG	ACATGGATGG	TCAGTATTTT	1200
	GGTCTACAGA	CAACTTCAAC	TTGTATCATT	AACATTGATG	ATGTAATGA	CCACTTGCCA	1260
	ACATTACTCT	GTACTTCTTA	TGTGACATCA	GTGGAAGAAA	ATACAGTTGA	TGTGGAATC	1320
45	TTACGAGTTA	CTGTGAGGGA	TAAGGACTTA	GTGAATACTG	CTAACTGGAG	AGCTAATTAT	1380
	ACCATTTTAA	AGGGCAATGA	AAATGGCAAT	TTTAAATTGG	TAACAGATGC	CAAAACCAAT	1440
	GAAGGAGTTT	TTTGTGTAGT	TAAGCCTTTG	AATTATGAAG	AAAAGCAACA	GATGATCTTG	1500
	CAAAATGGTG	TAGTTAATGA	AGCTCCATT	TCCAGAGAGG	CTAGTCCAAG	ATCAGCCATG	1560
	AGCAGAGCAA	CAGTTACTGT	TAATGTAGAA	GATCAGGATG	AGGGCCCTGA	GTGTAACCTT	1620
50	CCAATACAGA	CTGTTGCGAT	GAAAGAAAAT	GCAGAAGTGG	GAACAACAAG	CAATGGATAT	1680
	AAAGCATATG	ACCCAGAAAC	AAGAAGTAGC	AGTGGCATAA	GGTATAAGAA	ATTAAGTATG	1740
	CCAAAGGGTG	GGGCTCTCTG	TGATGAAAAT	ACAGGATCAA	TCAAAGTTTT	CAGAAGCGAT	1800
	GATAGAGAGG	CAGAGACCAT	CAAAATGGC	ATATATAATA	TTACAGTCTT	TGCATCAGAC	1860
	CAAGGAGGGA	GAACATGTAC	GGGACACTG	GGCATTATAC	TTCAAGACGT	GAATGATAAC	1920
55	AGCCCATCTA	TACCTAAAAA	GACAGTGATC	ATCTGCAAA	CCACCATGTC	ATCTGCGGAG	1980
	ATTGTTGCGG	TTGATCTCTG	TGAGCCTATC	CATGGCCCAT	CCTTTGACTT	TAGTCTGGAG	2040
	AGTTCTACTT	CAGAAGTACA	GAGAATGTGG	AGACTGAAAG	CAATTAATGA	TACAGCAGCA	2100
	CGTCTTTCTT	ATCAGAATGA	TCCTCCATT	GGCTCATATG	TAGTACCTAT	AACAGTGAGA	2160
	GATAGACTTG	GCATGCTAG	GTCTACTTCA	TTGGATGTTA	CACGTGTGTA	CTGCATTACC	2220
60	GAAATGACT	GCACACATCG	TGTAGATCCA	AGGATTGGCG	GTGGAGGAGT	ACAACTTGGA	2280
	AAGTGGGCCA	TCCTTGCAAT	ATTGTTGGGC	ATAGCATTCG	TCTTTTGCA	CCTGTTTACG	2340
	CTGCTCTGTG	GGGCTCTCTG	GACGCTCTAA	CAACCAAAAG	TAATTCCTGA	TGATTAGCCG	2400
	CAGCAGAAC	TAATGTATC	AAACACAGAA	GCTCCTGGAG	ATGACAAAGT	GTATTCTCGG	2460
	AATGGCTTCA	CAACCCAAAC	TGTGGGCGCT	TCTGCTCAGG	GAGTTTGTGG	CACCGTGGGA	2520
65	TCAGGAATCA	AAAACGGAGG	TCAGGAGACC	ATCGAAATGG	TGAAAGGAGG	ACACCAGACC	2580
	TCGGAATCCT	GCCGGGGGGC	TGGCCACCAT	CACACCTTGG	ACTCCTGCG	GGGAGSACAC	2640
	ACGAGGTTGG	ACAACTGCAG	ATACACTTAC	TCGGAGTGGC	ACAGTTTATC	TCAGCCCGGT	2700
	CTTGGTGAAA	AAGTGTATCT	GTGTAATCAA	GATGAAAATC	ACAAGCATGC	CCAAGACTAT	2760
	GTCCCTGACAT	ATAACTATGA	AGGAAGAGGA	TCCGTGGCTG	GGTCTGTAGG	TTGTTGCAGT	2820
70	GAACGACAAG	AAGAAGATGG	GCTTGAATTT	TTGGATAATT	TGGAGCCCAA	ATTTAGGACA	2880
	CTAGCAGAAG	CATGCATGAA	GAGATGAGTG	TGTTCTAATA	AGTCTCTGAA	AGCCAGTGGC	2940
	TTTATGACTT	TTAAAAAATA	TTACAAACCA	AGAATTTTTT	AAAGCAGAAG	ATGCTATTGG	3000
	TGGGGGTTTT	TCTCTCATTA	TTTGGATGGA	ATCTCTTTGG	TCAAATGCAC	ATTTACAGAG	3060
	AGACACTATA	AACAAGTACA	CAAAATTTTC	AATTTTTCAC	TATTTTAAAT	TTACTTATCT	3120
75	TCTATCCAAG	GAGGTCTACA	GAGAAATTAA	AGTCTGCCTT	ATTGTTTACA	TTGGGTATATA	3180
	ATGACAACAG	CCAATTTATA	GTGCAATAAA	ATGTAATTAA	TTCAAGTCTT	TATTATAGAC	3240
	TATTTGAAGC	ACAACCTAAT	GGAAAATTGT	AGAGACCTTG	CTTTAATCATT	ATCTCCAGTT	3300
	AATTAAGTGT	TCAATGTTGT	CTTGGAAACT	GTGTTTTCCT	TGAACATCTA	AAGTGTGTAG	3360
80	ACTGCATTCT	TGCTATTATT	TTATTCTTGT	AATGTGACCT	TTTCACTGTG	CAAAAGGGAGA	3420
	TTTCTAGCCA	GGCATTGACT	ATTACAATTT	CATT			

Seq ID NO: 617 Protein sequence
Protein Accession #: NP_077740.1

85	1	11	21	31	41	51	
	MEARPSGWSW	NGALCRLLLL	TLAILIFASD	ACKNVTLHVP	SKLDAEKLVG	RVNLKECPTA	60
	ANLIHSSDPD	FQILEDGSVY	TTNTILLSSE	KRSFTILLSN	TENQEKKKIF	VFLEHQTKVL	120

KKRHTKEKVL RRAKRRWAPI PCSMLENSLG PFPLFLQQVQ SDTAQNYTIY YSIRGPGVDQ 180
 EERNLFYVER DTGNLYCTRP VDREQYESFE IIAFATTPDG YTPLEPLPLI IKIEDENDNY 240
 TIFTEETYTF TIFENCVRGT TVGQVCATDK DEPDTHMTRL KYSIGQVPP SPTLFMSHPT 300
 5 TGVITTTSSQ LDRELIDKYQ LKIKVQMDMG QYFGLQTTST CIINIDVDND HLPFTFRTSY 360
 VTSVEENTVD VRIILRVTVED KDLVNTANWR ANYTILKONE NGNFKIVTDA KTNFVLCVV 420
 KPLNVEEKQQ MILQIGVVNE APFSREASPR SAMSTATVTV NVEDQDEGPE CNPPIQTVRM 480
 KENAEVGTTS NGYKAYDPET RSSSGIRYKK LTDPTGWVTI DENTGSIKVF RSLDREASTI 540
 KNGIYNITVL ASDQGRCTCT GTLQILQDV NDNSPFIPKK TVIICKPTMS SAEIVAVDFD 600
 10 EPIHGPPPDF SLESSTSEVQ RMWRLKAIND TAARLSYQND PPFQSYVVPV TVRDRLGMS 660
 VTSLDVTLCD CITENDCTHR VDPRIQGGGV QLGKNAILAI LLGIALLFPI LFTLVCGASG 720
 TSKQPKVIPD DLAQONLIVS NTEAPGDDKV YSANGFTTQT VGASAQGVCG TVSGIKNGG 780
 QETIEMVKGQ HQTSESCRGH GHHTLDSR GGHTEVDNCR YTVSEWHSFT QPRLGEKVYL 840
 CNQDENHKA QDYVLTNYE GRGSVAGSVG CCSERQEEDG LEFLDNLEPK FRTLAEACMK 900
 R

Seq ID NO: 618 DNA sequence
 Nucleic Acid Accession #: NM_004949.1
 Coding sequence: 202..2745

20 1 11 21 31 41 51
 CGCCAAAGGA AAAGCCCTT GGATGAGAGG CAGGCGCTTC AGAGAAGCTA AGAAAAGCAC 60
 CTCTCCGCGC GCCCCACCTC CTCGCGCTCG CGCTCCTCCT GAGCAGCGGG CCCAGACTGC 120
 25 GCTCCGCGCG CCGCCCTGCG CCGCGGAGC CCTCCTACCC CGGCGGACG CTCGCGCCGC 180
 GACCTGCCCC GAGCCCTCTC CATGGAGGCA GCCCGCCCTC CCGGCTCCTG GAACGGAGCC 240
 CTCTGCGCGC TGCTCCTGCT GACCTCGCG ATCTTAATAT TTGCCAGTGA TGCCTGCAA 300
 AATGTGACAT TACATGTTC CTCCAACTA GATGCCGAGA AACTTGTGG TAGAGTTAAC 360
 CTGAAAGAGT GCTTTACAGC TGCAAACTA ATTCACTCAA GTGATCCTGA CTTCCAAAT 420
 30 TTGGAGGATG GTTCAGTCTA TACAACAAAT ACTATTCTAT TGTCCTCGGA GAAGAGAAGT 480
 TTTACCATAT TACTTTCCAA CACTGAGAAC CAAGAAAAGA AGAAAATATT TGCTTTTGTG 540
 GAGCATCAA CAAAGGTCTT AAAGAAAAGA CATACTAAG AAAAAGTTCT AAGGCGCGCC 600
 AAGAGAAGAT GGGCTCCAAT TCCTTGTTCT ATGTAGAAA ACTCCTTGGG TCCTTTTCCA 660
 CTTTTCCTTC AACAGSTTCA ATCTGACACG GCCCAAACT ATACCATATA CTATTCCATA 720
 35 AGAGGTCTCG GAGTTGACCA AGAACCTCGG AATTTATTTT ATGTGGAGAG AGACACTGGA 780
 AACTTGTATT GTACTCGTCC TGTAGATCGT GAGCAGTATG AATCTTTTGA GATAATTGCC 840
 TTTGCAACAA CTACTACTGG GTATACTCCA GAACCTCCAC TGCCCTTAAT AATCAAAATA 900
 GAGGATGAAA ATGATACTA CCCAATTTT ACAGAGAAA CTTATACTTT TACAATTTT 960
 40 GAAAATTGCA GAGTGGGCAC TACTGTGGGA CAAGTGTGTG CTACTGACAA AGATGAGCCT 1020
 GACACGATGC ACACACGCTT GAAGTACTCC ATCATTGGGC AGGTGCCACC ATCACCACC 1080
 CTATTTTCTA TGCATCCAACT TACAGGCGTG ATCACCACAA CATCATCTCA GCTAGACAGA 1140
 GAGTTAATTG ACAAGTACCA GTTGAAAATA AAAGTACAA ACATGGATGG TCAGTATTT 1200
 GGTCTACAGA CAACCTCAAC TTGTATCATT AACATTGATG ATGTAAATGA CCACTTGCCA 1260
 ACATTTACTT GACTTCTCTA TGTGACATCA GTGGAAGAAA ATACAGTTGA TGTGGAAT 1320
 45 TTACGAGTTA CTGTTGAGGA TAAGGACTTA GTGAATACTG CTAAGTGGAG AGCTAATTAT 1380
 ACCATTTTAA AGGCAATGTA AATGGCAAT TTTAAATTTG TAACAGATGC CAAAACCAAT 1440
 GAAGGAGTTT TTTGTGTAGT TAAGCCTTTG AATTATGAG AAAAGCAACA GATGATCTTG 1500
 CAAATTTGGT TAGTTAATGA AGCTCCATT TCCAGAGAGG CTAGTCCAAG ATCAGCCATG 1560
 AGCACAGCAA CAGTTACTGT TAATGTAGAA GATCAGGATG AGGGCCCTGA GTGTAACTCT 1620
 50 CCAATACAGA CTGTTGCGAT GAAAGAAAAT GCAGAAGTGG GAACAACAAG CAATGGATAT 1680
 AAAGCATATG ACCCAGAAAC AAGAAGTAGC AGTGGCATAA GGTATAAGAA ATTAAGTATG 1740
 CCAACAGGTG GGGTCAACAT TGATGAAAAT ACAGGATCAA TCRAAGTTT CAGAAGCCTG 1800
 GATAGAGAGG CAGAGACCAT CAAAATGGC ATATATAATA TTACAGTCTC TGATCAGAC 1860
 CAAGGAGGGA GAACATGTAC GGGGACACTG GGCATTATAC TTCAAGACGT GAATGATAAC 1920
 AGCCCATTC TACCTAAAAA GACAGTGATC ATCTGCAAA CCAACCATGTC ATCTGCGGAG 1980
 55 ATTGTTGCGG TTGATCTCTG TGAGCCTATC CATGCCCCAC CCTTTGACTT TAGTCTGGAG 2040
 AGTTCTACTT CAGAAGTACA GAGAATGTGG AGACTGAAAG CAATTAATGA TACAGCAGCA 2100
 CGTCTTTCTC ATCAGAATGA TCCTCCATT GGCTCATATG TAGTACCTAT AACAGTGAGA 2160
 GATAGACTTG GCATGCTTAG GTCTCACTTA TTGGATGTTA CACTGTGTGA CTGCATTACC 2220
 60 GAAAATGACT GCACACATCG TGTAGATCCA AGGATTGGCG GTGGAGGAGT ACAACTTGA 2280
 AAGTGGGCCA TCCTTGCAAT ATTGTTGGGC ATAGCATTCG TCTTTTGCAT CCGTTTACG 2340
 CTGGTCTGTG GGGCTTCTGG GAGCTCTAAA CAACCAAAAG TAATTCCTGA TGATTTAGCC 2400
 CAGCAGAAC TAATTGTATC AAACACAGAA GCTCCTGGAG ATGACAAAGT GTATTCTGCG 2460
 AATGGCTTCA CAACCAAAAC TGTGGGCGCT TCTGCTCAGG GAGTTTGTGG CACCGTGGGA 2520
 65 TCAGGAATCA AAAACGGAGG TCAGGAGACC ATCGAAATGG TGAAGGAGG ACACCAGACC 2580
 TCGGAATCCT GCCGGGGGCG TGCCACCCTG CACACCCTG ACTCCTGCAG GGGAGGACAC 2640
 ACGGAGGTGG ACAAATGCG ATACACTTAC TCGGAGTGGC ACGTCTTTAC TCAGCCCGGT 2700
 CTTGGTGAAG AATCCATTAG AGGACACACT CTGATTAAAA ATTAACAAT GAAAGAAAGT 2760
 GTATCTGTGT AATCAAGATG AAAATCACAA GCATGCCCAA GACTATGTCC TGACATATAA 2820
 70 CTATGAAGGA AGAGGATCGG TGGCTGGGTC TGTAGTTTGT TGCAGTGAAC GACAAGAGA 2880
 AGATGGGCTT GAATTTTGGG ATAATTGGA GCCCAAATTT AGGACACTAG CAGAAGCATG 2940
 CATGAAGAGA TGAGTGTGTT CTAATAAGTC TCTGAAAGCC AGTGGCTTTA TGACTTTTAA 3000
 AAAAAATTAC AAACAAGAA TTTTAAAG CAGAAGATGC TATTTGTGGG GGTTTTCTC 3060
 TCATTATTTG GATGGAATCT CTTTGGTCAA ATGCACATT ACAGAGAGAC ACTATAACA 3120
 75 AGTACACAAA TTTTCAATT TTTACATATT TTTAAATTAC TTATCTTCTA TCCAAGGAGG 3180
 TCTACAGAGA AATTAAGTC TGCTTATTT GTTACATTG GGTATAATGA CAACAGCCAA 3240
 TTTATAGTGC AATAAAATGT AATTAATTCA AGTCTTATT ATAGACTATT TGAAGCACA 3300
 CCTAATGGAA AATTGTAGAG ACCTTGCTTT AACATTATCT CCAAGTTAAT AAGTGTTCAT 3360
 GTGGTGCTTG GAACTGTGTT TTTTCTGAA CATCTAAAGT GTGTAGACTG CATTCTTGCT 3420
 80 ATTATTTTAT TCTTGTAAAT TGACCTTTTC ACTGTGCAAA GGGAGATTTC TAGCCAGGCA 3480
 TTGACTATTA CAATTCATT

Seq ID NO: 619 Protein sequence
 Protein Accession #: NP_004940.1

85 1 11 21 31 41 51
 MEAARPSGSW NGALCRLLLL TLAILIFASD ACKQVTLHVP SKLDAEKLVG RVNLKECFPTA 60

ANLIHSSDPD FOILEDGGSVY TTNTILLSSE KRSPTILLSN TENQEKKKIF VFLEHQTKVL 120
 KKRHTKEKVL RRAKRRWAPI PCSMLNSLG PFPLFLQQVQ SDTAQNYTIY YSIRGPGVDQ 180
 EPRNLFFYVER DTGNLYCTRP VDREQYESFE IIAFATTPDG YYPELPLPLI IKIEDENDNY 240
 PIFTEETYP TIFENCRVGT TVGQVCATDK DEPDTHMTRL KYSIIGQVPP SPTLFSMHPT 300
 TGVITTTSSQ LDRELIDKYQ LKIKVQDMDG QYFGLQTTST CIINIDVDND HLPFTFRTSY 360
 VTSVEENTVD VEILRVTVED KDLVNTANWR ANYTILKNE NGNFKIIVTDA KTNBGLVLCVV 420
 KPLNYEEKQKQ MILQIGVVNE APFSREASPR SAMSTATVTV NVEDQDEGPE CNPPIQTVRM 480
 KENAEVGTTS NGYKAYDPET RSSSGIRYKK LTDPTGWVTI DENTGSIKVF RSLDREAEI 540
 KNGIYNITVL ASDQGGRTCT GTLGIILQDV NDNSPFIKK TVIICKPTMS SAEIVAVDPD 600
 EPIHGPFFDF SLESSTSEVQ RMWRLKAIN TAARLSYQND PPGSYVVPPI TVDRRLGMSS 660
 VTSLDVTLCD CITENDCTHR VDPRIIGGGV QLKWKAILAI LLGIALLFICI LFTLVCGASG 720
 TSKQPKVIPD DLAQONLIVS NTEAPGDDKV YSANGFTTQT VGASAQGVCG TVGSGIKNGG 780
 QETIEMVKGG HQTSESCRG AHHHTLDSGR GGHTVEDNCR YTYSEHNSPT QPRLGEESIR 840
 GHTLIKN

Seq ID NO: 620 DNA sequence
 Nucleic Acid Accession #: NM_032545.1
 Coding sequence: 46..718

1 11 21 31 41 51
 AAACGTGATCT TCAATGCACT AAGAGAAGGA GACTCTCAA CCAAAATGA CCTGGAGGCA 60
 CCATGTCAGG CTCTCTGTTA CGGTCACTTT GGCATTACAG ATCATCAATT TGGGAAACAG 120
 CTATCAAAGA GAGAAACATA ACGGCGGTAG AGAGGAAGTC ACCAAGGTTG CCACTCAGAA 180
 GCACCGACAG TCACCGCTCA ACTGGACCTC CAGTCATTTC GGAGAGGTGA CTGGGAGCGC 240
 CGAGGGCTGG GGGCCGAGG AGCCGCTCCC CTACTCCCGG GCTTTCGGAG AGGGTGCCTG 300
 CGCGCGGCGG CGCTGCTGCA GGAACGGCGG TACCTGCGTG CTGGGCGAGT TCTGCGTGTG 360
 CCGGCGCCAC TTCACCGGCC GCTACTGCGA GCATGACCAG AGGCGCAGTG AATGCGGCGC 420
 CCTGGAGCAC GAGAGCTTGA CCTCCGCGC CTGCCACCTC TGCAGGTGCA TCTTCGGGGC 480
 CCTGCACTGC CTCCTCTTCC AGACGCTTGA CCGCTGTGAC CCGAAAGACT TCCTGGCCCTC 540
 CCAAGCTCAC GGGCCGAGCG CGGGGGGCGG GCCCAGCCTG CTACTCTTGC TGCCCTGCGC 600
 ACTCCTGCAC CGCTCTCTGC GCCCGGATGC GCCCGCGCAC CCTCGGTCCC TGGTCCCTTC 660
 CGTCTCTCAG CGGGAGCGGC GCCCTGCGG AAGGCCGGGA CTGGGCAATC GCCCTTAATT 720
 TCTATGTTG TAAATAATAG ATGTGTTAG TTTACCGTAA CTGAAGCATC TGGGTGAATA 780
 TTTTATTGG GTAATAAATA TTTTCATGAA AGCGCCAAAA AAAAAAAAAA AAAAAAAAAA 840
 AAAAAA

Seq ID NO: 621 Protein sequence
 Protein Accession #: NP_115934.1

1 11 21 31 41 51
 MTWRHHVRL FTVSLALQII NLGNSYQREK HNGGREEVTK VATQKHRQSP LNWTSSHFE 60
 VTGSAEGWGP EEPFYSRAF GEGASARPRC CRNGGTCLVG SPCVCPAHT GRYCEHDQRR 120
 SECAGLEHGA WTLRACHLCR CTFGALHCLP LQTPDRCDPK DFLASHAHGP SAGGAPSLLL 180
 LLPCALHLRL LRPDAPAPHR SLVPSVLQRE RRPCGRPLG HRL

Seq ID NO: 622 DNA sequence
 Nucleic Acid Accession #: FGENESH predicted
 Coding sequence: 1..390

1 11 21 31 41 51
 ATGAGGTTCA GTGTCTCAGG CATGAGGACC GACTACCCCA GGAGTGTGCT GGCTCCTGCT 60
 TATGTGTGAG TCTGTCTCCT CTCTCTGTGT CCAAGGGAAG TCATCGCTCC CGCTGGCTCA 120
 GAACCATGGC TGTGCCAGCC GGCACCCAGG TGTGGAGACA AGATCTACAA CCCCTGGAG 180
 CAGTGTCTGT ACAATGACGC CATCGTGTCC CTGAGCGAGA CCCGCCAATG TGGTCCCCC 240
 TGCACCTTCT GGCCTCTGCT TGAGCTCTGC TGTCTTGATT CCTTTGGCCT CACAAACGAT 300
 TTTGTGTGA AGCTGAAGGT TCAGGGTGTG AATTCACAGT GCCACTCATC TCCCATCTCC 360
 AGTAAATGTG AAAGAGGCCG GATATGTTAG

Seq ID NO: 623 Protein sequence
 Protein Accession #: FGENESH predicted

1 11 21 31 41 51
 MRFSVSGMRT DYPRSVLAPA YVSVCLLLLC PREVIAPAGS EPWLCQAPAP CGDKIYNFLE 60
 QCCYNDAIVS LSETRQCGPP CTFWPCFELC CLDSFGLTND FVVKLVQVGV NSQCHSSPIS 120
 SKCERGRIC

Seq ID NO: 624 DNA sequence
 Nucleic Acid Accession #: M18728.1
 Coding sequence: 51..1085

1 11 21 31 41 51
 GGAGCTCAAG CTCCTCTACA AAGAGGTGGA CAGAGAAGAC AGCAGAGACC ATGGGACCCC 60
 CCTCAGCCCC TCCTCTGAGA TTGCTGTGCC CCTGGAAGGA GGTCTGTCTC ACAGCCTCAC 120
 TTCTAACCTT CTGGAACCCA CCCACCACTG CCAAGCTCAC TATTGAATCC ACGCCATTCA 180
 ATGTGCGAGA GGGGAAGGAG GTTCTTCTAC TCGCCACAA CCTGCCCCAG AATCGTATTG 240
 GTTACAGCTG GTACAAAGGC GAAAGAGTGG ATGGCAACAG TCTAATTGTA GGATATGTAA 300
 TAGGAACCTA ACAAGCTACC CCAGGGCCCG CATACAGTGG TCGAGAGACA ATATACCCCA 360
 ATGCATCCCT GCTGATCCAG AACGTCAACC AGAATGACAC AGGATTCTAT ACCCTACAAG 420
 TCATAAAGTC AGATCTTGTG ATGAAGAAG CAACCGGACA GTTCCATGTA TACCCGAGAG 480
 TGCCCAAGCC CTCCTCTCTC AGCAACAAC CCAACCCCGT GGAGGACAAG GATGCTGTGG 540
 CCTTCACCTG TGAACCTGAG GTTCAGAAAC CAACCTACCT GTGGTGGGTA AATGTCAGA 600
 GCCTCCCGGT CAGTCCACAG CTGCAGCTGT CCAATGGCAA CATGACCCTC ACTCTACTCA 660

	GCGTCAAAAG	GAACGATGCA	GGATCCTATG	AATGTGAAAT	ACAGAACCCA	GCGAGTGCCA	720
	ACCGCAGTGA	CCCAGTCACC	CTGAATGTCC	TCTATGGCCC	AGATGTCCCC	ACCATTTCCTC	780
	CCTCAAAGGC	CAATTACCGT	CCAGGGGAAA	ATCTGAACCT	CTCCTGCCAC	GCAGCCTCTA	840
5	ACCCACCTGC	ACAGTACTCT	TGGTTTATCA	ATGGGACGTT	CCAGCAATCC	ACACAAGAGC	900
	TCTTTATCCC	CAACATCACT	GTGAATAATA	GCGGATCCTA	TATGTGCCAA	GCCCAATACT	960
	CAGCCACTGG	CCTCAATAGG	ACCACAGTCA	CGATGATCAC	AGTCTCTGGA	AGTGCTCCTG	1020
	TCCTCTCAGC	TGTGGCCACC	GTCGGCATCA	CGATTGGAGT	GCTGGCCAGG	GTGGCTCTGA	1080
	TATAGCAGCC	CTGGTGATTT	TTGATATTTT	CAGGAAGACT	GGCAGATTGG	ACCAGACCCT	1140
10	GAATTCCTCT	AGCTCCTCCA	ATCCCATTCT	ATCCCATTGG	ACCACTAAAA	ACAAGGTCTG	1200
	CTCTGCTCCT	GAAGCCCTAT	ATGCTGGAGA	TGGACAACCT	AATGAAAAAT	TAAAGGGAAA	1260
	ACCCTCAGGC	CTGAGGTGTG	TGCCACTCAG	AGACTTCACC	TAACTAGAGA	CAGTCAAACT	1320
	GCAAACCATG	GTGAGAAATT	GACGACTTCA	CACATATGAC	AGCTTTTCCC	AAGATGTCAA	1380
	AACAAGACTC	CTCATCATGA	TAAGGCTCTT	ACCCCTTTT	AATTTGTCCT	TGCTTATGCC	1440
15	TGCTCTTTCT	GCTTGGCAGG	ATGATGCTGT	CATTAGTATT	TCACAAGAAG	TAGCTTCAGA	1500
	GGGTAACTTA	ACAGAGTGTC	AGATCTATCT	TGTCAATCCC	AACGTTTAC	ATAAAATAAG	1560
	AGATCCTTTA	GTGCACCCAG	TGACTGACAT	TAGCAGCATC	TTTAAACACAG	CCGTGTGTTT	1620
	AAATGTACAG	TGTCCTTTT	CAGAGTTGGA	CTTCTAGACT	CACCTGTTCT	CACTCCCTGT	1680
	TTTAATTCAA	CCCAGCCATG	CAATGCCAAA	TAATAGAATT	GCTCCCTACC	AGCTGAACAG	1740
20	GGAGGAGTCT	TGCAGTTTC	TGACACTTGT	TGTTGAACAT	GGCTAAATAC	AATGGGTATC	1800
	GCTGAGACTA	AGTTGTAGAA	ATTAACAAAT	GTGCTGCTTG	GTTAAAAATG	CTACACTCAT	1860
	CTGACTCATT	CTTTATTTCT	TTTGTATCTT	GCCTAAGGTG	CGTAGTCCAA	1920	
	CTCTTGGTAT	TACCTCTCTA	ATAGTCATAC	TAGTAGTCAT	ACTCCCTGGT	GTAGTGTATT	1980
	CTCTAAAGGC	TTTAAATGTC	TGCTGCAGC	CAGCCATCAA	ATAGTGAATG	GTCTCTCTTT	2040
25	GGCTGGAATT	ACAAAATGTC	GAGAAATGTG	TCATCAGGAG	AACATCATAA	CCCATGAAGG	2100
	ATAAAAGCCC	CAATGGTGG	TAACTGATAA	TAGCACTAAT	GCTTTAAGAT	TTGGTCACAC	2160
	TCTCACCTAG	GTGAGCGCAT	TAGGCCAGTG	GTGCTAAATG	CTACATACTC	CAACTGAAAT	2220
	GTTAAGGAAG	AAGATAGATC	CAATTAAAAA	AAATTAAAAA	CAATTAAAAA	AAAAAAAAGA	2280
	ACACAGGAGA	TTCAGTCTA	CTTGAGTTAG	CATAATACAG	AAGTCCCTTC	TACTTTAACT	2340
30	TTTACAAAAA	AGTAACCTGA	ACTAATCTGA	TGTTAAACCA	TGTATTATTT	TCTGTGGTTC	2400
	TGTTTCTCTG	TTTCAATTG	ACAAAACCCA	CTGTTCTTGT	ATTGTATTGC	CCAGGGGGAG	2460
	CTATCACTGT	ACTTGTAGAG	TGGTGCTGCT	TTAATTTCATA	AATCACAAAT	AAAAGCCAAAT	2520
	TAGCTCTATA	ACT					

Seq ID NO: 625 Protein sequence
Protein Accession #: AAA59907.1

	1	11	21	31	41	51	
40	MGPPSAPPCR	LHVPWKEVLL	TASLLTFWNP	PTTAKLTIES	TPFNVAEGKE	VLLLAHNLPO	60
	NRIGYSWYKG	ERVDGNLIV	GVVIGTQQAT	PGPAYSGRET	IYPNASLLIQ	NVTQNDTFY	120
	TLQVIKSDLV	NEEATQCFHV	YPFLPKPSIS	SNNSPVDEK	DAVAFTCEPE	VQNTTYLWV	180
	NGQSLFVSPR	LQLSNGNMTL	TLLSVKRNDG	GSYECEIQNP	ASANRSDPVT	LNVLVGPDPV	240
	TIISPSKANYR	PGENLNLSC	AASNPQAQYS	WFINGTFQQS	TQELFIPNIT	VNNSGVSVMCQ	300
45	AHNSATGLNR	TTVTMITVSG	SAPVLSAVAT	VGITIGVLAR	VALI		

Seq ID NO: 626 DNA sequence
Nucleic Acid Accession #: M18728.1
Coding sequence: 1355..1657

	1	11	21	31	41	51	
50	GGAGCTCAAG	CTCCTCTACA	AAGAGGTGGA	CAGAGAAGAC	AGCAGAGACC	ATGGGACCCC	60
	CCTCAGCCCC	TCCCTCTGCT	TGCAATGTCC	CCTGGAAGGA	GGTCTGCTC	ACAGCCTCAG	120
55	TTCTAACCTT	CTGGAACCCA	CCCACCACTG	CCAAGCTCAC	TATTGAATCC	ACGCCATTCA	180
	ATGTGCGAGA	GGGGAAGGAG	GTTCTTCTAC	TGCGCCCAAA	CCTGCCCCAG	AATCGTATTG	240
	GTTACAGCTG	GTACAAAGGC	GAAAGAGTGG	ATGGCAACAG	TCTAATTGTA	GGATATGTAA	300
	TAGGAACCTA	ACAGGCTACC	CCAGGGCCCC	CATACAGTGG	TGAGAGAGCA	ATATACCCCA	360
	ATGCATCCCT	GCTGATCCAG	AACGTCAACC	AGAATGACAC	AGGATTCTAT	ACCCCTACAAG	420
60	TCATAAAGTC	AGATCTTGTG	AATGAAGAAG	CAACCGGACA	GTCCATGTGA	TACCCGGAGC	480
	TGCCCAAGCC	CTCCATCTCC	AGCAACAAC	CCAACCCCGT	GGAGGACAAG	GATGCTGTGG	540
	CCTTCACCTG	TGAACCTGAG	GTTCAGAAAC	CAACCTACCT	GTGGTGGGTA	AATGGTCAGA	600
	GCCTCCCGGT	CAGTCCCAGG	CTGCAGCTGT	CCAATGGCAA	CATGACCCCT	ACTCTACTCA	660
	GCGTCAAAAG	GAACGATGCA	GGATCCTATG	AATGTGAAAT	ACAGAACCCA	GCGAGTGCCA	720
65	ACCGCAGTGA	CCCAGTCACC	CTGAATGTCC	TCTATGGCCC	AGATGTCCCC	ACCATTTCCTC	780
	CCTCAAAGGC	CAATTACCGT	CCAGGGGAAA	ATCTGAACCT	CTCCTGCCAC	GCAGCCTCTA	840
	ACCCACCTGC	ACAGTACTCT	TGGTTTATCA	ATGGGACGTT	CCAGCAATCC	ACACAAGAGC	900
	TCTTTATCCC	CAACATCACT	GTGAATAATA	GCGGATCCTA	TATGTGCCAA	GCCCAATACT	960
	CAGCCACTGG	CCTCAATAGG	ACCACAGTCA	CGATGATCAC	AGTCTCTGGA	AGTGCTCCTG	1020
70	TCCTCTCAGC	TGTGGCCACC	GTCGGCATCA	CGATTGGAGT	GCTGGCCAGG	GTGGCTCTGA	1080
	TATAGCAGCC	CTGGTGATTT	TTGATATTTT	CAGGAAGACT	GGCAGATTGG	ACCAGACCCT	1140
	GAATTCCTCT	AGCTCCTCCA	ATCCCATTCT	ATCCCATTGG	ACCACTAAAA	ACAAGGTCTG	1200
	CTCTGCTCCT	GAAGCCCTAT	ATGCTGGAGA	TGGACAACCT	AATGAAAAAT	TAAAGGGAAA	1260
	ACCCTCAGGC	CTGAGGTGTG	TGCCACTCAG	AGACTTCACC	TAACTAGAGA	CAGTCAAACT	1320
75	GCAAACCATG	GTGAGAAATT	GACGACTTCA	CACATATGAC	AGCTTTTCCC	AAGATGTCAA	1380
	AACAAGACTC	CTCATCATGA	TAAGGCTCTT	ACCCCTTTT	AATTTGTCCT	TGCTTATGCC	1440
	TGCTCTTTCT	GCTTGGCAGG	ATGATGCTGT	CATTAGTATT	TCACAAGAAG	TAGCTTCAGA	1500
	GGGTAACTTA	ACAGAGTGTC	AGATCTATCT	TGTCAATCCC	AACGTTTAC	ATAAAATAAG	1560
	AGATCCTTTA	TGTCACCCAG	TGACTGACAT	TAGCAGCATC	TTTAAACACAG	CCGTGTGTTT	1620
80	AAATGTACAG	TGTCCTTTT	CAGAGTTGGA	CTTCTAGACT	CACCTGTTCT	CACTCCCTGT	1680
	TTTAATTCAA	CCCAGCCATG	CAATGCCAAA	TAATAGAATT	GCTCCCTACC	AGCTGAACAG	1740
	GGAGGAGTCT	GTGCAGTTTC	TGACACTTGT	TGTTGAACAT	GGCTAAATAC	AATGGGTATC	1800
	GCTGAGACTA	AGTTGTAGAA	ATTAACAAAT	GTGCTGCTTG	GTTAAAAATG	CTACACTCAT	1860
85	CTGACTCATT	CTTTATTTCT	TTTGTATCTT	GCCTAAGGTG	CGTAGTCCAA	1920	
	CTCTTGGTAT	TACCTCTCTA	ATAGTCATAC	TAGTAGTCAT	ACTCCCTGGT	GTAGTGTATT	1980
	CTCTAAAGGC	TTTAAATGTC	TGCTGCAGC	CAGCCATCAA	ATAGTGAATG	GTCTCTCTTT	2040
	GGCTGGAATT	ACAAAACCTCA	GAGAAATGTG	TCATCAGGAG	AACATCATAA	CCCATGAAGG	2100
	ATAAAAGCCC	CAATGGTGG	TAACTGATAA	TAGCACTAAT	GCTTTAAGAT	TTGGTCACAC	2160

WO 02/086443

PCT/US02/12476

TCTCACCTAG GTGAGCGCAT TGAGCCAGTG GTGCTAAATG CTACATACTC CAACTGAAAT 2220
GTTAAGGAAG AAGATAGATC CAATTAAAAA AAATTAAAAA CAATTAAAAA AAAAAAAGA 2280
ACACAGGAGA TTCCAGTCTA CTGAGTTAG CATAATACAG AAGTCCCCTC TACTTTAACT 2340
TTTACAAAAA AGTAACCTGA ACTAATCTGA TGTAAACCAA TGTATTATTT TCTGTGGTTC 2400
TGTTCCTTGG TTCCAATTTG ACAAAACCCA CTGTTCTTGT ATTGTATTGC CCAGGGGGAG 2460
CTATCACTGT ACTGTAGAG TGGTGTGCT TTAATTCATA AATCACAAT AAAAGCCAAT 2520
TAGCTCTATA ACT

Seq ID NO: 627 Protein sequence
Protein Accession #: AAA59908.1

1 11 21 31 41 51
MDSFSDVKT RLLIMIRLLP PPNLSLLMPA SFAWQDDAVI SISQEVASEG NLTECQIYLV 60
NPNVLHKIRD PLVHPVTDIS SIFNTAVCSN VQWSFSELDI

Seq ID NO: 628 DNA sequence
Nucleic Acid Accession #: M18728.1
Coding sequence: 2370..2501

1 11 21 31 41 51
GGAGCTCAAG CTCCTCTACA AAGAGGTGGA CAGAGAAGAC AGCAGAGACC ATGGGACCCC 60
CCTCAGCCCC TCCTCTGAGA TTGCATGTCC CCTGGAAGGA GGTCTGTCTC ACAGCTCAC 120
TTCTAACCTT CTGGAACCCA CCCACCACTG CCAAGCTCAC TATTGAATCC ACGCCATTCA 180
ATGTGCGAGA GGGGAAGGAG GTTCTTCTAC TCGCCCAACA CCTGCCACAG AATCGTATTG 240
GTTACAGCTG GTACAAAGGC GAAAGAGTGG ATGGCAACAG TCTAATTGTA GGATATGTAA 300
TAGGAACCTA ACAAGCTACC CCAGGGCCCC CATAAGTGG TCGAGAGACA ATATACCCCA 360
ATGCATCCCT GCTGATCCAG AACGTCAACC AGAATGACAC AGGATTCTAT ACCCTACAGA 420
TCTCAAAGTC AGATCTTGTG AATGAAGAAG CAACCGGACA GTTCCATGTA TACCGGAGGC 480
TGCCCAAGCC CTCCTCTCC AGCAACAAC CCAACCCCGT GGAGGACAAG GATGCTGTGG 540
CCTTCACCTG TGAACCTGAG GTTCAGAAC CAACCTACCT GTGGTGGGTA AATGGTCAGA 600
GCCTCCCGGT CAGTCCCAGG CTGCAGCTGT CCAATGGCAA CATGACCCTC ACTCTACTCA 660
GCGTCAAAAG GAACGATGCA GGATCCTATG AATGTGAAAT ACAGAACCCA GCGAGTGCCA 720
ACCGCAGTGA CCCAGTCAAC CTGAATGTCC TCTATGGCCC AGATGTCCCC ACCATTTCCTC 780
CCTCAAAGGC CAATTACCGT CCAGGGGAAA ATCTGAACCT CTCCTGCCAC GCAGCCTCTA 840
ACCCACCTGC ACAGTACTCT TGGTTTATCA ATGGGACGTT CCAGCAATCC ACACAAGAGC 900
TCTTTATCCC CAACATCACT GTGAATAATA GCGGATCCTA TATGTGCCAA GCCATAACT 960
CAGCCACTGG CCTCAATAGG ACCACAGTCA CGATGATCAC AGTCTCTGGA AGTGGCTCCTG 1020
TCCTCTCAGC TGTGGCCACC GTCCGCATCA CGATTGGAGT GCTGGCCAGG GTGGCTCTGA 1080
TATAGCAGCC CTGGTGTATT TCGATATTT CAGGAAGACT GGCAGATTGG ACCAGACCCT 1140
GAATCTCTCT AGCTCCTCCA ATCCCATTTT ATCCCATGGA ACCACTAAAA ACAAGGTCTG 1200
CTCTGCTCCT GAAGCCCTAT ATGCTGGAGA TGGACAACCT AATGAAAATT TAAAGGGAAA 1260
ACCCCTCAGC CTGAGGTGTG TGCCACTCAG AGACTTCACC TAACTAGAGA CAGTCAAAT 1320
GCAAACCATC GTGAGAAATT GACGACTTCA CACTATGGAC AGCTTTTCCC AAGATGTCAA 1380
AACAAGACTC CTCAATCATG TAAGGCTCTT ACCCCCTTTT AATTGTCTCT TGCTTATGCC 1440
TGCCCTCTTC GCTTGGCAGG AGATGCTGT CATTAGTATT TCACAAGAAG TAGCTTCAGA 1500
GGGTAACCTA ACAGAGTGTG AGATCTATCT TGTCAATCCC AACGTTTAC ATAAAATAAG 1560
AGATCCTTTA GTGCACCCAG TGACTGACAT TAGCAGCATC TTAAACACAG CCGTGTGTTC 1620
AAATGTACAG TGGTCTCTTT CAGAGTTGGA CTCTTAGACT CACCTGTCTC CACTCCCTGT 1680
TTTAAATCAA CCCAGCCATG CAATGCCAAA TAATAGAATT GCTCCCTACC AGCTGAACAG 1740
GGAGGAGTCT GTGCAGTTTC TGACACTTGT TGTGGAACAT GGCTAAATAC AATGGGTATC 1800
GCTGAGACTA AGTTGTAGAA ATTAACAAAT GTGCTGCTTG GTTAAATGG CTACACTCAT 1860
CTGACTCATT CTTTATCTTA TTTTAGTTGG TTTGTATCTT GCCTAAGGTG CGTAGTCCAA 1920
CTCTTGGTAT TACCTCCTTA ATAGTCATAC TAGTAGTCAT ACTCCCTGGT GTAGTGTATT 1980
CTCTAAAAGC TTTAAATGTC TGCAATGCAG CAGCCATCAA ATAGTGAATG GTCTCTCTTT 2040
GGCTGGAATC ACAAACCTCA GAGAAATGTG TCATCAGGAG AACATCATAA CCCATGAAGG 2100
ATAAAGGCC CAAAGTGTGG TAACTGATAA TAGCACTAAT GCTTTAAGAT TTGGTCACAC 2160
TCTCACCTAG GTGAGCGCAT TGAGCCAGTG GTGCTAAATG CTACATACTC CAACTGAAAT 2220
GTTAAGGAAG AAGATAGATC CAATTAAAAA AAATTAAAAA CAATTAAAAA AAAAAAAGA 2280
ACACAGGAGA TTCCAGTCTA CTGAGTTAG CATAATACAG AAGTCCCCTC TACTTTAACT 2340
TTTACAAAAA AGTAACCTGA ACTAATCTGA TGTAAACCAA TGTATTATTT TCTGTGGTTC 2400
TGTTCCTTGG TTCCAATTTG ACAAAACCCA CTGTTCTTGT ATTGTATTGC CCAGGGGGAG 2460
CTATCACTGT ACTGTAGAG TGGTGTGCT TTAATTCATA AATCACAAT AAAAGCCAAT 2520
TAGCTCTATA ACT

Seq ID NO: 629 Protein sequence
Protein Accession #: AAA59909.1

1 11 21 31 41 51
MLTNVVISVV LPPCSNLTKP TVLVLYCPGG AITVLVEWCC FNS

Seq ID NO: 630 DNA sequence
Nucleic Acid Accession #: NM_016639.1
Coding sequence: 40..429

1 11 21 31 41 51
GCGGCGGGCG CAGACAGCGG CGGGCGCAGG ACGTGCACTA TGGCTCGGGG CTCGCTGCBC 60
CGGTTGTCTG GGTCTCTCGT GCTGGGGCTC TGGCTGGCGT TGGCTGCGTC CGTGGCCGGG 120
GAGCAAGCGC CAGGACCCGC CCCCTGTCTC CGCGGACGCT CCTGGAGCGC GGACCTGGAC 180
AAGTGCAATG ACTGCGGCTC TTGCAGGGCG CGACCGCACA GCGACTTCTG CCTGGGCTGC 240
GCTGCAGCAT CCTCTGCCCC CTTCGGGCTG CTTTGGCCCA TCCTTGGGGG CGCTCTGAGC 300
CTGACCTTCG TGCTGGGGCT GCTTTCTGTC TTTTGGTCTG GGAGACGATG CCGCAGGAGA 360
GAGAAGTTCA CCACCCCAT AGAGGAGACC GCGCGAGAGG GCTGCCACGC TGTGGCGCTG 420

ATCCAGTGAC AATGTGCCCC CTGCCAGCCG GGGCTCGCCC ACTCATCATT CATTTCATCCA 480
 TTCTAGAGCC AGTCTCTGCC TCCCAGACGC GCGGGGAGCC AAGCTCCTCC AACCAACAGG 540
 GGGGTGGGGG GCGGTGAATC ACCTCTGAGG CCTGGGCCCA GGGTTCAGGG GAACCTTCCA 600
 AGGTGTCTGG TTGCCCTGCC TCTGGCTCCA GAACAGAAAG GGAGCCTCAC GCTGGCTCAC 660
 ACAAACAGC TGACACTGAC TAAGGAACCTG CAGCATTTGC ACAGGGGAGG GGGGTGCCCT 720
 CCTTCTTTAG GACCTGGGGG CCAGGCTGAC TTGGGGGGCA GACTTGACAC TAGGCCCCAC 780
 TCACTCAGAT GTCCTGAAAT TCCACCACG3 GGGTCACCCT GGGGGGTTAG GGACCTATTT 840
 TTAACACTAG GGGCTGGCCC ACTAGGAGGG CTGGCCCTAA GATACAGACC CCCCCAACTC 900
 CCCAAAGCGG GGAGGAGATA TTTATTTTGG GGAGAGTTTG GAGGGGAGGG AGAATTTATT 960
 AATAAAGAA TCITTAACCT TAAAAAATAA AAAAAAAA

Seq ID NO: 631 Protein sequence
Protein Accession #: NP_057723.1

1 11 21 31 41 51
 MARGSLRRLL RLLVLGLWLA LLRSVAGEQA PGTAPCSRGS SWSADLDKCM DCASCRARPH 60
 SDFCLGCAAA PPAPFRLLPW ILGGALSLTF VLGLLSGLFV WRRRREKREF TPIEETGGE 120
 GCPAVALIQ

Seq ID NO: 632 DNA sequence
Nucleic Acid Accession #: NM_003816.1
Coding sequence: 79..2538

1 11 21 31 41 51
 CGGCAGGGTT GGAATATGAT GGAAGAGGCG GAGGTGGAGG CGACCGAGTG CTGAGAGGAA 60
 CCTGCGGAAT CGGCCGAGAT GGGGTCTGGC GCGCGCTTTC CCTCGGGGAC CCTTCGTGTC 120
 CGGTGGTTGC TGTGTCTTGG CCTGGTGGCG CCAGTCTCTCG GTGCGGCGCG GCCAGGCTTT 180
 CAACAGACCT CACATCTTTC TTCTTATGAA ATTATAACTC CTGGGAGATT AACTAGAGAA 240
 AGAAGAGAAG CCCCTAGGCC CTATTCAAAA CAAGTATCTT ATGTTATTCA GGCTGAAGGA 300
 AAAGAGCATA TTATTCACCT GGAAGGAAC AAAGACCTTT TGCTGAAGA TTTGTGGTT 360
 TATACCTACA ACAAGGAAGG GACTTTAATC ACTGACCATC CCAATATACA GAATCATTTG 420
 CATATATCGG GCTATGTGGA GGGAGTTTCA AATTCATCCA TTGCTCTTAG CGACTGTTT 480
 GGACTCAGAG GTATGTCTGCA TTTAGAGAAT GCGAGTTATG GGATTGAACC CCTGCAGAAC 540
 AGCTCTCATT TTGAGCACAT CATTTATCGA ATGGATGATG TCTACAAAGA GCCTCTGAAA 600
 TGTGGAGTTT CCAACAAGGA TATAGAGAAA GAAACTGCAA AGGATGAAGA GGAAGAGCCT 660
 CCCAGCATGA CTCAGCTACT TCGAAGAAGA AGAGCTGTCT TGCCACAGAC CCGTATGTG 720
 GAGCTGTTCA TTGTCTGAGA CAAGGAAAGG TATGACATGA TGGGAAGAAA TCAGACTGCT 780
 GTGAGAGAAG AGATGATTCT CCTGGCAAAC TACTTGGATA GTATGTATAT TATGTTAAAT 840
 ATTCGAATTG TGCTAGTTGG ACTGGAGATT TGGACCAATG GAAACCTGAT CAACATAGTT 900
 GGGGTGTGCT GTGATGTGCT GGGGAACTTC GTGCAGTGGC GGGAAAGATT TCTTATCACA 960
 CGTCGGAGAC ATGACAGTGC ACAGCTAGTT CTAAGAAAGG GTTTTGGTGG AACTGCAGGA 1020
 ATGGCATTGG TGGGAACAGT GTGTTCAAGG AGCCACGCGAG GCGGGATTAA TGTGTTTGA 1080
 CAAATCACTG TGAGACATT TGCTTCCATT GTTGCTCATG AATTGGGTCA TAATCTTGA 1140
 ATGAATCAGG ATGATGGGAG AGATTGTTCC TGTGGAGCAA AGAGCTGCAT CATGAATTCA 1200
 GGAGCATCGG GTTCCAGAAA CTTTAGCAGT TGCAGTCAG AGGACTTGA GAAGTTAACT 1260
 TTAATAAAG GAGGAACTG CCTTCTTAAT ATTCCAAAGC CTGATGAAGC CTATAGTGCT 1320
 CCTCTCTGTG GTAATAAGTT GGTGGACGCT GGGGAAGAGT GTGACTGTGG TACTCCAAAG 1380
 GAATGTGAAT TGGAACCTTG CTGCGAAGGA AGTACCTGTA AGCTTAAATC ATTTGCTGAG 1440
 TGTGCATATG GTGACTGTGG TAAAGACTGT CGGTTCCTTC CAGGAGGTAC TTTATGCCGA 1500
 GGAAAAACCA GTGAGTGTGA TGTTCAGAG TACTGCAATG GTTCTTCTCA GTTCTGTGAG 1560
 CCAGATGTTT TTATTCAGAA TGGATATCCT TGCCAGAAATA ACAAAGCCTA TTGCTACAAC 1620
 GGCAATGTGC AGATTATGA TGCTCAATGT CAAGTCATCT TTGGCTCAA AGCCAAGGCT 1680
 GCGCCCAAG ATGTTTTCAT TGAAGTGAAT TCTAAAGGTG ACAGATTGG CAATTGTGGT 1740
 TTCTCTGGCA ATGAATACAA GAAAGTGTGC ACTGGGAATG CTTTGTGTGG AAAGCTTCAG 1800
 TGTGAGAATG TACAAGAGAT ACCTGTATTT GGAATTGTGC CTGCTATTAT TCAAACGCTC 1860
 AGTCGAGGCA CCAATGTTG GGGTGTGAT TTCCAGCTAG GATCAGATGT TCCAGATCCT 1920
 GGGATGTTA ACGAAGGCAC AAAATGTGGT GCTGGAAGA TCTGTAGAAA CTTCCAGTGT 1980
 GTAGATGCTT CTGTCTGTGA TTATGACTGT GATGTTTACA AAAAGTGTCA TGGACATGGG 2040
 ATATGTAATA GCAATAAGAA TTGTCACTGT GAAATGGCT GGGCTCCCC AAATGTGAG 2100
 ACTAAAGGAT ACGGAGGAAG TGTGGACAGT GGACCTACAT ACAATGAAAT GAATACTGCA 2160
 TTGAGGGAGG GACTTCTGGT CTCTTCTTC CTAATTGTTT CCCTTATTGT CTGTGCTATT 2220
 TTTATCTTCA TCAAGAGGGA TCAACTGTGG AGAAGCTACT TCAGAAAGAA GAGATCACA 2280
 ACATATGAGT CAGATGGCAA AAATCAAGCA AACCTTCTA GACAGCCGGG GAGTGTTCCT 2340
 CGACATGTTT CTCCAGTGAC ACCCTCCAGA GAACTTCTTA TATATGCAAA CAGATTGCA 2400
 GTACCAACCT ATGCAGCCAA GCAACCTCAG CAGTTCCCAT CAAGGCCACC TCCACCACAA 2460
 CGAAAGTAT CATCTCAGGG AAACCTTAAT CCGTCCCGTC CTGCTCCTGC ACCTCCTTTA 2520
 TATAGTCCCC TCACTTGATT TTTTAACTT TCTTTTGTCA AATGTCTTCA GGGAACTGAG 2580
 CTAATACCTT TTTTCTTCT TGATGTTTTC TTGAAAAGCC TTTCTGTGTC AACTATGAAT 2640
 GAAAAAATAA CACCACAAAA CAGACTTCAC TAACACAGAA AACACAGAAAC TGAGTGTGAG 2700
 AGTTGTGAAA TACAAGGAAA TGCAGTAAAG CCAGGGAATT TACAATAACA TTTCCGTTTC 2760
 CATCATTGAA TAAGTCTTAT TCAGTCATCG GTGAGGTTAA TGCACTAATC ATGGATTTTT 2820
 TGAACATGTT ATTGCAGTGA TTCTCAAAT AACTGTATTG GTGTAGATT TTTGTCTTCA 2880
 AGTGTTTAAG TGTATTCTG AATTTTCTAC CTTAGTTATC ATTAATGTAG TTCTCATTG 2940
 AACATGTGAT AATCTAATAC CTGTGAAAAC TGACTAATCA GCTGCCAATA ATATCTAATA 3000
 TTTTTCATCA TGACAGCAAT AATAATCATC ATACTCTAGA ATCTTGTCTG TCACTCACA 3060
 CATGAATAAG CAAATATTGT CTTCAAAAGA ATGCACAAGA ACCACAATTA AGATGTCATA 3120
 TTATTTTGAA AGTACAAAAT ATACTAAAAG AGTGTGTGTG TATTCACGCA GTTACTCGCT 3180
 TCCATTTTAA TGACCTTTCA ACTATAGGTA ATAACCTCTA GAGAAATTAA TTTAATATTA 3240
 GAATTTCTAT TATGAATCAT GTGAAAGCAT GACATTCGTT CACAATAGCA CTATTTTAAA 3300
 TAAATATATA GCTTTAAGGT ACGAAGTATT TAATAGATCT AATCAATAT GTTGATTCAT 3360
 GGCTATAATA AAGCAGGAGC AATTATAAAA TCTTCAATCA ATTGAACCTT TACAAAACCA 3420
 CTTGAGAAAT TCATGAGCAC TTTAAATCT GAACTTCAA AGCTTGCTAT TAAATCATTT 3480
 AGAATGTTTA CATTTACTAA GGTGTGCTGG GTCATGTAAA ATATTAGACA CTAATATTTT 3540
 CATAGAAATT AGGCTGGAGA AAGAAGGAAG AAATGGTTTT CTTAAATACC TACAAAAAG 3600
 TTACTGTGGT ATCTATAGAT TATCATCTTA GCTGTGTAA AAATGAATTT TTACTATGGC 3660

AGATATGGTA TGGATCGTAA AATTTTAAGC ACTAAAAATT TTTTCATAAC CTTTCATAAT 3720
 AAAGTTTAAT AATAGGTTTA TTAAGTGAAT TTCATTAGTT TTTTAAAGT GTTTTGGTT 3780
 TGTGTATATA TACATATACA AATACAACAT TTACAATAAA TAAATACTT GAAATCTCA 3840
 AAAAAAAAAA AAAAAAAAAA AAAAA

Seq ID NO: 633 Protein sequence
 Protein Accession #: NP_003807.1

1 11 21 31 41 51
 MGSARFPSPG TLRVRWLLLL GLVGPVLGAA RPPGQOTSHL SSYEIITPWR LTRERREAPR 60
 PYSKQVSIVI QAEGKEHIIH LERNKDLLPE DFVVYTYNKE GTLITDHPNI QNHCHRYGYV 120
 EGVHNSIAL SDGFLRLGLL HLENASYGIE PLQNSSHFEH IYRMDVYK EPLKCGVSNK 180
 DIEKETAIDE EEPEPMTQL LRRRAVLFPQ TRYVELPIVV DKERYDMMGR NQTAVREMI 240
 LLANYLDSMY IMLNIRIVLV GLEIWTGNL INIVGGAGDV LGNFVQWREK FLITRRRHDS 300
 AQLVLKKGFG GTAGMARFVGT VCSRSAGGI NVFGQITVET FASIVAHELQ HNLGMNHDDG 360
 RDCSCQAKSC IMNSGASGSR NFSSCSAEDF EKLTNLKGGN CLLNIPKPE AYSAPSCGNK 420
 LVDAGEEEDC GTPKCELDLP CCEGSTCKLK SFAECAYGDC CKDCRFLPGG TLRCRKTSEC 480
 DVPEYCNSSS QFCOPDVFIQ NGYPCQNNKA YCYNGMCQYY DAQCQVIFGS KAKAAPKDCP 540
 IEVNSQKGRF GNCQPSGNEY KKCAGTGNALC GKLCQENQVE IPVFGIVPAI IQTPSRGKTC 600
 WGVDFQLGSD VPDGPMVNEG TKCGAGKICR NFQCVDAVL NYDCDVQKKC HGHGVCNSNK 660
 NCHCENGWAP PNCETKGYGG SVDSGPTYNE MNTALRDGLL VFFFLIVPLI VCAIFIFIKR 720
 DQLWRSYFRK KRSQTYESDG KNQANPSRQP GSVPRHVSFV TTPPREVIYA NFAVPTYAA 780
 KQPQGFPPRP PPOPKVSSQ GNLIARPAP APPLYSSLT

Seq ID NO: 634 DNA sequence
 Nucleic Acid Accession #: NM_002091.1
 Coding sequence: 56..503

1 11 21 31 41 51
 AGTCTCTGCT CTTCCAGGCC TCTCCGGCGC GCTCCAAGGG CTTCCTGTCG GGACCATGCG 60
 CGGCAGTGAG CTCCTGCTGG TCTGCTGCGC GCTGGTCTCT TGCTAGCGC CCCGGGGGCG 120
 AGCGGTCCCG CTGCTGCTGG GCGGAGGGAC CGTGTCTGACC AAGATGTACC CGCGCGGCAA 180
 CCCTGCGGCG GTGCGGCACT TAATGGGGAA AAAGAGCACA GGGGAGTCTT CTCTGTGTTT 240
 TGAGAGAGGG AGCCTGAAGC AGCAGCTGAG AGAGTACATC AGGTGGGAAG AAGCTGCAAG 300
 GAATTGCTG GGTCTCATAG AAGCAAAGGA GAACAGAAAC CACCAGCCAC CTCAACCCAA 360
 GGCCTTGGGC AATCAGCAGC CTTCTGTTGA TACAGAGGAT AGCAGCAACT TCAAAGATGT 420
 AGGTTCAAAA GGCAGAGTTG GTAGACTCTC TGCTCCAGTG TCTCAACGTG AAGGAAGGAA 480
 CCCCAGCTG AACCAGCAAT GATAATGATG GCCTCTCTCA AAAGAGAAAA ACAAAACCCC 540
 TAAGAGACTG AGTCTGTCAA GCATCAGTTC TACGAGTATC CAACAAGATT TCCTGTGTGA 600
 AAATATTGTA CTATTCTGTA TCTTTCATCC TTGACTAAAT TCGTATTGTT CAAGCAGCAT 660
 CTTCTGGTTT AAACCTGTTT GCTGTGAACA ATTGTGAAAA AGAGTCTTCC AATTAATGCT 720
 TTTTATATC TAGGCTACCT GTTGGTTAGA TTCAAGGCCC CGAGCTGTGA CCATTACAAA 780
 TAAAAGCTTA AACACAT

Seq ID NO: 635 Protein sequence
 Protein Accession #: NP_002082.1

1 11 21 31 41 51
 MRGSELPLVL LALVLCIAPR GRAVPLPAGG GTVLTMYPR GNHWAVGHLM GKKTGESSS 60
 VSERGSLKQQ LREYIRWEEA ARNLLGLIEA KENRNHQPPQ PKALGNQPPS WDSEDSBNFK 120
 DVGSKGKVR LSAPGSQREG RNPQLNQ

Seq ID NO: 636 DNA sequence
 Nucleic Acid Accession #: NM_016522.1
 Coding sequence: 265..1299

1 11 21 31 41 51
 GCGGAAGCAG CGAGGAGGGA GCCCCTTTTG GCCGTCTCC GTGGAACCGG TTTCCGAGG 60
 CTGGCAAAAG CCGAGGCTGG ATTGGGGGA GGAATATTAG ACTCGGAGGA GTCTGCGCGC 120
 TTTTCTCTC CCCGCGCTC CCGGTGCGCG CGGGTTTACC GCTCAGTCCC CGCGCTCGCT 180
 CGGCACCCCA CCCACTTCCT GTGCTGCGCC GGGGGGCGTG TGCCGTGCGG CTGCGGAGT 240
 TCGGGGAAGT TGTGGCTGTC GAGAATGGGG GTCTGTGGGT ACCTGTTCCT GCCCTGGAAG 300
 TGCCCTCGTG TCGTGTCTCT CAGGCTGCTG TTCTTTGTAC CCACAGGAGT GCCCGTGCBC 360
 AGCGGAGATG CCACCTTCCC CAAAGCTATG GACAACGTGA CGGTCCGGCA GGGGGAGAGC 420
 GCCACCTTCA GGTGCACTAT TGACAACCGG GTCACCCGGG TGGCTGTGCT AAACCGCAGC 480
 ACCATCTCT ATGCTGGGAA TGACAAGTGG TGCTGGATC CTGCGTGGT CCTTCTGAGC 540
 AACACCCAAA CGCAGTACAG CATCGAGATC CAGAACGTGG ATGTGTATGA CGAGGGCCCT 600
 TACACCTGCT CGGTGCAGAC AGACAACACC CAAAGACCT CTAGGTGCTA CCTCATTTGT 660
 CAAGTATCTC CCAAAATTGT AGAGATTCT TCAGATATCT CCATTAATGA AGGGAACAAT 720
 ATTAGCCTCA CCGCATAGC AACTGGTAGA CCAGAGCCTA CGGTACTTGT GAGACATC 780
 TCTCCCAAG CGGTTGGCTT TGTGAGTGAA GACGAATACT TGGAAATTCA GGCATCACC 840
 CGGGAACAGT CAGGGGACTA CGAGTGCAGT GCCTCCAATG ACGTGGCCCG GCCCTGGTA 900
 CGGAGAGTAA AGGTCAACGT GAACATATCA CCATACATTT CAGAAAGCAA GGTACAGGT 960
 GTCCCGTGG GACAAAAGGG GACACTGCAG TGTGAAGCCT CAGCAGTCCC CTCAGCAGAA 1020
 TTCCAGTGGT ACAAGGATGA CAAAGACTG ATTGAAGGAA AGAAAGGGGT GAAAGTGGAA 1080
 AACAGACCTT TCCTCTCAAA ACTATCTTC TTCAATGTCT CTGAACATGA CTATGGGAAC 1140
 TACACTTGGC TGGCCTCCAA CAAGCTGGGC CACACCAATG CCAGCATCAT GCTATTGGT 1200
 CTAGCGCGCG TCAGCAGAGT GAGCAACCGC ACGTCGAGGA GGGCAGGCTG CGTCTGGCTG 1260
 CTGCTCTTTC TGTCTTTCGA CTTGCTTCTC AAATTTTGTAT GTGAGTGCCA CTTCCCCACC 1320
 CGGGAAGGCG TGCGCGCACC ACCACACCA ACACAACAGC AATGGCAACA CCGACAGCAA 1380
 CCAATCAGAT ATATACAAAT GAAATTAGAA GAAACACAGC CTCATGGGAC AGAAATTTGA 1440
 GGGAGGGGAA CAAAGAATAC TTTGGGGGGA AAAGAGTTTT AAAAAAGAAA TTGAAATTG 1500
 CCTTGAGAT ATTTAGGTAC AATGGAGTTT TCTTTTCCCA AACGGGAAGA ACACAGCACA 1560

CCGGCTTGG ACCCACTGCA AGCTGCATCG TGCAACCTCT TTGGTGCCAG TGTGGGCAAG 1620
 GGCTCAGCCT CTCTGCCAC AGACTGCCCC CACGTGGAAC ATTCTGGAGC TGGCCATCCC 1680
 AAATTCATC AGTCCATAGA GACGAACAGA ATGAGACCTT CCGGCCCAAG CGTGGCGCTT 1740
 CCGGCCAAG CGTGGCGCTG CGGGCACTTT GGTAGACTGT GCCACCACGG CGTGTGTTGT 1800
 GAAACGTGAA ATAAAAAGAG CAAAAAATAA AAAAAAATAA

Seq ID NO: 637 Protein sequence
 Protein Accession #: NP_057606.1

1 11 21 31 41 51
 MGVCGLFLP WKCLVVVSLR LLFLVPTGVP VRSGDATFPK AMDNVTVRQG ESATLRCTID 60
 NRVTTRVAVLN RSTILYAGND KWCLDRPVVL LSNTQTQYSI EIQNVDVYDE GPYTCVSVQTD 120
 NHPKTSRVHL IVQVSPKIVE ISSDISINEG NNISLTCTAT GRPEPTVTWR HISP KAVGFV 180
 SEDEYLEIQG ITRQSGDYB CSASNDVAAP VVRRVKVTVN YPPYISEAKG TGVVPVQKGT 240
 LQCEASAVPS AEFQWYKDDK RLLEGKKGVK VENRPFSLKL IFFNVSEHDY GNYTCVASNK 300
 LGHTNASIML FPGAVSEVS NGTSRRAGCV WLLPLLVHL LLLK

Seq ID NO: 638 DNA sequence
 Nucleic Acid Accession #: NM_012261.1
 Coding sequence: 203..1045

1 11 21 31 41 51
 GATTGTCTCT GCCAGCAGCT GTCGGTGCCG CGCTCGACAC CGAGTCCTAG CTAGGCGCTC 60
 ACAGAAATAG CGCTCCCTCC CTCCCTCTTC TCTGTCCGCC GCCTCTCGCT CACCCCGGCT 120
 CACTCCAGCG GCGACTTTGA GGGATTCCCT CTCTGGCGGC CTCTGCAGCA GCACAGCCGG 180
 CCTCATTCGG GGCACCTGCG ATATGGATCT CCAAGGAAGA GGGGTCCCCA GCATCGACAG 240
 ACTTCGAGTT TCTCTGATGT TGTTCATATC AATGGCTCAA ATCATGGCAG AACAAAGAGT 300
 GGAAATCTCT TCAGGCTCTT CCACTAACCC TGAAAAAGAT ATATTGTGG TCGCGGAAAA 360
 TGGGACGACG TGTCTCATGG CAGAGTTTGC AGCCAAATTT ATTGTACCTT ATGATGTGTG 420
 GGCCAGCAAC TACGTAGATC TGATCACAGA ACAGGCCGAT ATCGCATTGA CCGGGGAGC 480
 TGAGGTGAAG GGCCTCTGTG GCCACAGCCA GTCGGAGCTG CAAGTGTCTT GGGTGGATCG 540
 CGCATATGCA CTCAAAATGC TCTTTGTAAA GGAAAGCCAC AACATGTCCA AGGGACCTGA 600
 GGCGACTTGG AGGCTGAGCA AAGTGCAGTT TGTCTACGAC TCCTCGGAGA AAACCCACTT 660
 CAAAGACGCA GTCACTGCTG GGAAGCACAC AGCCAACTCG CACCACCTCT CTGCCTTGGT 720
 CACCCCGCTT GGAAGTCTCT ATGAGTGTCA AGCTCAACAA ACCATTTCAC TGGCCTCTAG 780
 TGATCCGCGA AAGACGCTCA CCATGATCCT GTCTGCGGTC CACATCCAAC CTTTGTGACAT 840
 TATCTCAGAT TTGTCTTCTA GTGAAGAGCA TAAATGCCCA GTGGATGAGC GGGAGCAACT 900
 GGAAGAAACC TTGCCCCTGA TTTTGGGGCT CATCTTGGGC CTGTCATCA TGGTAACACT 960
 CGCGATTAC CACGTCCACC ACAAAATGAC TGCCAAACAG GTGCAGATCC CTCGGGACAG 1020
 ATCCCACTAT AAGCAGATGG GCTAGAGGCC GTTAGGCAGG CACCCCTAT TCCTGCTCCC 1080
 CCAACTGGAT CAGGTAGAAC AACAAAAGCA CTTTCCATC TTGTACACGA GATACACCAA 1140
 CATAGCTACA ATCAAAACAG CTTGGGTATC TGAGGCTTGC TTGGCTTGTG TCCATGCTTA 1200
 AACCCACGGA AGGGGGAGAC TCTTTCGGAT TTGTAGGGTG AAATGGCAAT TATTCTCTCC 1260
 ATGCTGGGGA GGAAGGAGG AGGCTCTCAG ACAGCTTTGC TGCTCATGGT GGGCTTGGCT 1320
 TGACTCTCCA AAGAGCAATA AATGCCACTT GGAGCTGTAT CTGGCCCAA AGTTTAGGGA 1380
 TTGAAACAT GCTTCTTGA GGAAGAAACC CCTTGTAGTT CAGAAGAATA TGGGGTGGCT 1440
 TGCTCCCTTG GACACAGCTG GCTTATCCTA TACAGTTGTC AATGCACACA GAATACAACC 1500
 TCATGCTCCC TCGAGCAAGA CCCTGAAAG TGATTCATGC TTCTGGCTGG CATTCTGCAT 1560
 GTTTAGTAGT TGTCTTGGGA ATGTTTCACT GCTACCCGCA TCCAGCGAGT GCAGCACCAG 1620
 AAAACGACTA ATGTAACAT GCAGAGTTGT TTGACTTCT TCCTGTGCCA GGTCCAAGTC 1680
 GGGGACCTG AAGAATCAAT CTGTGTGAGT CTGTTTTTCA AAATGAATA AAACACACTA 1740
 TTCTCTGGC

Seq ID NO: 639 Protein sequence
 Protein Accession #: NP_036193.1

1 11 21 31 41 51
 MDLQGRGVPS IDRLRVLLML PHTMAQIMAE QEVENLSGLS TNPEKDIFV RENGTTCLMA 60
 EFAAKFIVPY DVWASNYVDL ITEQADIALT RGAEVKGRCG HSQSELQVFW VDRAYALKML 120
 FVKESHNSMK GPEATWRLSK VQFVYDSSEK THFKDAVSAG KHTANSHLS ALVTPAGKSY 180
 ECQAQQTISL ASSDPQRTVT MILSAVHIQF FDIISDFVFS ESHKCPVDER EQLEETLPLI 240
 LGLILGLVIM VTLAIYVHH KMTANQVQIF RDRSQYKHM

Seq ID NO: 640 DNA sequence
 Nucleic Acid Accession #: NM_002993.1
 Coding sequence: 64..408

1 11 21 31 41 51
 GGCACGAGCC AGTCTCCGCG CCTCCACCCA GCTCAGGAAC CCGCGAACCC TCTCTTGACC 60
 ACTATGAGCC TCCGCTCCAG CCGCGCGGCC CGTGTCCCGG GTCTCTCGGG CTCCTTGTGC 120
 GCGCTGCTCG CGCTGCTGCT CCGCTGAGC CCGCGGGGCG CCTCGCCAG CGCTGGTCTC 180
 GTCTCTGCTG TGCTGACAGA GCTGCGTTGC ACTTGTATTAC CGGTACGCT GAGAGTAAAC 240
 CCCAAACGTA TTGTGTAACCT GCAGGTGTTT CCGCGAGGCC CGCAGTGCTC CAAGGTGGAA 300
 GTGGTAGCCT CCGTGAAGAA CGGGAAGCAA GTTTGTCTGG ACCCGGAAGC CCCTTTTCTA 360
 AAGAAAGTCA TCCAGAAAT TTTGGACAGT GGAACAAGA AAACTGAGT AACAAAAAG 420
 ACCATGCAAT ATAAATTTGC CAGTCTTCA GCGGAGCAGT TTTCTGGAGA TCCCTGGACC 480
 CAGTAAGAAT AAGAAGGAAG GGTGGTTTT TTTCCATTTT CTACATGGAT TCCCTACTTT 540
 GAAGAGTGTG GGGGAAAGCC TACGCTTCT CCGTGAAGTT ACAGCTCAG TAATGAAGTA 600
 CTAATATAGT ATTTCCACTA TTTACTGTTA TTTTACCTGA TAAGTTATTG AACCTTTGG 660
 CAATTGACCA TATTGTGAGC AAGAAATCAC TGGTTATTAG TCTTCAATG AATATTGAAT 720
 TGAAGATAAC TATTGTATT CTATCATACA TTCCTTAAAG TCTTACCAG AAGCTGTGG 780
 ATTTGATATG GAAATAATGT TTTATTAGT TGCTGTTGAG GGAGGTATCC TGTGTTCTT 840
 ACTCACTCT CTCATAAAT AGGAAATATT TTAGTTCTGT TTTCTGGGG AATATGTTAC 900

TCTTTACCTT AGGATGCTAT TTAAGTTGTA CTGTATTAGA ACACTGGGTG TGTACATCCG 960
 TTATCTGTGC AGAATATATT TCCTTATTCA GAATTTCTAA AAATTTAAGT TCTGTAAGGG 1020
 CTAATATATT CTCTTCTCAT GGTTTTAGAT GTTTGATGTC TTCTTAGTAT GGCATAATGT 1080
 CATGATTTAC TCATTAAACT TTGATTTTGT ATGCTATTTT TTCACATAG GATGACTATA 1140
 ATTCTGGTCA CTAATATAC ACTTTAGATA GATGAAGAAG CCCAAAAACA GATAAATTCC 1200
 TGATTGCTAA TTATCATAGA AATGTATTCT CTGGTTTTT TAAATAAAG CAAAATTAAAC 1260
 AATGATCTGT GCTCTGCAAA GTTTTGAAAA TATATTTGAA CAATTTGAAT ATAAATTCAT 1320
 CATTTAGTCC TCAAAATATA TACAGCATTG CTAAGATTTT CAGATATCTA TTGTGGATCT 1380
 TTTAAAGGTT TTGACCATTT TGTATGAGG AATTATACAT GTATCACATT CACTATATTA 1440
 AAATTGCACT TTTATTTTTT CCTGTGTGTC ATGTTGGTTT TTGGTACTTG TATTGTCTAT 1500
 TGGAGAAACA ATAAAGATT TCTAAACCAA AAAAAA AAAA

Seq ID NO: 641 Protein sequence

Protein Accession #: NP_002984.1

1 11 21 31 41 51
 MSPLPSSRAAR VPGPSGSLCA LLALLLLLTP PGPLASAGPV SAVLTELRCT CLRVLRLVNP 60
 KITIGKLQVFP AGPQCSKVEV VASLKNGKQV CLDPEAPFLK KVIQKILDSG NKKN

Seq ID NO: 642 DNA sequence

Nucleic Acid Accession #: NM_013271.1

Coding sequence: 27..809

1 11 21 31 41 51
 TCCGGAGCCA GGCCTGCTGG GGCAGCATGG CGGGGTGCGC GCTGCTCTGG GGGCCGCGGG 60
 CCGGGGGCGT CGGCCCTTTT GTGCTGCTGC TGCTCGGCCT GTTTCGGCCG CCCCCCGCGC 120
 TCTGCGCGCG GCGCGTAAAG GAACCCCGCG GCCTAAGCGC AGCGTCTCCG CCCTTGGCTG 180
 AGACTGGGCG TCCTCGCCCG TTCCGGCGGT CAGTGCCCGG AGGTGAGGCG GCGGGGGCGG 240
 TGCAGGAGCT GCGCGCGGGG CTGGCGCATC TGCTGGAGGC CGAACGTCTG GAGCGGGCGC 300
 GGGCCGAGGC GCAGGAGGCT GAGGATCAGC AGGCGCGCGT CCTGGCGCAG CTGCTGCGCG 360
 TCTGGGGCGC CCCCAGCAAC TCTGATCCGG CTCTGGGCCT GGACGACGAC CCGGACGCGC 420
 CTGACGCGCA GCTGCTCGCG GCTCTGCTCC GCGCCCGCCT TGACCTTGCC GCCCTAGCAG 480
 CCCAGCTTGT CCCCAGCCCG GTCCCCCGCG CGGCGCTCCG ACCCGGCGCC CCGGTCTAAG 540
 ACGACGGGCG GAGGCTGAGG GATGCTGAGG AGGCAGGCGA CGAGACACCC GACGTGGACC 600
 CCGAGCTGTT GAGGTACTTG CTGGACGCGA TTCTTGCGGG AAGCGCGGAC TCCGAGGGGG 660
 TGGCAGCCCC GCGCCGCGCT CGCCGTGCGG CCGACCAAGA TGTGGGCTCT GAGCTGCCCC 720
 CTGAGGGGCT GCTGGGGGCG CTGCTGCGTG TGAAACGCGT AGAGACCCCG GCGCCCCAGG 780
 TGCCTGCAAG CCGCCTCTTG CCACCTGAG CACTGCCCGG ATCCCGTGCA CCCTGGGACC 840
 CAGAAAGTGC CCGCCATCC CGCCACCAAG ACTTCTCCCC GCCAGCACGT CCAGAGCAAC 900
 TTACCCCGGC CAGCCAGCCC TCTACCCGA GGATCCCTAC CCCCCTGGCC ACAATAACAT 960
 GATCTGAGC

Seq ID NO: 643 Protein sequence

Protein Accession #: NP_037403.1

1 11 21 31 41 51
 MAGSPLLWGP RAGGVGLLV LLLGLFRPPP ALCARPVKEP RGLSAASPPL AETGAPRRFR 60
 RSVPRGEAAG AVQELARALA HLLAERQER ARAEAQEAED QARVLAQLL RVWGAPRNSD 120
 PALGLDDDDP APAQLARAL LRLRLDPAAL AAQLVPAVPV AAALRPRFPV YDDGPAGPDA 180
 EEAGDETCDV DPELLRVLG RILAGSADSE GVAAPRRLRR AADHDVGSSEL PEGVLGALL 240
 RVKRLTAP QVPARRLLPP

Seq ID NO: 644 DNA sequence

Nucleic Acid Accession #: NM_002214

Coding sequence: 681..2990

1 11 21 31 41 51
 CCCAGAGCCG CCTCCCCCTG TTGCTGGCAT CCGAGGCTTC CTCCCTTGCC AGCCAGGACG 60
 CTGCCGACTT GTCTTTGCCG GCTGCTCCGC AGACGGGGCT GCAAAGCTGC AACTAATGGT 120
 GTTGGCTTCC CTGCCACCT GTGGAAGCAA CTGCGCTGAT TGATGCGCA CAGACTTTT 180
 TCCCTCGAC CTGCGCGCGG TACCCTCCCA CAGATCCAGC ATCACCAGT GAATGTACAT 240
 TAGGGTGGTT TCCCCCCAG CTTCGGGCTT TGTTTGGGTT TGATTGTGTT TGGCTCTTCG 300
 CTAAGCTGAT TTATGAGCA GAAGCCCCAC CGGCTGGAGA GAAACAAAAG CTCTTTCTT 360
 TGTCCCGGAG CAGGCTGCGG AGCCCTTGCA GAGCCCTCTC TCCAGTCGCC GCCGGGCCCT 420
 TGGCCGTGCA AGGAGGTGCT TCTCGCGGAG ACCGCGGAC CCGCGGTGCC GAGCCGGGAG 480
 GGCCGTAGGG GCCCTGAGAT GCCGAGCGGT GCCCGGGGCC GCTTACCTGC ACCGCTTGT 540
 CCGAGCCGCG GGGTCCGCT GCTAGGCCTG CGGAAAACGT CCTAGCGACA CTCGCCGCG 600
 GGCCCGGAGG TCGCCCGGGA GGCCGAGCCC GCGTCCGGA GGCAGCCAGG CCGCGGGCGC 660
 GGGGCGGGCT GTTTTGCAAT ATGTGCGGCT CGGCCCTGGC TTTTTTACC GCTGCAITTT 720
 TCTGCTGCA AAACGACCGG CAGGTCCTCG CCTGTTCTCT CTGGGAGCC TGGGTGTTTT 780
 CACTTGTCT TGGACTGGGC CAAGGTGAAG ACAATAGATG TGCATCTTCA AATGCAGCAT 840
 CCTGTGCCAG GTGCCCTTGC CTGGTCCAG AATGTGGATG GTGTGTTCAA GAGGATTTCA 900
 TTTCAAGTGG ATCAAGAAAGT GAACGTTGTG ATATTGTTTC CAATTTAATA AGCAAAGGCT 960
 GCTCAGTTGA TTCAATAGAA TAACCATCTG TGCATGTTAT AATACCCACT GAAATGAAA 1020
 TTAATACCCA GTGACACCA GGAGAAAGTGT CTATCCAGCT GCGTCCAGGA GCCGAAGCTA 1080
 ATTTATGCTT GAAAGTTTCT CCTCTGAAGA AATATCCTGT GGATCTTTAT TATCTTGTG 1140
 ATGTCTCAGC ATCAATGCAC AATAATATAG AAAAATTAAA TTCCGTTGGA AACGATTAT 1200
 CTAGAAAAAT GGCATTTTTC TCCCGTGAAT TTGCTCTTGG ATTTGGCTCA TACGTTGATA 1260
 AAACAGTTTC ACCATCCACC CCGAAAGGAT TCATAATCAA TGCAGTGACT 1320
 ACAATTTAGA CTGCATGCCT CCCCATGGAT ACATCCATGT GCTGCTTTG ACAGAGACA 1380
 TCACTAGATT TGAGAAAGCA GTTCATAGAC AGAAGATCTC TGGAAACATA GATACACCAG 1440
 AAGGAGGTTT TGACGCCATG CTTCAGGCAG CTGCTCTGTA AAGTCATATC GGATGGCGAA 1500
 AAGAGGCTAA AAGATTGCTG CTGGTGATGA CAGATCAGAC GTCTCATCTC GCTCTTGATA 1560

	GCAAATTGGC	AGGCATAGTG	GTGCCCAATG	ACGGAAACTG	TCATCTGAAA	AACAACGTCT	1620
	ACGTCAAAATC	GACAACCATG	GAACACCCCT	CACTAGGCCA	ACTTTCAGAG	AAATTAATAG	1680
	ACAACAACAT	TAATGTATC	TTTGCAGTTC	AAGGAAAACA	ATTTTCATTG	TATAAGGATC	1740
5	TTCTACCCCT	CTTGCCAGGC	ACCATTGCTG	GTGAAATAGA	ATCAAAGGCT	GCAAACTCA	1800
	ATAATTTGGT	AGTGGAAAGC	TATCAGAAGC	TCATTTTCAGA	AGTGAAGATT	CAGGTGGAAA	1860
	ACCAGGTACA	AGGCATCTAT	TTTAACATTA	CGCCATCTG	TCCAGATGGG	TCCAGAAAGC	1920
	CAGGCATGGA	AGGATGCAGA	AACGTGACGA	GCAATGATGA	AGTTCTTTTC	AATGTAACAG	1980
	TTACAATGAA	AAAATGTGAT	GTCAACAGGAG	GAATAAATA	TGCAATAATC	AAACCTATTG	2040
10	GTTTTAATGA	AACCGCTAAA	ATTCATATAC	ACAGAAACTG	CAGCTGTCTG	TGTGAGGACA	2100
	ACAGAGGACC	TAAAGGAAAG	TGTGTAGATG	AAACTTTTCT	AGATTCCAAG	TGTTTCCAGT	2160
	GTGATGAGAA	TAAATGTCTAT	TTTGTATGAG	ATCAGTTTTC	TTCTGAGAGT	TGCAAGTCAC	2220
	ACAAGGATCA	GCCTGTTTGC	AGTGGTCSAG	GAGTTTGTGT	TTGTGGGAAA	TGTTTCATGTC	2280
	ACAAAATTAA	GCTTGGAAAA	GTGTATGGAA	AATACTGTGA	AAAGGATGAC	TTTTCTTGTG	2340
	CATATCACCA	TGTAATCTCG	TGTGCTGGGC	ATGGAGAGTG	TGAAGCAGGC	AGATGCCAAT	2400
15	GCCTTCAGTG	CTGGGAAGGT	GATCGATGCC	AGTGCCCTTC	AGCAGCAGCC	CAGCACTGTG	2460
	TCAATTCAA	GGGCAAGTG	TGCAGTGGAA	GAGGCACGTG	TGTGTGTGGA	AGGTGTGAGT	2520
	GCACCGATCC	CAGGAGCATC	GGCCGCTTCT	GTGAACACTG	CCCCACCTGT	TATACAGCCT	2580
	GCAAGGAAAA	CTGGAATTGT	ATGCAATGCC	TTCACTCTCA	CAATTTGTCT	CAGGCTATAC	2640
	TTGATCATAG	CAACACCTCA	TGTGCTCTCA	TGGAACAACA	GCATTATGTC	GACCAAACTT	2700
20	CAGAATGTTT	CTCCAGCCCA	AGCTACTTGA	GAATATTTT	CATCATTTTC	ATAGTTACAT	2760
	TCTTGTATGG	TTGCTCTAAA	GTCTGATCA	TTAGACAGGT	GATACTACAA	TGGAATAGTA	2820
	ATAAAATTAA	GTCTCTATCA	GATTACAGAG	TGTGACGCTC	AAAAAAGGAT	AAGTTGATTG	2880
	TGCAAGTGT	TTGCACAAGA	GCAGTCACCT	ACCGACGTGA	GAAGCCTGAA	GAATAAAAA	2940
25	TGGATATCAG	CAAAATTAAT	GCTCATGAAA	CTTTCAGGTG	CAACTTCTAA	AAAAAGATT	3000
	TTAAACACTT	AATGGGAAAC	TGGAATTGTT	AATAATTGCT	CCTAAAGATT	ATAATTTTAA	3060
	AAGTCACAGG	GGGCAACAAA	TTGCTCACGG	TCATGCCAGT	TGCTGGTTGT	ACACTCGAAC	3120
	GAAGACTGAC	AAGTATCCTC	ATCATGATGT	GACTCACATA	GCTGCTGACT	TTTTCAGAGA	3180
	AAAAATGTGT	TTACTACTGT	TTGAGACTAG	TGTCGTTGTA	GCACCTTACT	GTAATATATA	3240
	ACTTATTTAG	ATCAGCATAG	AATGTAGATC	CTCTGAAGAG	CAGTGATTAC	ACTTTACAGG	3300
30	TACCTGTAT	CCCTACGCTT	CCCAGAGAGA	ACAATGCTGT	GAGAGAGTTT	AGCATTGTGT	3360
	CACTACAAGG	GTACAGTAAT	CCCTGCACTG	GACATGTGAG	GAATAAATA	ATCTGGCAAG	3420
	TATATTCTAA	GGTTGCCCAA	CACCTCAACA	GTGTGTGGTT	GAATAGACAA	GAACAGCTAG	3480
	ATGAATAAAT	GATTCTGTGT	TCACCTTTTC	AAGAGGTGAA	CAGATACAAC	CTTAATCTTA	3540
35	AAAGATTATT	GCTTTTAAAT	GTGTGTAGTT	TTATGCATGT	GTGTTTATGG	TTTGCTTATT	3600
	TTTGCAAGAT	GGATACTAAT	TCCAGCATTC	TCTCTCTTTT	GCCTTTATGT	TTTGTTTTCT	3660
	TTTTTACAGG	ATAAGTTTAT	GTATGTCACA	GATGACTGGA	TTAATTAAAGT	GCTAAGTTAC	3720
	TACTGCCATA	AAAAACTAAT	AATACATGT	CACCTTTATCA	GAATACTAGT	TTTAAAGCT	3780
	GAATGTTAA						

Seq ID NO: 645 Protein sequence
Protein Accession #: NP_002205

	1	11	21	31	41	51	
45	MCGSALAPFT	AAVFLQNDNR	RGPAFLWAA	WVFLVLGLG	QGEDNRCASS	NAASCARCLA	60
	LGPECGVCVQ	EDFISGGRS	ERCDIVSNLI	SKGCSVDSE	YPSVHVLIPT	ENEINTQVTP	120
	GEVSIQLRPG	AEANFMKLVH	PLKKYPVDLY	YLVDVSASMH	NNIEKLSVNG	NDLSRKMAFF	180
	SRDFRLGFGS	YVDKTVSPYI	SIHPERIHNQ	CSQYNLDCMP	PHGYIHVLSL	TENITEFEKA	240
50	VHRQKISGNI	DTPEGGFDAM	LQAACVCEHI	GWRKEAKRL	LVMTDQTSHL	ALDSKLAGIV	300
	VPNDGNCHLK	NNVVKSTTM	EHPSLGQLSE	KLIDNNINVI	FAVQGGQFHW	YKDLLFLLEPG	360
	TIAGEIESKA	ANLNNLVVEA	YQKLISEVKV	QVENQVQGIY	FNITAICPDG	SRKPGMEGCR	420
	NVTNDEVLFP	NVTVTMKKCD	VTGKKNYAI	KPIGFNETAK	IHIHRNCSQ	CEDNRGPKGK	480
	CVDETFLDSK	CFQCDENKCH	FDEDQFSSSE	CKSHKQDQVC	SGRGVCVCGK	CSCHKIKLKG	540
55	VYGYKCEKDD	PSCPHYHGNL	CAGHGECEAG	RQCQPSGWE	DRQCQPSAAA	QHCNVSKGQV	600
	CSGRGTGCVG	RCECTDPRSI	GRFCEHCPTC	YTACKENWNC	MQCLHHPNLS	QAILDQCKTS	660
	CALMEQGHYV	DQTECEPSSP	SYLRIFFIIF	IVTFILIGLLK	VLIIRQVILQ	WNSNRKIKSSS	720
	DYRVSASKID	KLILQSVCTR	AVTYRREKPE	EIKMDISKLN	AHETFRFCNF		

Seq ID NO: 646 DNA sequence
Nucleic Acid Accession #: NM_003318.1
Coding sequence: 1..2574

	1	11	21	31	41	51	
65	ATGGAATCCG	AGGATTTAAG	TGGCAGAGAA	TTGACAATTG	ATTCCATAAT	GAACAAAGTG	60
	AGAGACATTA	AAAATAAGTT	TAAAAATGAA	GACCTTACTG	ATGAACATAA	CTTGAATAAA	120
	ATTTCTGCTG	ATACTACAGA	TAACTCGGGA	ACTGTTAAAC	AAATTATGAT	GATGGCAAA	180
	AAACCAGAGG	ACTGGTTGAG	TTTGTGCTC	AAACTAGAGA	AAAACAGTGT	TCCGCTAAGT	240
	GATGCTCTTT	TAAATAAATT	GATTGGTCGT	TACAGTCAAG	CAATTGAAGC	GCTTCCCCCA	300
70	GATAAATATG	GCCAAATGGA	GAGTTTGTCT	AGAATTCAG	TGAGATTGTC	TGAATTAAGA	360
	GCTATTCAAG	AGCCAGATGA	TGCACGTGAC	TACTTTCAAA	TGGCCAGAGC	AAACTGCAAG	420
	AAATTGCTTT	TTGTTCTAT	ATCTTTTGCA	CAATTGTAAC	TGTCAACAAG	TAATGTCAAA	480
	AAAAGTAAAC	AACTTCTTCA	AAAAGCTGTA	GAACGTGGAG	CAGTACCAC	AGAAATGCTG	540
	GAAATGCCCC	TGCGGAATTT	AAACCTCCAA	AAAAAGCAGC	TGCTTTTCAG	GGAGGAAAG	600
75	AAGAATTTAT	CAGCATCTAC	GGTATTAAC	GCCCAAGAA	CATTTTCCCG	TTCACTTGGG	660
	CATTTACAGA	ATAGGAACAA	CAGTTGTGAT	TCCAGAGGAC	AGACTACTAA	AGCCAGGTTT	720
	TTATATGAGG	AGAATCATGC	ATCACAAGAT	GCAGAAATAG	GTTACCGGAA	TTCAATTGAGA	780
	CAAACTAACA	AACTAACA	GTCATGCCCA	TTTGAAGAG	TCCCAAGTAA	CCTTCTAAAT	840
	AGCCAGATT	GTGATGTGAA	GACAGATGAT	TCAGTTGTAC	CTTGTTTTAT	GAAGAGACAA	900
80	ACCTCTAGAT	CAGATGCGG	AGATTGGTT	GTGCCTGGAT	CTAAACCAAG	TGGAATGAT	960
	TCCTGTGAAT	TAAGAAATTT	AAAGTCTGTT	CAAAATAGTC	ATTTCAGGGA	ACCTCTGGTG	1020
	TCAGATGAAA	AGAGTTCTCA	ACTTATTATT	ACTGATTCAA	TAACCTTGAA	GAATAAAACG	1080
	GAATCAAGTC	TTCTAGCTAA	ATTAGAAGAA	ACTAAAGAGT	ATCAAGAAC	AGAGGTTCCA	1140
	GAGAGTAACC	GAAGACAGTG	GCAATCTAAG	AGAAAGTCAG	AGTGTATTAA	CCAGATCTCT	1200
85	GCTGCATCT	CAATCACTG	GCAGATTCCG	GAGTTAGCCC	GAAGAGTTAA	TACAGAGCAG	1260
	AAACATACCA	CTTTTGAACA	ACCTGTCTTT	TCAGTTTCAA	AACAGTCACC	ACCAATATCA	1320
	ACATCTAAT	GGTTTGACCC	AAAATCTATT	TGTAAGACAC	CAAGCAGCAA	TACCTTGGAT	1380

	GATTACATGA	GCTGTTTGTAG	AATCCAGTT	GTAAAGAATG	ACTTTCACAC	TGCTTGTGAG	1440
	TTGTCAACAC	CTTATGGCCA	ACCTGCCTGT	TCCAGCAGC	AACAGCATCA	AATACCTGCC	1500
	ACTCCACTTC	AAAATTTACA	GGTTTGTAGCA	TCTTCTTCAG	CAAAATGAATG	CATTTCGGTT	1560
5	AAAGGAAGAA	TTTATTCAT	TTTAAAGCAG	ATAGGAAGTG	GAGGTTCAAG	CAAGGTATTT	1620
	CAGGTGTTAA	ATGAAAGAA	ACAGATATAT	GCTATAAAAT	ATGTGAACCT	AGAAGAAGCA	1680
	GATAACCAAA	CTCTTGATAG	TTACCGGAAC	GAAATAGCTT	ATTTGAATAA	ACTACAACAA	1740
	CACAGTGATA	AGATCATCCG	ACTTTATGAT	TATGAAATCA	CGGACCACTA	CATCTACATG	1800
	GTAATGGAGT	GTGGAAATAT	TGATCTTAAT	AGTTGGCTTA	AAAAGAAAAA	ATCCATTGAT	1860
10	CCATGGGAAC	GCAAGAGTTA	CTGGAATAAT	ATGTTAGAGG	CAGTTCACAC	AATCCATCAA	1920
	CATGGCATTG	TTACAGTGTA	TCTTAAACCA	GCTAACTTTC	TGATAGTTGA	TGGAATGCTA	1980
	AAGCTAATTG	ATTTTGGGAT	TGCAAAACCA	ATGCAACCAG	ATACAACAAG	TGTTGTTAAA	2040
	GATTCTCAGG	TTGGCACAGT	TAATTATATG	CCACCAGAAG	CAATCAAAGA	TATGTCCTCC	2100
	TCCAGAGAGA	ATGGGAATATC	TAAGTCAAAG	ATAAGCCCCA	AAAGTGATGT	TTGGTCCTTA	2160
	GGATGTATTT	TGTACTATAT	GACTTACGGG	AAAACACCAT	TTCAGCAGAT	AATTAATCAG	2220
15	ATTTCTAAAT	TACATGCCAT	AATTGATCCT	AATCATGAAA	TTGAATTTCC	CGATATTCCA	2280
	GAGAAAGATC	TTCAGATGTG	GTTAAAGTGT	TGTTTAAAAA	GGGACCCAAA	ACAGAGGATA	2340
	TCCATTCTCG	AGCTCCTGGC	TCATCCCTAT	GTTCAAATTC	AAACTCATCC	AGTTAACCAA	2400
	TTGGCCCAAG	GAAACACTGA	AGAAATGAAA	TATGTTCTGG	GCCAACTTGT	TGGTCTGAAT	2460
20	TCTCCTAACT	CCATTTTGAA	AGCTGCTAAA	ACTTTATATG	AACACTATAG	TGGTGGTGAA	2520
	AGTCATAATT	CTTCATCCTC	CAAGACTTTT	GAIAAAAAAA	GGGGAIAAAA	ATGA	

Seq ID NO: 647 Protein sequence
Protein Accession #: NP_003309.1

25	1	11	21	31	41	51	
	MESEDLSGRE	LTIDSIMNKV	RDINKNPKNE	DLTDELSLNK	ISADTTDMSG	TVNQIMMMAN	60
	NPEDWLSLLL	KLEKNSVPLS	DALLNKLIGR	YSQAIELAPP	DKYQNESFA	RIQVRFALIK	120
	ATQEPDDARD	YFQMARANCK	KFAFVHISFA	QFELSQQNVK	KSKQLLQKAV	ERGAVPLEML	180
30	ETALRNLNQ	KKQLLSSEEEK	KNLSASTVLT	AQESFSSGLG	HLQNRNNSCD	SRGQTTKARF	240
	LYGENMPPQD	AEIGYRNSLR	QTNKTKQSCP	FGRVFPVNLN	SPDCVKTTDD	SVPFCFMKRO	300
	TSRSECDRLV	VPGSKPSGND	SCELRNLKSV	QNSHPKEPLV	SDEKSELII	TDSITLKNKT	360
	ESSLLAKLEE	TKYQEPPEVP	ESNQKQWQSK	RKSECINQNP	AASSNHQWIP	ELARKVNTBQ	420
	KHTTFEPQVF	SVSQSPPIIS	TSKWFDPKSI	CKTPSNTLTD	DYMSCRPTPV	VKNDFPPACQ	480
35	LSTPYGQPAC	FQQQOHQILA	TPLQNLQVLA	SSSANECISV	KGRIVSILKQ	IGSGGSSKVF	540
	QVLNEKKQY	AIKIVNLEEA	DNQTLDSYRN	EIAYLNKLQO	HSDKIRLYD	YEITDQIYIM	600
	VMECGNIDLN	SWLKKKKSID	PWERKSYWKN	MLEAVHTIHO	HGIVHSDLKP	ANFLIVDGM	660
	KLIDFGIANQ	MQPDTSVVVK	DSQVGTVMYM	PPEAIKDMSS	SRENKSKSK	ISPKSDVWSL	720
	GCILYMYTYG	KTPPQIINQ	ISKLHAIIDP	NHEIEFPDIP	EKDLQDVLKC	CLKRDPKQRI	780
40	SIPELLAHFY	VQIQTHPVNQ	MAKGTTEEMK	VVLGQLVGLN	SPNSILKAAK	TLYEHYSGGE	840
	SHNSSSSKTF	EKKRGKK					

Seq ID NO: 648 DNA sequence
Nucleic Acid Accession #: NM_015507
Coding sequence: 241..1902

45	1	11	21	31	41	51	
	CCGCAGAGGA	GCCTCGGCCA	GGCTAGCCAG	GGCGCCCCCA	GCCCCCTCCC	AGGCCGCGAG	60
	CGCCCCCTGC	GCGGTGCTGT	GCCTCCCTTC	CCAGACTGCA	GGGACAGCAC	CCGGTAACTG	120
50	CGAGTGGAGC	GGAGGACCCG	AGCGGCTGAG	GAGAGAGGAG	GCGGCGGCTT	AGCTGCTACG	180
	GGGTCCGGCC	GGCGCCCTCC	CGAGGGGGGC	TCCAGAGGAG	GAGGAGGAGC	CCGTGCGAGA	240
	ATGCTCTGCG	CCTGAGAGCT	TGCGCTCCCG	CTGCTGCTCT	CCTGGGTGGC	AGGTGGTTTC	300
	GGGAACGCGG	CCAGTGCAAG	GCATCACGGG	TTGTTAGCAT	CGGCACGTCA	GCCTGGGGTC	360
55	TGTCACTATG	GAATCAAACT	GGCTGCTGCT	TACGCTGGA	GAAGAAGAGC	CAAGGAGATC	420
	TGTGAAGCTA	CATCGCAACC	TGGATGTAAG	TTTGGTGAGT	GCGTGGGACC	AAACAAATGC	480
	AGATGCTTTC	CAGGATACAC	CGGGAAGAAC	TGCAGTCAAG	ATGTGAATGA	GTGTGGAATG	540
	AAACCCCGGC	CAGTCAACAC	CAGATGTGTG	AATACACACG	GAAGCTACAC	GTGCTTTTGC	600
	CTCAGTGGCC	ACATGCTCAT	GCCAGATGCT	ACGTGTGTGA	ACTCTAGGAC	ATGTGCCATG	660
60	ATAAACTGTC	AGTACAGCTG	TGAAGACACA	GAAGAAGGGC	CACAGTGCCT	GTGTCCATCC	720
	TCAGGACTGC	CCCTGGGCCC	AAATGGGAAG	GACTGTCTAG	ATATTGATGA	ATGTGCCCTC	780
	GGTAAAGTCA	TCTGTCCCTA	CAATCGAAGA	TGTGTGAACA	CATTGGAAG	CTACTACTGC	840
	AAATGTACAC	TTGGTTTCGA	ACTGCAATAT	ATCAGTGGAC	GATATGACTG	TATAGATATA	900
65	AATGAATGTA	CTATGGATAG	CCATACGTGC	AGCCACCATG	CCAATTGCTT	CAATACCCAA	960
	GGGTCTTCTA	AGTGTAATAG	CAAGCAGGGA	TATAAAGGCA	ATGGACTTCC	GTGTTCTGCT	1020
	ATCCCTGAAA	ATTCTGTGAA	GGAAAGTCTC	AGAGCACCTG	GTACCATCAA	AGACAGAATC	1080
	AAGAAAGTGC	TTGCTCACAA	AAACAGCATG	AAAAAGAAAG	CAAAATTTAA	AAATGTTACC	1140
	CCAGAACCCA	CCAGGACTCC	TACCCCTAAG	GTGAACCTGC	AGCCCTTCAA	CTATGAAGAG	1200
70	ATAGTTTCCA	GAGGCGGGAA	CTCTCATGGA	GGTAAAAAAG	GGAATGAAGA	GAAGATGAAA	1260
	GAGGGGCTTG	AGGATGAGAA	AAGAGAAGAG	AAAGCCCTGA	AGAATGACAT	AGAGGAGCGA	1320
	AGCCTGCGAG	GAGATGTGTT	TTTCCCTAAG	GTGAATGAAG	CAGGTGAATT	CGGCTGATT	1380
	CTGGTCCAAA	GGAAAGCGCT	AACCTCCAAA	CTGGAACATA	AAGATTATAA	TATCTCGGTT	1440
	GACTGCGACT	TCAATCATGG	GATCTGTGAC	TGGAAACAGG	ATAGAGAAGA	TGATTTTGAC	1500
75	TGGAATCCTG	CTGATCGAGA	TAATGCTATT	GGCTTCTATA	TGGCAGTTCC	GGCCTTGGCA	1560
	GGTCAACAAG	AAGACATTGG	CCGATTGAAA	CTTCTCTTAC	CTGACCTGCA	ACCCCAAAGC	1620
	AACITCTGTT	TGCTTTTGA	TTACCGGCTG	GCCGGAGACA	AAGTCGGGAA	ACTTCGAGTG	1680
	TTTGTGAAAA	ACAGTAACAA	TGCCCTGGCA	TGGGAGAAGA	CCACGAGTGA	GGATGAAAAG	1740
	TGGAAGACAG	GGAAATTTCA	GTGTATATCA	GGAACTGATG	CTACCAAAG	CATCATTTT	1800
	GAAGCAGAAC	GTGGCAAGGG	CAAAACCGGC	GAAATCGCAG	TGGATGGCGT	CTTGCTTGTT	1860
80	TCCAGGCTTAT	GTCCAGATAG	CCTTTTATCT	GTGGATGACT	GAATGTTACT	ATCTTTATAT	1920
	TTGACTTTGT	ATGTCAGTTC	CCTGGTTTTT	TTGATATTGC	ATCATAGGAC	CTCTGGCATT	1980
	TAGAAATFAC	TAGCTGAAAA	ATTGTAATGT	ACCAACAGAA	ATATTATTGT	AAGATGCCTT	2040
	TCTTGATATA	GAAATGCCAA	TATTTGCTTT	AAATATCATA	TCACTGTATC	TTCTCAGTCA	2100
	TTTCTGAATC	TTTCCACATT	ATATTATAAA	ATATGGAAT	GTCAGTTTAT	CTCCCTCCT	2160
85	CAGTATATCT	GATTTGTATA	AGTAAGTTGA	TGAGCTTCTC	TCTACAACAT	TTCTAGAAAA	2220
	TAGAAAAAAA	AGCACAGAGA	AATGTTTAAC	TGTTTGACTC	TTATGATACT	TCTTGAAAC	2280
	TATGACATCA	AAGATAGACT	TTTGCCTAAG	TGGCTTAGCT	GGGTCTTTCA	TAGCCAAACT	2340

TGTATATTTA AATCTTTGT AATAATAATA TCCAAATCAT CAAAAAATAA AAAAAAAA

Seq ID NO: 649 Protein sequence
Protein Accession #: NP_056322

	1	11	21	31	41	51	
5	MPLPWSLALP	LLLSWVAGGF	GNAASARHHG	LLASARQPGV	CHYGTKLACC	YGWRRNSKGV	60
10	CEATCEPGCK	FGECVGNPKC	RCPPGYTGKT	CSQDVNECGM	KPRPCQHRVC	NTGHSYKCFE	120
	LSGHMLMPDA	TCVNSRTCAM	INCQYSCEDT	BEGPQCLCPS	SGLRLAPNGR	DCLDIDECAS	180
	GKVICPNRR	CVNTFGSYVC	KCHIGFELQY	ISGRYDCIDI	NECTMDSHTC	SHHANCFTNQ	240
	GSFKCKCKQG	YKGNGLRCSA	IPENSVKEVL	RAPGTIKDRI	KKLLAHKNSM	KKKAKIKNVT	300
15	PEPTRTPPK	VNLQPFNYEE	IVSRGGNSHG	GKKGNEEKMK	EGLEDEKREE	KALKNDIEER	360
	SLRGDVFFPK	VNEAGFGLI	LQQRKALTSK	LEHKDLNISV	DCSFNHGICD	WKQDREDDFD	420
	WNPADRDNAI	GFYMAVPALA	GKKKDIGRLK	LLLPDLQPS	NFCLLFIDYRL	AGDKVGLLRV	480
	FVKNSNNALA	WEKTTSEDEK	WKTGKIQLYQ	GTDAKTSIIF	EAERKGKGTG	EIAVDGVLLV	540
	SGLCPDLSLS	VDD					

Seq ID NO: 650 DNA sequence
Nucleic Acid Accession #: NM_003506.1
Coding sequence: 259..2379

	1	11	21	31	41	51	
25	GCAGCTCCAG	TCCCGGACGC	AACCCCGGAG	CCGTCTCAGG	TCCCTGGGGG	GAACGGTGGG	60
	TTAGACGGGG	ACGGGAAGGG	ACAGCGGCCT	TCGACCGCCC	CCCGAGTAAT	TGACCCAGGA	120
	CTCATTTTCA	GGAAAGCCTG	AAATAGAGTA	AAATAGTGAA	ATGAGGAATT	TGAACATTTT	180
30	ATCTTTGGAT	GGGGATCTTC	TGAGGATGCA	AAGAGTGATT	CATCCAAGCC	ATGTGGTAAA	240
	ATCAGGAATT	TGAAGAAAAT	GGAGATGTTT	ACATTTTGTG	TGACGTGTAT	TTTTCTACCC	300
	CTCCTAAGAG	GGCAGAGTCT	CTTCACCTGT	GAACCAATTA	CTGTTCCAG	ATGTATGAAA	360
	ATGGCCTACA	ACATGACGTT	TTTCCCTAAT	CTGATGGGTC	ATTATGACCA	GAGTATTGCC	420
	GCGGTGGAAA	TGGAGCATTT	TCTTCTCTCT	GCAAACTCGG	AATGTTCAAC	AAACATTGAA	480
35	ACTTTCCTCT	GCAAAGCATT	TGTACCAACC	TGCATAGAAC	AAATTCATGT	GGTTCACCT	540
	TGTCGTAAAC	TTTGTGAGAA	AGTATATTCT	GATTGCAAAA	AATTAATTGA	CACTTTGGG	600
	ATCCGATGGC	CTGAGGAGCT	TGAATGTGAC	AGATTACAAT	ACTGTGATGA	GACTGTTCCT	660
	GTAACCTTTG	ATCCACACAC	AGAATTTCTT	GGTCTCTAGA	AGAAAACAGA	ACAAGTCCAA	720
	AGAGACATTG	GATTTTGGTG	TCCAAGGCAT	CTTAAGACTT	CTGGGGGACA	AGGATATAAG	780
40	TTTCTGGGAA	TGACCCAGTG	TGCGCCTCCA	TGCCCAACA	TGTATTTTAA	AAGTGATGAG	840
	CTAGAGTTTG	CAAAAAGTTT	TATTGGAAAC	GTTCATATAT	TTTGTCTTTG	TGCAACTCTG	900
	TTCACTTTCC	TACTTTTCTT	AATTGATGTT	AGAAGATTCA	GATACCCAGA	GAGACCAATT	960
	ATATATTACT	CTGTCTGTGA	CAGCATGTGA	TCTCTTATGT	ACTTCATTGG	ATTTTGTGCTG	1020
	GGCGATATTC	TGTTTGGCCT	TGAGGAGATG	GAGAAGCTAG	AAGTTGGTGA	CACGTGTGTC	1080
45	CTAGGCTCTC	AAAATAAGGC	TTGCACCGTT	TTGTTCATGC	TTTTGTATTT	TTTCACAATG	1140
	GCTGGCAGTG	TGTGGTGGGT	GATTCTTACC	ATTACTTGGT	TCTTAGCTGC	AGGAAGAAAA	1200
	TGGAGTTTGG	AAGGACCTGA	GCAAAAAGCA	GTGTGGTTTC	ATGCTGTTGG	ATGGGGAACA	1260
	CCAGGTTTCC	TGACTGTGAT	GCTTCTTGCT	CTGAACAAGG	TTGAAGGAGA	CAACATTAGT	1320
	GGAGTTTGCT	TTGTTGGCCT	TTATGACCTG	GATGCTTCTC	GCTACTTTGT	ACTCTTGCCA	1380
50	CTGTGCTTTT	GTGTGTTTGT	TGGGCTCTCT	CTTCTTTTAG	CTGGCATTAT	TTCTTTAAAT	1440
	CATGTTCCAG	AAATCATACA	ACATGATGGC	CGGAACCAAG	AAAAACTAAA	GAATTTATG	1500
	ATTGCAATTG	GAGTCTTCAG	CGGCTTGTAT	CTTGTGCCAT	TAGTGACACT	TCTCGGATGT	1560
	TACGCTTAGT	AGCAAGTGAA	CAGGATTACC	TGGGAGATAA	CTTGGGCTCT	TGATCATTGT	1620
	CGTCAGTACC	ATATCCCATG	TCCTTATCAG	GCAAAAAGCA	AAGCTCGACC	AGAATTGGCT	1680
55	TTATTTATGA	TAAATACCTT	GATGACATTA	ATTGTTGGCA	TCTCTGCTGT	CTTCTGGGTT	1740
	GGAAGCAAAA	AGACATGCAC	AGAATGGGCT	GGGTTTTTTA	AACGAAATCG	CAAGAGAGAT	1800
	CCAATCAGTG	AAAGTCGAAG	AGTACTACAG	GAATCATGTG	AGTTTTTCTT	AAAGCACAAAT	1860
	TCTAAAGTTA	AACACAAAAC	GAAGCACTAT	AAACCAAGTT	CACACAGCT	GAAGGTCAAT	1920
	TCCAATCCGA	TGGGAACCCG	CACAGGAGCT	ACAGCAAATC	ATGGCACTTC	TGCAGTAGCA	1980
60	ATTACTAGCC	ATGATTACCT	AGGACAAGAA	ACTTTGACAG	AAATCCAAC	CTCACCAGAA	2040
	ACATCAATGA	GAGAGGTGAA	AGCGGACCGA	GCTAGCACCC	CCAGGTTAAG	AGAACAGGAC	2100
	TGTGGTGAAC	CTGCTTCGCC	AGCAGCATCC	ATCTCCAGAC	TCTCTGGGGA	ACAGGTCGAC	2160
	GGGAAGGGCC	AGGCAGGCAG	TGTATCTGAA	AGTGCAGCGA	GTGAAGGAAG	GATTAGTCCA	2220
	AAGAGTGATA	TTACTGACAT	TGGCCTGGCA	CAGAGCAACA	ATTTCAGAGT	CCCCAGTTCT	2280
65	TCAGAACCAA	GCAGCCTCAA	AGGTTCCACA	TCTCTGCTTG	TTCAACCCAGT	TTCAAGGAGTG	2340
	AGAAAAGAGC	AGGAGGTGCG	TTGTCTTCA	GATACTTGAA	GAACATTTTC	TCTCGTTACT	2400
	CAGAAGCAAA	TTTGTGTAC	ACTGGAAGTG	ACCTATGCAC	TGTTTTGTAA	GAATCACTGT	2460
	TACGTTCTTC	TTTTGCACTT	AAAGTTGCAT	TGCTTACTGT	TATCTAGGAA	AAATAGAGT	2520
	TCAAGAATAA	TATGACTCAT	TTCAACAAAA	GGTTAATGAC	AACAATATAC	CTGAAAACAG	2580
70	AAATGTGCAG	GTTAATAATA	TTTTTTTAAAT	AGTGTGGGAG	GACAGAGTTA	GAGGAATCTT	2640
	CCTTTTCTAT	TTATGAAGAT	TCTACTCTTG	GTAAGAGTAT	TTTAAGATGT	ACTATGCTAT	2700
	TTTACCTTTT	TGATATAAAA	TCAAGATATT	TCTTTGCTGA	AGTATTTAAA	TCTTATCTTT	2760
	GTATCTTTTT	ATACATATTT	GAAAATAAGC	TTATATGTAT	TTGAACCTTT	TTGAAATCCT	2820
	ATTCAAGTAT	TTTTATCATG	CTATTGTGAT	ATTTTAGCAC	TTTGGTAGCT	TTTCACTGTA	2880
75	ATTTCTAAGA	AAATTGTAAA	ATAGTCTTCT	TTTACTATGT	AAAAAAGAT	ATACCAAAAA	2940
	GTCTTATAAT	AGGAATTTAA	CTTTAAAAAC	CCACTTATTT	ATACCTTACC	ATCTAAAAATG	3000
	TGTGATTTTT	ATAGTCTCGT	TTTAGGAATT	TCACAGATCT	AAATTTATGTA	ACTGAAATAA	3060
	GGTGCTTACT	CAAAAGAGTG	CCACTATTGA	TGTATTATG	CTGCTCACTG	ATCCTTCTGC	3120
	ATATTAAAA	TAAAGGTTTC	TAAAGGTTTA	GTAGACAAAA	TGTTAGTCTT	TTGTATATTA	3180
80	GGCCAGGTGC	AATTGACTTC	CCTTTTTTAA	TGTTTCATGA	CCACCCATTG	ATTGTATTAT	3240
	AACCACTTAC	AGTTGCTTAT	ATTTTTTGT	TTAACTTTTG	TTTCTTAAAC	TTTAGAATAT	3300
	TACATTTTGT	ATTATACAGT	ACCTTTCTCA	GACATTTTGT	AG		

Seq ID NO: 651 Protein sequence
Protein Accession #: NP_003497.1

	1	11	21	31	41	51

WO 02/086443

PCT/US02/12476

MEMPTFLLTC IFLPLLRGHS LFTCEPITVP RCMKMYNMT FFPNLMGHVD QSIAAVERMEH 60
 FLPLANLECS PNIETFLCKA FVPTCIEQIH VVPPCRKLCE KVVSDCKKLI DTFGIRWPEE 120
 LBCDRLQYCD ETPVPTFDPH TEFLGPQKKT EQVQRDIGFW CPHRLKTSGG QGYKFLGIDQ 180
 CAPPCPNMYF KSDELEFAKS FIGTVSIFCL CATLFTPLTF LIDVRRFRYP ERPIIYYSVC 240
 YSIVSLMYFI GFLLGDSSTAC NKADEKLELG DTVVLGSSQNK ACTVLFMLLY FFTMAGTVMW 300
 VILTTITWFLA AGRKWSCEAI EQKAVWPHAV AWGTPGFLTV MLLALNKVEG DNISGVCFVG 360
 LYDLASRYF VLLPLCLCVF VGLSLLLAGI ISLNHVQRVI QHGRNQEKI KKFMRIGVF 420
 SGLYLVLPLVT LLGCVYVEQV NRITWEITWV SDHCQRQYHIP CPYQAKAKAR PELALFMIKY 480
 LMTLIVGISA VFWVGSKKT TEWAGFFKRN RKRDPISER RVLQESCEFP LKHSKVKHK 540
 KGHYKPSHK LKVISKSMGT STGATANHGT SAVAITSHDY LGQETLTIQ TSPETSMREV 600
 KADGASTPRL REQDCGEPAS PAASISRLSG EQVDGKGQAG SVSESARSEG RISPKSDITD 660
 TGLAQSNMLQ VPSSESPSSL KGSTSLLVHP VSGVRKEQGG GCHSDT

Seq ID NO: 652 DNA sequence
 Nucleic Acid Accession #: NM_014791.1
 Coding sequence: 171..2126

1 11 21 31 41 51
 TTGGCGGGCG GAAGCGGCCA CAACCGGGCG ATCGAAAAGA TTCTTAGGAA CGCGTACCA 60
 GCGCGGTCTC TCAGGACAGC AGGCCCTGT CCTTCTGTGG GCGCGGCTC AGCCGTGCC 120
 TCGCGCCCTC AGGTTCTTTT TCTAATTCCA AATAAACTTG CAAGAGGACT ATGAAAGATT 180
 ATGATGAAC TCTCAAATAT TATGAATTAC ATGAAACTAT TGGGACAGGT GGCTTTGCAA 240
 AGGTCAAAC TGCTGCCCAT ATCCTTACTG GAGAGATGGT AGCTATAAAA ATCATGGATA 300
 AAAACACACT AGGGAGTGAT TTGCCCCGGA TCAAAACGGA GATTGAGGCC TTGAAGAAC 360
 TGAGACATCA GCATCTATGT CAACTCTACC ATGTGCTAGA GACAGCCAAC AAAATATTCA 420
 TGGTCTCTGA GTACTGCCCT GGAGGAGAGC TGTTTGACTA TATAATTCC CAGGATCGCC 480
 TGTCAAGAAG GGAGACCCGG GTTGTCTTCC GTCAGATAGT ATCTGCTGTT GCTTATGTGC 540
 ACAGCCAGGG CTATGCTCAC AGGGACCTCA AGCCAGAAAA TTTGCTGTTT GATGAATATC 600
 ATAAATTAAG GCTGATTGAC TTGGTCTCT GTGCAAAACC CAAGGGTAAC AAGGATTACC 660
 ATCTACAGAC AGTCTGTGGG AGTCTGGCTT ATGCAGCACC TGAGTTAATA CAAGGCAAT 720
 CATATCTTGG ATCAGAGGCA GATGTTTGA GCATGGGCAT ACTGTTATAT GTTCTTATGT 780
 GTGGATTCTT ACCATTTGAT GATGATAATG TAATGGCTTT ATACAAGAAG ATTATGAGAG 840
 GAAATATAGA TGTTCCTAAG TGGCTCTCT CCAGTAGCAT TCTGCTTCTT CAACAAATGC 900
 TGCAGGTGGA CCCAAGAAAA CGGATTCTTA TGAAAAATCT ATTGAACCAT CCCTGGATCA 960
 TGCAAGATTA CAACTATGCT GTTGAAGTGG AAAGCAAGAA TCCTTTTATT CACCTCGATG 1020
 ATGATTGCGT AACAGAACTT TCTGTACATC ACAGAAACAA CAGGCAACAA ATGGAGGATT 1080
 TAATTTCACT GTGGCAGTAT GATCACCTCA CGGCTACCTA TCTTCTGCTT CTAGCCAAGA 1140
 AGGCTCGGGG AAAACCAAGT CGTTTAAGGC TTTCTTCTT CTCTGTGGA CAAGCCAGTG 1200
 CTACCCCATC CACAGACATC AAGTCAAATA ATTGGAGTCT GGAAGATGTG ACCGCAAGTG 1260
 ATAAAAATTA TGTGGCGGGA TTAATAGACT ATGATTGGTG TGAAGATGAT TTATCAACAG 1320
 GTGCTGTCTAC TCCCGGAACA TCACAGTTTA CCAAGTACTG GACAGATCA AATGGGGTGG 1380
 AATCTAAATC ATTAATCTCA GCCTTATGCA GAACACCTGC AAATAAATTA AAGAACAAG 1440
 AAAATGTATA TACTCTTAAG TCTGCTGTAA AGAATGAAGA GTACTTTATG TTTCTGAGC 1500
 CAAAGACTCC AGTTAATAAG AACACGATA AGAGAGAAAT ACTCACTACG CCAATTCGTT 1560
 ACATACATC CTCAAAAGT GCTGAAGA AACTCCAATT AAAATACAG 1620
 TAAATTCAC AGGAACAGAC AAGTTAATGA CAGGTGTCTAT TAGCCCTGAG AGGCGGTGCC 1680
 GCTCAGTGA ATTGCATCTC AACCAAGCAC ATATGGAGGA GACTCCAATA AGAAAGGGAG 1740
 CCAAAGTGT TGGGAGCCTT GAAAGGGGGT TGGATAAGGT TATCACTGTG CTCACCAGGA 1800
 GCAAAGGAA GGGTCTTGCC AGAGACGGGC CCAGAAAGCT AAAGCTTAC TATAATGTGA 1860
 CTACACCTAG ATTAGTGAAT CAGATCAAC TGTGAATGA AATAATGTCT ATTCTTCAA 1920
 AGAAGCATGT TGACTTTGTA CAAAGGGT ATCACTGAA GTGTCAAACA CAGTCAGATT 1980
 TTGGGAAAT GACAATGCAA TTTGAATTAG AAGTGTGCCA GCTTCAAATA CCGATGTGG 2040
 TGGGTATCAG GAGGCAGCGG CTTAAGGGCG ATGCCTGGGT TTACAAAGA TTAGTGAAG 2100
 ACATCCTATC TAGCTGCAAG GTATAATTGA TGGATTCTTC CATCCTGCCG GATGAGTGT 2160
 GGTGTGATAC AGCCTACATA AAGACTGTTA TGATCGCTTT GATTTTAAAG TTCATTGGA 2220
 CTACCAACTT GTTCTTAAAG AGCTATCTTA AGACCAATAT CTCTTTGTTT TTAACAAAA 2280
 GATATTATT TGTGTATGAA TCTAATCAA GCCCATCTGT CATTATGTTA CTGTCTTTT 2340
 TAATCATGTG GTTTTGTATA TTAATAATTG TTGACTTTCT TAGATTCACT TCCATATGTG 2400
 AATGTAAGCT CTTAACATAG TCTCTTGTGA ATGTGTAATT TCTTCTGAA ATAAACCAT 2460
 TTGTGAATAT

Seq ID NO: 653 Protein sequence
 Protein Accession #: NP_055606.1

1 11 21 31 41 51
 MKDYDELLKY YELHETIGT GFAKVKLACH ILTGEMVAIK IMDKNTLGSD LPRIKTEIEA 60
 LKNLRHQHIC QLYHVLETAN KIFMVLEYCP GGELEFDYIIS QDRLSEETR VVFRQIVSAV 120
 AYVHSQGYAH RDLKPENLFF DEYHKLKID FGLCAKPKGN KDYHLQTCG SLAYAPELI 180
 QGKSYLGSEA DVNSMGILLY VLMCGFLPPD DDNMALYKK IMRGKYDVPK WLSPPSILL 240
 QQMLQVDPFK RISMKNLLNH PWIMQDYNYP VEWQSKNFFI HLDDCVTEL SVHHRNNRQT 300
 MEDLISLWQY DHLTATYLL LAKKARGKEV RLRLSSPSCG QASATPFTDI KSNNWSLEDV 360
 TASDKNVVAG LIDYDWCEDD LSTGAATPRT SQFTKYWTES NGVESKSLTP ALCRTPANKL 420
 KNKENVYTPK SAVKNEEYFM FPEPKTFVNK NQHKREILT PNRYTTPSKA RNQCLKETPI 480
 KIPVNSTGTD KLMTGVISPE RRCRSVELDL NQAHMEETPK RKGAKEVFGSL ERGLDKVITV 540
 LTRSKRKGSA RDGPRRLKH YNVTTTRLVN PDQLNEIMS ILPKGHVDPV QRGYTLKQCT 600
 QSDFGKVMQ FELEVCQLQK PDVVGIRRRQ LKGDWVYKR LVEDILSSCK V

Seq ID NO: 654 DNA sequence
 Nucleic Acid Accession #: NM_000582
 Coding sequence: 88..990

1 11 21 31 41 51
 GCAGAGCACA GCATCGTCCG GACCAGACTC GTCTCAGGCC AGTTGCAGCC TTCTCAGCCA 60
 AACGCCGACC AAGGAAAAC TACTACCATG AGAATTGCAG TGATTGCTT TTGCTCCTCA 120

	GGCATCACT	GTGCCATACC	AGTTAAACAG	GCTGATTCTG	GAAGTTCTGA	GGAAAAGCAG	180
	CTTTACAACA	AATACCAG	TGCTGTGGCC	ACATGGCTAA	ACCCTGACCC	ATCTCAGAAG	240
	CAGAACTCC	TAGCCCCACA	GACCCCTCCA	AGTAAGTCCA	ACGAAAGCCA	TGACCACATG	300
5	GATGATATG	ATGATGAAGA	TGATGATGAC	CATGTGGACA	GCCAGGACTC	CATTGACTCG	360
	AACGACTCTG	ATGATGTAGA	TGACACTGAT	GATTCTCACC	AGTCTGATGA	GTCTCACCAT	420
	TCTGATGAAT	CTGATGAAC	GGTCACTGAT	TTTCCCACGG	ACCTGCCAGC	AACCGAAGTT	480
	TTCACCTCCAG	TTGTCCCCAC	AGTAGACACA	TATGATGGCC	GAGGTGATAG	TGTGGTTTAT	540
	GGACTGAGGT	CAAAATCTAA	GAAGTTTCGC	AGACCTGACA	TCCAGTACCC	TGATGCTACA	600
10	GACGAGGACA	TCACCTCACA	CATGGAAAGC	GAGGAGTTGA	ATGGTGCATA	CAAGGCCATC	660
	CCCGTTGGCC	AGGACCTGAA	CGCGCCTTCT	GATTGGGACA	GCCGTGGGAA	GGACAGTTAT	720
	GAAACGAGTC	AGCTGGATGA	CCAGAGTGCT	GAAACCCACA	GCCACAAGCA	GTCCAGATTA	780
	TATAAGCGGA	AAGCCAATGA	TGAGAGCAAT	GAGCATTCCG	ATGTGATTGA	TAGTCAGGAA	840
	CTTTCCAAAG	TCAGCCGTGA	ATTCCACAGC	CATGAATTC	ACAGCCATGA	AGATATGCTG	900
	GTTGTAGACC	CCAAAAGTAA	GGAAGAAGAT	AAACACCTGA	AATTTGCTAT	TTCTCATGAA	960
15	TTAGATAGTG	CATCTTCTGA	GGTCAATTAA	AAGGAGAAAA	AATACAATTT	CTCACTTTGC	1020
	ATTTAGTCAA	AGAAAAAAT	CTTTTATAGC	AAAATGAAAG	AGAACATGAA	ATGCTTCTTT	1080
	CTCAGTTTAT	TGGTTGAATG	TGTATCTATT	TGAGTCTGGA	AATAACTAAT	GTGTTTGATA	1140
	ATTAGTTTAG	TTTGTGGCTT	CATGGAAACT	CCCTGTAAAC	TAAAAGCTTC	AGGGTTATGT	1200
20	CTATGTTTAT	TTTATGAAG	AAATGCAAA	TATCACTGTA	TTTTAATATT	TGTTATTCTC	1260
	TCATGAATAT	AAATTTATGT	AGAAGCAAAC	AAAATACTTT	TACCCACTTA	AAAAGAGAAT	1320
	ATAACATTTT	ATGCTCATAT	ATCTTTTGT	TTTTTAAGTT	AGTGTATATT	TGTTGTGATG	1380
	TATCTTTTGT	TGGTGTGAAT	AAATCTTTTA	TCTTGAATGT	AATAAGAAAT	TGGTGGTGTC	1440
	AATTGCTTAT	TTGTTTTCCT	ACGGTTGTCC	AGCAATTAAT	AAAACATAAC	CTTTTCTACT	1500
25	GCCTAAAAAA	AAAAAAAATA	AAAA				

Seq ID NO: 655 Protein sequence
Protein Accession #: NP_000573

30	1	11	21	31	41	51	
	MRIIVICFCL	LGITCAIPVK	QADSGSSEK	QLYNKYPDV	ATWLNPDPSQ	KQNLLAPQTL	60
	PSKSNESHDH	MDDMDDDDDD	DHVDSDSDID	SNDSDDVDDT	DDSHQSDSH	HSDESDELVT	120
	DFPTDLFATE	VFTPVVPTVD	TYDGRGDSVV	YGLRSKSKKF	RRPDIOYVDA	TDEDITSHME	180
35	SEELNGAYKA	IPVAQDLNAP	SDWDSRGKDS	YETSQLDQDS	AEETHSHKQSR	LYKRRANDES	240
	NHSDVIDSQ	ELSKVSREPH	SHEFHSHEDM	LVVDFPKSKEE	DKHLKFRISH	ELDSASSEVN	

Seq ID NO: 656 DNA sequence
Nucleic Acid Accession #: NM_003108.1
Coding sequence: 76..1401

40	1	11	21	31	41	51	
	GGGGTGGGAG	GGGGAGGGGG	ACCTCCGCAC	GAGACCCAGC	GGCCCGGGTT	GGAGCGTCCA	60
45	GCCCTGCAAC	GGATCATGGT	GCAGCAGGCG	GAGAGCTTGG	AAGCGGAGAG	CAACCTGCCC	120
	CGGGAGGGCG	TGGACACGGA	GGAGGGCGAA	TTCAATGGCTT	GCAGCCCGGT	GGCCCTGGAC	180
	GAGAGCGACC	CAGACTGGTG	CAAGACGGCG	TCCGGCCACA	TCAAGCGGCC	GATGAACGCG	240
	TTCAATGGTAT	GGTCCAAGAT	CGAACGCGAG	AAGATCATGG	AGCAGTCTCC	GGACATGCAC	300
50	AACGCGGAGA	TCTCCAAGAG	GCTGGGCAAG	CGCTGGAAGA	TGCTGAAGGA	CAGCGAGAAG	360
	ATCCCGTTCA	TCCGGGAGGC	GGAGCGGCTG	CGGCTCAAGC	ACATGGCCGA	CTACCCCGAC	420
	TACAAGTACC	GGCCCCGGAA	AAAGCCCAAA	ATGGACCCCT	CGGCCAAGCC	CAGCGCCAGC	480
	CAGAGCCAG	AGAAGAGCGC	GGCCGGCGGC	GGCGCGGGGA	GGCGGGCGGG	AGCGCGGGGC	540
	GGTGCCAGCA	CCTCCAAAGG	CTCCAGCAAG	AAATGCGGCA	AGCTCAAGGC	CCCCCGGGCC	600
55	GCGGGCGCCA	AGGCGGGCGC	GGCAAGGCGC	GCCCACTCCG	GGGACTACGG	GGGCGGGGGC	660
	GACGACTACG	TGCTGGGCAG	CCTGCGCGTG	AGCGGCTCGG	GCGGCGGCGG	CGCGGGCAAG	720
	ACGGTCAAGT	GCCTGTTTCT	GGATGAGGAC	GACGACGACG	ACGACGACGA	CGACGAGCTG	780
	CAGCTGCAGA	TCAAAACAGGA	GCCGACGAG	GAGGACGAGG	AACCAACGCA	CCAGCAGCTC	840
	CTGACGCGCG	CGGGGACGCA	GCCGTCGCG	CTGCTGAGAC	GCTACAAAGT	CGCCAAAGTG	900
60	CCCGCCAGCC	CTACGCTGAG	CAGCTCGGCG	GAGTCCCCCG	AGGGAGCGAG	CCTCTACGAC	960
	GAGGTGCGGG	CCGCGCGGAC	CTCGGCGGCC	GGGGCGGCGA	GCCGCTCTTA	CTACAGCTTC	1020
	AAAGAACATCA	CCAAGCAGCA	CCCGCCGCGC	CTCGCGCAGC	CCGCGCTGTC	GGCCCGCTCC	1080
	TGCGCGCTCG	TGTCCACCTC	CTCGTCCAGC	AGCAGCGCGA	GCAGCAGCGG	CAGCAGCGGC	1140
	GAGGACGCGC	ACGACCTGAT	GTTCCGACCTG	AGCTTGAATT	TCTCTCAAAG	CGCGCACAGC	1200
65	GCCAGCGAGC	AGCAGCTGGG	GGGCGGCGCG	GCGGCGGGGA	ACCTGTCCCT	GTGCTGTTGT	1260
	GATAAGGATT	TGGATTCGTT	CAGCGAGGCG	AGCCTGGGCT	CCCACTTCGA	GTTCCCGGAC	1320
	TACTGCACGC	CGGAGCTGAG	CGAGATGATC	GCGGGGAGCT	GGCTGGAGGC	GAACCTTCTC	1380
	GACCTGGTGT	TCACATATTG	AAAGGCGCCC	GCTGCTCGCT	CTTTCTCTCG	GAGGGTGATG	1440
	AGCTGGGTTT	CTGGGAGGA	AGTTGTAGTG	GTGATGATGA	TGATGATGAT	AATGATGATG	1500
70	ATGATGGTGG	TGTTGATGGT	GGCGGTGGTA	GGGTGGAGGG	GAGAGAAGAA	GATGCTGATG	1560
	ATATTGTATA	GATGTCGTGA	CGCAAGAAAA	TTGGAAGAAA	TGATGAAAT	TTGGTGGAG	1620
	TTAAAGTGAA	ATGAGTAGTT	TTTAAACATT	TTTCTGTGTC	TTTTTTTGTC	CCCCCTCCCT	1680
	TCCTTTATCG	TGTTCTCAAGG	TAGTTGCATA	CCTAGTCTGG	AGTTGTGATT	ATTTTCCCAA	1740
	AAAATGTGTT	TTTGTAAATTA	CTATTTCTTT	TTCTGAAAT	TCGTGATTGC	AACAAAGGCA	1800
75	GAGGGGGCGG	CGCGGCGGAG	GGGAGGTAGG	ACCCGCTCCG	GAAGGCGCTG	TTTGAAGCTT	1860
	GTCGGTCTTT	GAACTCTGGA	AGACGCTGCG	AGAGGACCTT	TTTGGCAGCA	CAACTGTTAC	1920
	TCTAGGGAGT	TGGTGGAGAT	ATTTTCTTTT	CTTAAGAGAA	CTTAAAGAAC	TGGTGATTTT	1980
	TTTTTAACAA	AAAAAGGG					

Seq ID NO: 657 Protein sequence
Protein Accession #: NP_003099.1

80	1	11	21	31	41	51	
	MVQQAESLEA	ESNLPREALD	TEEGEFMACS	PVALDESDPD	WCKTASGHIK	RPMNAFMVWS	60
85	KIERRKIMQ	SFDMHNAEIS	KRLGKRWKML	KDSEKIPFIR	EAERLRKLMH	ADYFDYKYRP	120
	RKKPKMDPSA	KPSASQSPK	SAAGGGGGSA	GGGAGGAKTS	KGSSKKCKGL	KAPAAAGAKA	180
	GAGKAAQSGD	YGGAGDDYVL	GSRLVSGSGG	GGAGKTVKCV	FLDEDDDDDD	DDDELQLQIK	240

QEPDEDEEP PHQQLLPFG QQPSQLLRRY NVAKVPASPT LSSSAESPEG ASLYDEVVRAG 300
 ATSGAGGGSR LYSYFKNITK QHPPLAQA LSPASSRSVS TSSSSSSGSS SGSSGEDADD 360
 LMFDSLNLFS QSAHSASEQQ LGGAAAAGNL SLSLVDKDL D SPSEGLSGH FEPFDYCTPE 420
 LSEMIAGDWL EANFSDLVFT Y

Seq ID NO: 658 DNA sequence
 Nucleic Acid Accession #: NM_001719
 Coding sequence: 123..1418

10 1 11 21 31 41 51
 | | | | | |
 GGGCGCAGCG GGGCCCGTCT GCAGCAAGTG ACCGACGGCC GGGACGGCCG CCTGCCCCCT 60
 CTGCCACCTG GGGCGGTGCG GGGCCGGAGC CGGAGCGCGT AGAGCCGGCG 120
 CGATGCACGT GCGCTCACTG CGAGCTGCGG CGCCGCACAG CTTCGTGGCG CTCTGGGCAC 180
 15 CCCTGTTCTT GCTGCGTCCG GCCTTGCCCG ACTTCAGCCT GGACAACGAG GTGCACTCGA 240
 GCTTCATCCA CCGCGCGCTC CGCAGCCAGG AGCGGCGGGA GATGCAGCGC GAGATCCTCT 300
 CCATTTTGGG CTTGCCCCAC CGCCCGCGCC CGCACCCTCA GGGCAAGCAC AACTCGGCAC 360
 CCATGTTTCT GCTGGACCTG TACAACGCCA TGGCGGTGGA GGAGGGCGGC GGGCCCGGCG 420
 GCGAGGGCTT CTCTACACCC TACAAGGCGG TCTTCAGTAC CCAGGGCCCC CCTCTGGCCA 480
 20 GCCTGCAAGA TAGCAATTTC CTCACGACG CCGACATGGT CATGAGCTTC GTCAACCTCG 540
 TGGAAACATGA CAAGGAATTC TTCCACCCAC GCTACCACCA TCGAGAGTTC CGGTTTGATC 600
 TTTCCAAGAT CCCAGAAGGG GAAGCTGTCA CGGCAGCCGA ATTCCGGATC TACAAGGACT 660
 ACATCCGGGA ACGCTTCGAC AATGAGACGT TCCGGATCAG CGTTTATCAG GTGCTCCAGG 720
 AGCACTTGGG GCGGGAATCG GATCTCTTCC TGCTCGACAG CCGTACCCTC TGGGCTCGG 780
 25 AGGAGGGCTG GCTGGTGTTC GACATCACAG CCACAGCAA CCACTGGGTG GTCAATCCGC 840
 GGCACAACCT GGGCTGTGCG CTCTCGGTGG AGACGCTGGA TGGGCGAGAG ATCAACCCCA 900
 AGTTGGCGGG CCTGATTGGG CGGCACGGGC CCCAGAACAA GCAGCCCTTC ATGGTGGCTT 960
 TCTTCAAGGC CACGGAGGTC CACTTCCGCA GCATCCGGTC CACGGGGAGC AAACAGCGCA 1020
 GCGAGAACC CGCTCAAGAC CCAGAAGACC AGGAAGCCCT CGGATGGCGT AACGTGGCGA 1080
 30 AGAAGCAGCA CAGGACACAG AGGACGGCCT GTAAGAAACA CGAGCTGTAT GTCACTTCC 1140
 GAGACCTGGG CTGGCAGGAC TGGATCATCG CGCCTGAAGG CTACGCGGCC TACTACTGTG 1200
 AGGGGGAGTG TGCCTTCCTT CTGAATCCTT ACATGAACGC CACCAACCAC GCCATCGTGC 1260
 AGACGCTGGT CCACCTTCATC AACCCGGAAA CGGTGCCCAA GCCCTGCTGT GCGCCACGCG 1320
 AGCTCAATGC CATCTCCGTC CTCTACTTCG ATGACAGCTC CAACGTCTAT CTGAAGAAAT 1380
 35 ACAGAAACAT GGTGGTCCGG GCCTGTGGCT GCCACTAGCT CCTCCGAGAA TTCAGACCTT 1440
 TTGGGGCCAA GTTTTCTGG ATCTTCCATT GCTCGCCTTG GCCAGGAACC AGCAGACCAA 1500
 CTGCCCTTTG TGAGACCTTC CCTCCCTAT CCGCAACTTT AAAGGTGTGA GAGTATTAGG 1560
 AAACATGAGC AGCATATGGC TTTTGTATCAG TTTTTCAGTG GCAGCATCCA ATGAACAAGA 1620
 40 TCTTACAAGC TGTGCAGGCA AAACCTAGCA GGAAAAAACA ACACGCATA AAGAAAAATG 1680
 GCGGGGCGAG GTACATTGGCT GGGAAAGTCT AGCCATGCAC GGACTCGTTT CCAGAGGTAA 1740
 TTATGAGGCG CTCACCAAGG GGCACCCAG CCGTGGGAGG AAGGGGGCGT GGCAAGGGGT 1800
 GGGCACATTG GTGTCTGTGC GAAAGGAAAA TTGACCCGGA AGTTCCTGTA ATAAATGTCA 1860
 CAATAAAACG AATGAATG

Seq ID NO: 659 Protein sequence
 Protein Accession #: NP_001710

1 11 21 31 41 51
 | | | | | |
 50 MHVRSRLRAA PHSFVALWAP LFLRLSALAD FSLDNEVHSS FIHRRRLRSQB RREMQRILS 60
 ILGLPHRRPP HLQGHKHSAP MFMLDLYNAM AVEEGGGPGG QGFSPYKAV FSTQGPPLAS 120
 LQDSHFLTDA DMVMSFVNLV EHDKEFFHPR YHREFRFDL SKIPEGEAVT AAEFRIYKDY 180
 IRERFDNETF RISVYQVLQE HLGRESDLPL LDSRTLWASE EGVLFVDITA TSNHWVNVPR 240
 55 HNLGLQLSVE TLDGQSINPK LAGLIGRHGP QNKQPPMVAF FKATEVHFRS IRSTGSKQRS 300
 QNRSTPKPNQ EALRMANVAE NSSSDQRQAC KKHELYVSFR DLGWQDWIIA PEGYAAYYCE 360
 GECAFPNLSY MNATNHAIVQ TLVHFINPET VFKPCCAPTQ LNAISVLYFD DSSNVILKKY 420
 RNMVVRACGC H

Seq ID NO: 660 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 211..1895

1 11 21 31 41 51
 | | | | | |
 65 GGATCTGAGG GGCGCCAGT CACTTCCTCC ACGTTCTCGT GCTGGGCGGG AGGAGCGGAT 60
 GGGGCTTGGG AGGCAGCCTG CTCTCCAGTC CCTATCCACC CACAGGTTTT TTGGGTGCGA 120
 GAGGAATTAT CTGATAAAAT TCCTGGGTGA ATATTTTAA AAACGGAGAG TTTTAAATAA 180
 TGATTTTTTT CCCTCGAAAA TGACCTTTTT ATGCTTCGAA GCAGTTTGTC AACCCAGCATA 240
 70 GTGCTTTTTT TTTTCTCTTC TTTTCTACG ATAAATGAAA GCATTTCTTC AAGAAAAAGG 300
 CACAGGTTCC TTGAACAGCT GGATTCTGAT GGCACCATTA CTATAGAGGA GCAGATTGTC 360
 CTGTGCTGTA AAGCGAAAGT ACAATGTGAA CTCACATCA CAGCTCAACT CCAGGAGGGA 420
 GAAGGTAATT GTTTCCCTGA ATGGGATGGA CTCATTGTGT GGCCAGAGG AACAGTGGG 480
 AAAATATCGG CTGTTCCATG CCTCCTTAT ATTTATGACT TCAACCATAA AGGAGTTGCT 540
 75 TTCCGACACT GTAACCCCAA TGGACATGG GATTTTATGC ACAGCTTAA TAAACATGG 600
 GCCAATTATT CAGACTGCCT TCGCTTTCTG CAGCCAGATA TCAGCATAGG AAAGCAAGAA 660
 TTCTTTGAAC GCCTCTATGT AATGTATACC GTTGGCTACT CCATCTCTTT TGGTTCTTGT 720
 GCTGTGGCTA TTCTCATCAT TGGTTACTTC AGACGATTGC ATTGCATAG GAACTATATC 780
 CACATGCATC TATTGTGTC TTTCATGCTG AGAGCTACAA GCATCTTTGT CAAAGACAGA 840
 80 GTAGTCCATG CTCACATAGG AGTAAAGGAG CTGGAGTCCC TAATAATGCA GGATGACCCA 900
 CAAAATTCCTA TTGAAGCAAC TTTCTGGGAC AAATCACAAT ATATCGGGTG CAAGATTGCT 960
 GTTGTGATGT TTATTTACTT CCTGGCTACA AATTATTATT GGATCCTGGT GGAAGGTCTC 1020
 TACCTGCATA ATCTCATCTT TGTGGCTTTC TTTTCGGACA CCAATACCT GTGGGGCTTC 1080
 ATCTTGATAG GCTGGGGGTT TCAGCAGCA TTTGTTCAG CATGGGCTGT GGCACAGCA 1140
 85 ACTCTGGCTG ATGCGAGGTG CTGGGAACCT AGTGTCTGAG ACATCAAGTG GATTTATCAA 1200
 GCACGATCT TAGCAGCTAT TGGGCTGAAT TTTATCTGT TTCTGAATAC GGTTAGAGTT 1260
 CTAGCTACCA AAATCTGGGA GACCAATGCA GTTGGGCATG ACACAAGGAA GCAATACAGG 1320
 AAATGGCCA AATCGACACT GGTCTCTGTC CTAGTCTTTG GAGTGCATTA CATCGTGTTC 1380

GTATGCCCTGC CTCACCTCCTT CACTGGGCTC GGGTGGGAGA TCCGCATGCA CTGTGAGCTC 1440
 TTCTTCAACT CCTTTCAGGG TTTCTTTGTG TCTATCATCT ACTGCTACTG CAATGGAGAG 1500
 GTTCAGGCAG AGGTGAAGAA GATGTGGAGT CCGTGAATC TCTCCGTGGA CTGGAAGAG 1560
 ACACCGCCAT GTGGCAGCCG CAGATGCGCG TCAGTGCTCA CCACCGTGAC GCACAGCACC 1620
 AGCAGCCAGT CACAGGTGGC GGCCAGCACA CGCATGGTGC TTATCTCTGG CAAAGCTGCC 1680
 AAGATCGCCA GCAGACAGCC TGACAGCCAC ATCACTTTAC CTGGCTATGT CTGGAGTAAC 1740
 TCAGAGCAGG ACTGCCCTGCC ACACCTCTTC CACGAGGAGA CCAAGGAAGA TAGTGGGAGG 1800
 CAGGAGATGC ATATTCTAAT GGAGAGCCCT TCCAGGCCCTA TGGAACTCAA CCCAGACACT 1860
 GAAGGATGCC AAGGAGAAAC TGAGGATGTT CTCTGA

Seq ID NO: 661 Protein sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 MLRSSLSSTSI VLFLPSSFST INESSISRKR HRFLEQLDSD GTITIEEQIV LVLKAKVQCE 60
 LNITAQLQEG EQNCFPEWDG LICWPRGTVG KISAVFCPPY IYDFNHKGVA FRHCNPNGTW 120
 DFMHSLNKTW ANYSDCLRFL QPDISIGKQE FFERLYVMYT VGYSISFGSL AVAILLIIGYF 180
 RRLHCTRNYYI HMHLFVSPML RATSIFVKDR VVHAHIGVKE LESLIMQDDP QNSIEATSVD 240
 KSOYIGCKIA VVMFIYPLAT NYYWILVEGL YLHNLIFVAF FSDTKYLWGP ILIGWFPFAA 300
 FVAWAVARA TLADARCWEL SAGDIKWIYQ ABILAAIGLN FILFLNTRV LATKIWETNA 360
 VGHDRKQYR KLAKSTLVLV LVFGVHYIVF VCLPHSFTGL GWEIRMHCEL PFNSFQGFV 420
 SLIYCYCNGE VQAEVKMWS RWNLSVDWKR TPCCGSRRCG SVLTTVTHTS SSQSQAAS 480
 RMVLISGKAA KIASRQPDSD ITPGTVWSN SEQDCLPHSF HEETKEDSGR QGDDILMEKP 540
 SRPMESNPDT EGCQGETEDV L

Seq ID NO: 662 DNA sequence
 Nucleic Acid Accession #: NM_005048
 Coding sequence: 143..1795

1 11 21 31 41 51
 GGCCGGTGGC CCGGGCCCGA CCACCCAGC TGCGCGTCGT TACTGGCCAC AAGTTTGCTC 60
 TGGGCCAGCC AAGTTGGCAA CTGGGAAGCT TCTCCCGGGC TCTGGAGGAG GGTCCCTGCT 120
 TCTTCTTACA GCGGTTCCGG GCATGGCCCG GCTGGGGGCG TCGCTCCACG TCTGGGGTTG 180
 GCTAATGCTC GGCAGCTGCC TCCTGGCCAG AGCCAGCTG GATTCTGATG GCACCATPAC 240
 TATAGAGGAG CAGATTGTCC TTGTGCTGAA AGCGAAAGTA CAATGTGAAC TCAACATCAC 300
 AGCTCAACTC CAGGAGGGAG AAGGTAATG TTTCCCTGAA TGGGATGGAC TCATTGTGTT 360
 GCCCAGAGGA ACAGTGGGGA AAATATCGGC TGTTCCATGC CCTCCTTATA TTTATGACTT 420
 CAACCATAAA GGAAGTTGCTT TCCGACACTG TAACCCCAAT GGAACATGGG ATTTTATGCA 480
 CAGCTTAAAT AAAACATGGG CCAATTATTC AGACTGCCTT CGCTTCTGCG AGCCAGATAT 540
 CAGCATAGGA AAGCAAGAA TCTTTGAACG CCTCTATGTA ATGTATACCG TTGGCTACTC 600
 CATCTCTTTT GGTTCCTTGG CTGTGGCTAT TCTCATCAT GGTACTTCA GACGATTGCA 660
 TTGCACTAGG AACTATATCC ACATGCACTT ATTTGTGTCT TTATGCTGA GAGCTACAAG 720
 CATCTTTGTC AAAGACAGAG TAGTCCATGC TCACATAGGA GTAAAGGAGC TGGAGTCCCT 780
 AATAATGAGC AAGATCCAT AAAAATCCAT TGAGGCAACT TCTGTGGACA AATCACAATA 840
 TATCGGGTGC AAGATTGCTG TTGTGATGTT TATTTACTTC CTGGCTACAA ATTATTATTG 900
 GATCCTGCTG GAAGGCTCTC ACCTGCATAA TCTCATCTTT GTGGCTTCTT TTTCCGACAC 960
 CAAATACCTG TGGGGCTTCA TCTTGATAGG CTGGGGGTTT CCAGCAGCAT TTGTTGCAGC 1020
 ATGGGCTGTC GCACGAGCAA CTCTGGCTGA TGCGAGGTGC TGGGAACCTA GTGCTGGAGA 1080
 CATCAAGTGG ATTTCTCAAG CACCGATCTT AGCAGCTATT GGGCTGAATT TTATTCTGTT 1140
 TCTGAATACG GTTAGAGTTC TAGCTACCAA AATCTGGGAG ACCAATGCAG TTGGGCATGA 1200
 CACAAGGAAG CAATACAGGA AACTGGCCAA ATCGACACTG GTCTGTGCTC TAGTCTTTGG 1260
 AGTGCAATAC ATCGTGTTCG TATGCTGCTC TCACTCCTTC ACTGGGCTCG GGTGGGAGAT 1320
 CCGCATGCGA TGTGAGCTCT TCTTCAACTC CTTTCAGGGT TTCTTTGTGT CTATCATCTA 1380
 CTGCTACTGC AATGAGGAGG TTCAGGCAGA GGTGAAGAAG ATGTGGAGTC GGTGGAATCT 1440
 CTCCGTGGAG TGGAAAAGGA CACCGCCATG TGGCAGCCCG AGATGCGGCT CAGTGCTCAC 1500
 CACCGTGACG CACAGCACA CACGCACTG ACAGGTGGCG GCCAGCACAC GCATGGTGCT 1560
 TATCTCTGGC AAAGCTGCCA AGATCGCCAG CAGACAGCCT GACAGCCACA TCACTTTACC 1620
 TGGCTATGTC TGGAGTAACT CAGAGCAGGA CTGCTGCGCA CACTCTTTCC ACGAGGAGAC 1680
 CAAGGAAGAT AGTGGGAGGC AGGAGATGTA TATTCTAATG GAGAAGCCCT CCAGGCCTAT 1740
 GGAATCTAAC CCAGACACTG AAGGATGCCA AGGAGAACT GAGGATGTTT TCTGAATGGA 1800
 CATTTGTGGC TGACTTTTCAT GGGCTGGTCC AATGGCTGGT TGTGTGAGAG GGCTTGGCTG 1860
 ATACTCCTAT GCTGAGTTC AAAGGCTGAA AATTCAGTTA AGGTGTACTT TAATAATAGT 1920
 TTTTAGGCTC CATGAATTGG CTCTGTAAA TACTAACGAC ATGAAAATGC AAGTGTCAAT 1980
 GGAGTAGTAT ATTACCTTCT ATTGGCATCA AGTTTTCCTC TAAATTAATG TATGGTATTT 2040
 GCTCTGTGAT TGTTCAATTT TTTCTGCTAC TTTTGGGTAG AAAAAAGATT CAATTGCTTG 2100
 GCTGTAGCTT TCTCTCATAT ATATCACCTT AAATATAATG AAGATCTTTT AGTGTGTATC 2160
 ATTTTCTCTT TAGAACTAG TATTCTCTTA TTTCTTACTT TAATGTACTT CTATCACTGC 2220
 ATTTATTTTG CCTGTGCATA GGAGCAATTA GATCTAAAA AAATATATGG GAAGATAAAA 2280
 GATCTAAGAA CAAGTACTTG CTGGAAAAAT AGTTGGCTGG ACATTGATAA AATAATGCAT 2340
 TTATAACAAT TACATGTGTT TTTGGGAACA AGGAAAAATT CTCAAAAAAG AATATTTCAC 2400
 ACATCCCTTC TTTTGAATGG CCTCTTGTG ACCAGCCAGA CCTCAGGTCT TCACTCTTTC 2460
 TTCTTTGTAA ACCATGTCAT GTGGAAAGAT TTCTCAGTT AGTGAGCTTG TGTCTGCAAA 2520
 TTGATTTTGT TTGTAATGTA TTTTGATAGC AAATCATGCT GCATCTATAT CTTTTCCTTG 2580
 TTTGAGCTGT TACTACATTG TACATGGCAT GTGGGATCAA TTAATAATTT GTTTTAAAAA 2640

Seq ID NO: 663 Protein sequence
 Protein Accession #: NP_005039

1 11 21 31 41 51
 MAGLQASLHV WGLMLGSLC LARAQLDSDG TITIEBQIVL VLKAKVQCEL NITAQLQEGE 60
 GNCPEWDGL ICWPRGTGK ISAVPCPPYI YDFNHKGVA FRHCNPNGTW FMSLNLKNTWA 120
 NYSDCLRFLQ PDISIGKQEF FERLYVMYT VGYSISFGSLA VAILLIIGYPR RLHCTRNYYI 180
 MHLFVSPMLR ATSFVVDKRV VHAHIGVKEL ESLIMQDDPQ NSIEATSVDK SQYIGCKIAV 240

VMPIYFLATN YYWILVEGLY LHNLIIVVAF SDTKYLWGF IIGWGFPAAF VAAVAVARAT 300
 LADARCWELS AGDIKWIYQA PILAAIGLNF ILFLNIVRVL ATKIWETNAV GHDTRKQYRK 360
 LAKSTLVLVL VFGVHYIVFV CLPHSFTGLG WEIRMHCELF FNSFGGFVVS IYCYCNGEV 420
 QAEVKMWSR WNLSDVWKRT PPCGSRRCS VLTTVTHSTS SQSQVAASR MVLISGKAAR 480
 IASRQPDSEI TLPGYVWSNS EQDCLPHSFH EETKEDSGRQ GDDILMEKPS RPEMESNPDE 540
 GCQGETEDVL

Seq ID NO: 664 DNA sequence
 Nucleic Acid Accession #: NM_012152
 Coding sequence: 43..1104

1 11 21 31 41 51
 CTCTTTTAAA TTTCTTTCTA GGATGTTTAC TTCTTCTCCA CAATGAATGA GTGTCACTAT 60
 GACAAGCACA TGGACTTTTT TTATAATAGG AGCAACACTG ATACTGTGCA TGACTGGACA 120
 GGAACAAAGC TTGTGATTGT TTTGTGTGTT GGGACGTTTT TCTGCCTGTT TATTTTTTTT 180
 TCTAATCTCT TGGTCATCGC GGCAGTGATC AAAACAGAAA AATTTCATT CCCTTCTTAC 240
 TACCTGTGGG CTAATTTAGC TGCTGCCGAT TTCTTCGCTG GAATTGCCTA TGTATTCTCG 300
 ATGTTTAAAC CAGGCCAGT TTCAAAAAC TTGACTGTCA ACCGCTGGTT TCTCCGTGAG 360
 GGGCTTCTGG ACAGTAGCTT GACTGCTTCC CTCACCAACT TGCTGGTTAT CGCCGTGGAG 420
 AGGCACATGT CAATCATGAG GATGCGGGTC CATAGCAACC TGACCAAAAA GAGGGTGACA 480
 CTGCTCATTT TGCTTGTCTG GGCATCTGCC ATTTTATGCG GGGCGGTCCC CACACTGGGC 540
 TGAATTTGCC TCTGCAACAT CTCTGCCTGC TCTTCCCTGG CCCCATTATA CAGCAGGAGT 600
 TACCTTGTGT TCTGGACAGT GTCCAACTTC ATGGCCTTCC TCATCATGGT TGTGGTGATC 660
 CTGCGGATCT ACGGTAGCT CAAGAGGAAA ACCAACCTCT TGTCTCCGCA TACAAGTGGG 720
 TCCATCAGCC GCGCGAGGAC ACCCATGAAG CTAATGAAGA CGGTGATGAC TGTCTTAGGG 780
 GCGTTTGTGG TATGCTGGAC CCGGGGCTTG GTGGTCTGCT TCCTCGACGG CCTGAACTGC 840
 AGGCAGTGTG CCGTGCAGCA TGTGAAAAGG TGGTTCCTGC TGCTGGCGCT GCTCAACTCC 900
 GTCTGGAACC CCATCTCTCA CTCTACAAG GACGAGGACA TGTATGGCAG CATGAAGAAG 960
 ATGATCTGCT GCTTCTCTCA GGAGAACCCA GAGAGGCGTC CCTCTCGCAT CCCCTCCACA 1020
 GTCTCAGCA GAGTGAACAC AGGCAGCCAG TACATAGAGG ATAGTATTAG CCAAGGTGCA 1080
 GTCTGCAATA AAAGCACTTC CTAACTCTG GATGCCTCTC GGGCCACCCA GGTGATGACT 1140
 GTCTTAGG

Seq ID NO: 665 Protein sequence
 Protein Accession #: NP_036284

1 11 21 31 41 51
 MNECHYDKHM DFFYNRSNTD TVDDWTGTKL VIVLCVGTFF CLFIFFSNLS VIAAVIKNRK 60
 PHEPFYYLLA NLAAADFPAG IAYVFLMFT GPVSKTLTVN RWPLRQGLLD SSLTASLTNL 120
 LVIAVERHMS IMRMVHSNL TKKRVTLIL LVMATAIFMG AVPTLGNCL CNISACSSLA 180
 PIYSRSLVF WTVSNLMAFL IMVVYLYRIY VVVKRKTNLV SPHTSGSISR RRTFPMKLMKT 240
 VMTVLGAFV CWTPLVLL LDGLNCRQCG VQHKRWFLP LALLNSVNP IYSYKDEDM 300
 YGTMKIMICC FSQNPERRP SRIPSTVLSR SDTGSQYIED SISQGAVCNK STS

Seq ID NO: 666 DNA sequence
 Nucleic Acid Accession #: NM_002821
 Coding sequence: 150..3362

1 11 21 31 41 51
 AACTCCCGCC TCGGGACGCC TCGGGGTCGG GCTCCGGCTG CGGCTGCTGC TCGGGGCCCC 60
 GCGCTCCGGT GCGTCCGCCT CCTGTGCCCG COGCGAGACA GTCTCGCGCC CGCGTGCCGC 120
 CCTCAGCTCC TTTTCTGAG CCGCGCGCGA TGGGAGCTGC GCGGGGATCC CCGGCCAGAC 180
 CCGCGCGGTT GCTCTGCTC AGCGTCCCTG TGCTCGCGCT GCTGGCGGTT ACCCAGACAG 240
 CCATTGTCTT CATCAGCAG CCGTCTCTCC AGGATGCACT GCAGGGGCGC CGGGCGCTGC 300
 TTGCTGTGA GGTGTAGGCT CCGGGCCCGG TACATGTGTA CTGGCTGCTC GATGGGGCCC 360
 CTGTCCAGGA CACGAGCGGG CGTTTCGCCC AGGCGAGCAG CCTGAGCTTT GCAGCTGTGG 420
 ACCGGCTGCA GGAATCTGGC ACCTTCCAGT GTGTGGCTCG GGATGATGTC ACTGGAGAAG 480
 AAGCCCGCAG TGCCCAACGCC TCCTTCAACA TCAAATGGAT TGAGGCAGGT CCTGTGGTCC 540
 TGAAGCATCC AGCCTCGGAA GCTGAGATCC AGCCACAGAC CCAGGTGACA CTTCGTGTCC 600
 ACATTGATGG GCACCTCGG CCACTTACC AATGGTTCCG AGATGGGACC CCCCTTTCTG 660
 ATGGTCAGAG CAACACACA GTGAGCAGCA AGGAGCGGAA CCTGAGCTCT CGGCCAGCTG 720
 GTCTCTGAGC TAGTGGGCTG TATCTCTGCT GCGCCACAG TGCTTTTGGC CAGGCTTGCA 780
 GCAGCCAGAA CTTCACCTTG AGCATTGCTG ATGAAAGCTT TGCCAGGGTG GTGCTGGCAC 840
 CCGCAGACGT GGTAGTAGCG AGGTATGAGG AGGCCATGTT CCATTGCCAG TTCTCAGCCC 900
 AGCCACCCCC GAGCTGCGAG TGGCTCTTTG AGGATGAGAC TCCCATCACT AACCGCAGTC 960
 GCGCCCCACA CCTCCGAGA GCCACAGTGT TTGCCAACGG GTCTCTGCTG CTGACCCAGG 1020
 TCOGGCCAGC CAATGCAAGG ATCTACCGCT GCATTGGCCA GGGGCGAGAG GGGCCACCCA 1080
 TCATCTGGA AGCCACACTT CACTAGCAG AGATTGAAGA CATGCCGCTA TTTGAGCCAC 1140
 GGGTGTATTAC AGCTGGCAGC GAGGAGCGTG TGACCTGCCT TCCCCCAAG GGTCTGCCAG 1200
 AGCCAGCGGT GTGGTGGGAG CACGCGGGAG TCCGGCTGCC CACCCATGGC AGGGTCTACC 1260
 AGAAGGGCCA CGAGCTGGTG TTGGCCAATA TTGCTGAAAG TGATGCTGGT GTCTACACCT 1320
 GGCACGCGGC CAACCTGGCT GGTGAGCGGA GACAGGATGT CAACATCACT GTGGCCACTG 1380
 TTCCCTCTCT GCTGAAGAAG CCCCAGACA GCCAGCTGGA GGAGGGCAAA CCGGCTACT 1440
 TGGATTGCGT GACCCAGGCC ACACCAAAAC CTACAGTTGT CTGTGACAGA AACCATGATC 1500
 TCATCTGGA GAGCTCAGG TCGAGGTCT TCAAGAAATG GACCTTGCGC ATCAACAGCG 1560
 TGGAGTGTA TGATGGGACA TGGTACCGTT GTATGAGCAG CACCCAGGCC GGCAGCATCG 1620
 AGGCGCAAGC CCGTGTCCAA GTGCTGGAAG AGCTCAAGTT CACACCAACA CCCAGCCAC 1680
 AGCAGTGCAT GGAGTTTGAC AAGGAGGCCA CGGTGCCCTG TTCAGCCACA GCGGAGAGA 1740
 AGCCCACTAT TAAGTGGGAA CGGGCAGATG GGAGCAGCCT CCCAGATGGG GTGACAGACA 1800
 ACGCTGGGAC CTGTGATTTT CCGCGGGTGA CTCGAGATGA CGCTGGCAAC TACACTTGCA 1860
 TTGCTCCAA CGGGCCGAG GGCAGATTC GTGCCCATGT CCAGCTCACT GTGGCAGTTT 1920
 TTATCACCTT CAAAGTGGAA CCAGAGCGTA CGACTGTGTA CCAGGGCCAC ACAGCCCTAC 1980
 TGCAGTGCGA GCGCCAGGGG GACCCCAAGC CGCTGATTCA GTGGAAGGCG AAGGACCGCA 2040
 TCCTGGACCC CACCAAGCTG GGACCCAGGA TGACATCTT CCAGAAATGGC TCCTGGTGA 2100

	TCCATGACGT	GGCCCCCTGAG	GACTCAGGCC	GCTACACCTG	CATTGCAGGC	AACAGCTGCA	2160
	ACATCAAGCA	CACGGAGGCC	CCCTCTATG	TCGTGGACAA	GCCTGTGCCG	GAGGAGTCGG	2220
	AGGGCCCTGG	CAGCCCTCCC	CCCTACAAGA	TGATCCAGAC	CATTGGGTTG	TCGGTGGGTG	2280
5	CGCTGTGGC	CTACATCATT	GCCGTGCTGG	GCCTCATGTT	CTACTGCAAG	AAGCGCTGCA	2340
	AAGCCAAAGC	GCTGCAGAAG	CAGCCCCGAG	GCGAGGAGCC	AGAGATGGAA	TGCCTCAACG	2400
	GAGGGCCCTT	GCAGAACGGG	CAGCCCTCAG	CAGAGATCCA	AGAAGAAGTG	GCCTTGACCA	2460
	GCTTGGGCTC	CGGCCCGCG	GCCACCAACA	AACGCCACAG	CACAAGTGAT	AAGATGCACT	2520
	TCCACGCTC	TGACCTGTC	CCCATCACCA	CGCTGGGAA	GAGTGAGTTT	GGGGAGGTGT	2580
10	TCCTGGCAAA	GGCTCAGGGC	TTGGAGGAGG	GAGTGGCAGA	GACCCTGGTA	CTTGTGAAGA	2640
	GCCTGCAGAC	GAAGGATGAG	CAGCAGCAGC	TGGACTTCCG	GAGGGAGTTG	GAGATGTTTG	2700
	GGAAAGCTGAA	CCACGCCAAC	GTGGTGGCGC	TCCTGGGGCT	GTGCCGGGAG	GCTGAGCCCC	2760
	ACTACATGGT	GCTGGAATAT	GTGGATCTGG	GAGACCTCAA	GCAGTTCCTG	AGGATTTCCA	2820
	AGAGCAAGGA	TGAAAAATTG	AAGTCACAGC	CCCTCAGCAC	CAAGCAGAAG	GTGGCCCTAT	2880
15	GCACCCAGGT	AGCCCTGGGC	ATGGAGCACC	TGTCCAACAA	CCGCTTTGTG	CATAAGGACT	2940
	TGGCTGCGCG	TAACCTGCTG	GTCACTGCCC	AGAGACAAGT	GAAGGTGTCT	GCCCTGGGCC	3000
	TCAGCAAGGA	TGTTGACAAC	AGTGAAGTACT	ACCACCTTCG	CCAGGCTCGG	GTGCGCTGCG	3060
	GCTGGATGTC	CCCCGAGGCC	ATCCTGGAGG	GTGACTTCTC	TACCAAGTCT	GATGTCTGGG	3120
	CCTTCGGTGT	GCTGATGTGG	GAAGTGTTTA	CACATGGAGA	GATGCCCAT	GGTGGGCAGG	3180
20	CAGATGATGA	AGTACTGGCA	GATTTGCAGG	CTGGGAAGGC	TAGACTTCTC	CAGCCCGAGG	3240
	GCTGCGCTTC	CAAACTCTAT	CGGCTGATGC	AGCCTCTGCT	GGCCCTCAGC	CCCAGGACC	3300
	GGCCCTCCTT	CAGTGAGATT	GCCAGCGCCC	TGGGAGACAG	CACCGTGGAC	AGCAAGCCGT	3360
	GAGGAGGAG	CCGCTCAGG	ATGGCCTGGG	CAGGGGAGGA	CATCTCTAGA	GGGAAGCTCA	3420
	GCCATGATG	GGCAAGATTG	CTGTCTCTCT	GGGCCCTGAG	GTGCCCTAGT	GCAACAGGCA	3480
25	TTGCTGAGGT	CTGAGCAGGG	CCTGGCCTTT	CCTCCTCTTC	CTCACCTCA	TCCTTTGGGA	3540
	GGCTGACTTG	GACCCAAACT	GGGCGACTAG	GGCTTTGAGC	TGGGCAGTTT	CCCCTGGCAC	3600
	CTCTCTCCTT	ATCAGGGACA	GTGTGGGTGC	CACAGGTAAC	CCCAATTCTT	GGCCTTCAAC	3660
	TTCTCCCTTT	CAGCGGTCC	AACTCTGCCA	CTCATCTGCC	AACTTTGGCT	GGGGAGGGCT	3720
	AGGCTTGGGA	TGAGCTGGGT	TTGTGGGGAG	TTCTCAAGTT	CTGGGCACAC		3780
30	AGGGTTAATG	AGTCTCTTGC	CCACTGGTCC	ACTTGGGGGT	CTAGACCAGG	ATTATAGAGG	3840
	ACACAGCAAG	TGAGTCTCTCC	CCACTCTGGG	CTTGTGCACA	CTGACCCAGA	CCCACGTCTT	3900
	CCCCACCTTT	CTCTCTTTTC	CTCATCTTAA	GTGCTTGSCA	GATGAAGGAG	TTTTCAGGAG	3960
	CTTTTGACAC	TATATAAACC	GGCCTTTTTG	TATGCACCAC	GGGCGGCTTT	TATATGTAAT	4020
	TGACGCTGG	GGTGGGTGGG	CATGGGAGGT	AGGGGTGGGC	CCTGAGATG	AGGAGGGTGT	4080
35	GCCATCCTTA	CCCCACACTT	TTATTGTTGT	CGTTTTTTGT	TTGTTTTGTT	TTTTTGTTTT	4140
	TGTTTTTGT	TTTACACTCG	CTGCTCTCAA	TAAATAAGCC	TTTTTTA		

Seq ID NO: 667 Protein sequence

Protein Accession #: NP_002812

40	1	11	21	31	41	51	
	MGAARGSPAR	PRRLPLLSVL	LLPLLGGTQT	AIVFIKQPSS	QDALQRRAL	LRCEVEAPGP	60
	VHVYVLLDGA	PVQDTERFFA	QSSLSFAAV	DRLQDSGTFO	CVARDDVTGE	EARSANASFN	120
45	IKWIEAGPVV	LKHFAEAEI	QPTQVTLRC	HIDGHPRETY	QWFRDGTPLS	DGQSNHTVSS	180
	KERNLTLRPA	GPEHSGLYSC	CHSAFQGAC	SSQNFSLIA	DESFAFVFLA	PDVUVVARYE	240
	EAMFHCQFSA	QPPPSLQWLF	EDETPTNRS	RPPHLRRATV	FANGSLLLTQ	VRPRNAGIYR	300
	CIGGQQRGPP	IILEATLHLA	ETEDMPLFEP	RVFTAGSEER	VTCLPFKGLP	EPFVWWEHAG	360
	VRLPHTGRVY	QKGEHLVLAN	IAESDAGVYT	CHAANLAGOR	RQDVNITVAT	VPFWLKKPQD	420
50	SQLBEGKPGY	LDCLTQATPK	PTVWVYRNQM	LISEDSEFEV	FKNGTLRINS	VEVYDGTWYR	480
	CMSSTFAGSI	EAGARVQVLE	KLKFTPPFPQ	QQCMFEDKEA	TVPCSATGRE	KPTIKWERAD	540
	GSSLPFWVTD	NAGTLHFARV	TRDDAGNYTC	IASNGPQQQI	RAHVQLTVAV	FITFRKVEPER	600
	TTVYQGHATL	LQCEAQGDPK	PLIQWKGKDR	ILDPTKLGR	MHIFQNGSLV	IHDVAPEDSG	660
	RYTCIAGNSC	NKHTTEAPLY	VVDKVPVEBS	EGPGSPPPYK	MIQTIGLSVG	AAYAYIIAIV	720
55	GLMPYCKKRC	KAKRLQKQPE	GEEPEMECLN	GGPLQNGQPS	AEIQEEVALT	SLGSGPAATN	780
	KRHSTSDKMH	FPRSSTLQPI	TLGKSEFGEV	FLAKAAGLEE	GVAETLVLVK	SLQTKDEQQQ	840
	LDPRRELEMF	GKLNHANVVR	LLGLCREAEP	HYMVLEYVDL	GDLKQFLRIS	RSKDEKLSQ	900
	PLSTKQKVAL	CTQVALGMEH	LSNNRPFVKD	LAARNCLVSA	QRQVKVSALG	LSKDVYNSEY	960
	YHFRQAWVPL	RWMSPEAILE	GDFSTKSDVW	AFGLVMWEVF	THGEMPHGGQ	ADDEVLDLQ	1020
60	AGKARLPQPE	GCPSKLYRLM	QRCWALSPKD	RPSFSEIASA	LGDSTVDSKP		

Seq ID NO: 668 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 1..1389

65	1	11	21	31	41	51	
	ATGGGCTACC	AGAGGCAGGA	GCCTGTCTATC	CCGCCGACAGA	GAGATTAGA	TGACAGAGAA	60
	ACCTTTGTTT	CTGAACATGA	GTATAAAGAG	AAAACCTGTC	AGTCTGCTGC	TCTTTTAAAT	120
70	GTTGTCAACT	CGATTATAGG	ATCTGGTATA	ATAGGATTGC	CTTATTCAAT	GAAGCAAGCT	180
	GGGTTTCCTT	TGGGAATATT	GCTTTTATTC	TGGGTTTCAT	ATGTTACGGA	CTTTCCCTTT	240
	GTTTATTATGA	TAAAGGAGG	GGCCCTCTCT	GGAACAGATA	CCTACCAGTC	TTTGGTCAAT	300
	AAAACCTTCG	GCTTCCAGG	GTATCTGCTC	CTCTCTGTTC	TTCACTTTT	GTATCCTTTT	360
	ATAGCAATGA	TAAGTTACAA	TATAATAGCT	GGAGATACTT	TGAGCAAAGT	TTTTCAAAGA	420
75	ATCCAGGAG	TTGATCCTGA	AAACGTGTTT	ATTGGTGGCC	ACTTCATTAT	TGGACTTTCC	480
	ACAGTTACTT	TTACTCTGCC	TTTATCCTTG	TACCGAAATA	TAGCAAAGCT	TGGAAAGGTC	540
	TCCCTCATCT	CTACAGGTTT	AACAACCTCTG	ATTCCTGGAA	TTGTAATGGC	AAGGGCAATT	600
	TCACCTGGTC	CACACATACC	AAAAACAGAA	GACGCTGGG	TATTTGCAAA	GCCCAATGCC	660
	ATTCAAGCGG	TCGGGGTTAT	GTCTTTTGCA	TTTATTGGCC	ACCATAACTC	CTTCTTAGTT	720
80	TACAGTCTCT	TAGAAGAACC	CACAGTAGCT	AAGTGGTCCC	GCCTTATCCA	TATGTCCATC	780
	GTGATTTCTG	TATTTATCTG	TATATTCTTT	GCTACATGTG	GATACCTGAC	ATTTACTGGC	840
	TTACCCCAAG	GGGACTTATT	TGAAAATTAC	TGCAGAAATG	ATGACCTGGT	AACATTTGGA	900
	AGATTTTGTG	ATGGTGTGAC	TGTCAATTTG	ACATACCCTA	TGGAAATGCT	TGTGACAAGA	960
	GAGGTAATG	CCAATGTGTT	TTTTGGTGGG	AATCTTTTCT	CGGTTTTCCT	CATGTTGTTA	1020
85	ACAGTGAATG	TCATCACTGT	AGCCAGCTTT	GTGTCATTGC	TGATTGATTG	CCTCGGGATA	1080
	GTTCTAGAAC	TCAATGAGTG	GCTCTGTGCA	ACTCCCTTCA	TTTTTATCAT	TCCATCAGCC	1140
	TGTATCTGA	AACGTCTGTA	AGAACCAGAG	ACACACTCCG	ATAAGATTAT	GTCTTGTGTC	1200
	ATGCTTCCA	TTGGTGTCTG	GGTGATGGTT	TTTGGATTGC	TCATGGCTAT	TACAAATACT	1260

WO 02/086443

PCT/US02/12476

CAAGACTGCA CCCATGGGCA GGAAATGTTT TACTGCTTTC CTGACAATTT CTCTCTCACA 1320
AATACCTCAG AGTCTCATGT TCAGCAGACA ACACAACCTT CTACTTTAAA TATTAGTATC 1380
TTTCAATGA

5 Seq ID NO: 669 Protein sequence
Protein Accession #: Eos sequence

1	11	21	31	41	51	
MGYQRQEPVI	PPQRDLDDRE	TLVSEHEYKE	KTCQSAALFN	VVNSIIGSGI	IGLPYSMKQA	60
GFPLGILLFF	WVSYYTDFSL	VLLIKGGALS	GTDTYQSLVN	KTFGPPGYLL	LSVLQFLYPF	120
IAMISYNIIA	GDTLKVFQFR	IPGVDPENVF	IGRHFIIGLS	TVFTPLPLSL	YRNIAKLGKV	180
SLISTGLTTL	ILGIVMARAI	SLGPHIEKTE	DAMVFAKENA	IQAVGVMSFA	FICHENSFLV	240
YSSLEPTVA	KWSRLIHMSI	VISVFICIFF	ATCGYLTFPTG	FTQGDLPFENY	CRNDDLVTFG	300
RFCYGVTVIL	TYPMECFVTR	EVIANVFFGG	NLSSVPHIVV	TMVITVATL	VSLLIDCLGI	360
VLELNGVLCA	TPLIIFIIPSA	CYLKLSSEEP	THSKIMSCV	MLPIGAVVMV	FGFVMAITNT	420
QDCTHGQEMF	YCFPDNFSLT	NTSESHVQQT	TQLSTLNISI	FQ		

20 Seq ID NO: 670 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..1284

1	11	21	31	41	51	
ATGGGCTACC	AGAGGCAGGA	GCCTGTCATC	CCGCCGCGAGA	GAGGATTGCC	TTATTCAATG	60
AAGCAAGCTG	GGTTTCTCTT	GGGAATATTG	CTTTTATTCT	GGGTTTCATA	TGTTACAGAC	120
TTTTCCCTTG	TTTTATTGAT	AAAAGGAGGG	GCCCTCTCTG	GAACAGATAC	CTACCACTCT	180
TGTGTCATA	AACTTTCGG	CTTCCAGGG	TATCTGCTCC	TCTCTGTTCT	TCAGTTTTTG	240
TATCCTTTTA	TAGCAATGAT	AAGTTACAAT	ATAATAGCTG	GAGATACTTT	GAGCAAAAGT	300
TTTCAAGAAA	TCCCAGGAGT	TGATCCTGAA	AACGTGTTTA	TTGGTGGCCA	CTTCATTATT	360
GGACTTTTCA	CAGTTACCTT	TACTCTGCCT	TTATCCTTGT	ACCGAAATAT	AGCAAAGCTT	420
GGAAAGGCTT	CCCTCATCTC	TACAGGTTTA	ACAACTCTGA	TTCTTGGAA	TGTAATGGCA	480
AGGGCAATTT	CACCTGGGTC	ACACATACCA	AAAACAGAAG	ACGCTTGGGT	ATTTGCAAG	540
CCCAATGCCA	TTCAGCGGT	CGGGGTATG	TCTTTTGCAT	TTATTTGCCA	CCATAACTCC	600
TTCTTAGTTT	ACAGTTCTCT	AGAAGAAGCC	ACAGTAGCTA	AGTGGTCCCG	CCTTATCCAT	660
ATGTCATCG	TGATTTCTGT	ATTATCTGT	ATATTCTTTG	CTACATGTGG	ATACTTGACA	720
TTTACTGGCT	TCACCAAGG	GGACTTATTT	GAATAATACT	GCAGAAATGA	TGACCTGGTA	780
ACATTGGAA	GATTTTGTTA	TGGTGTCACT	GTCATTTTGA	CATACCCCTAT	GGAAATGCTTT	840
GTGACAAGAG	AGGTAATTGC	CAATGTGTTT	TTTGGTGGGA	ATCTTTCATC	GGTTTTCCAC	900
ATTGTTGTAA	CAGTGATGGT	CATCACTGTA	GCCACGCTTG	TGTCATTGCT	GATTGATTGC	960
CTCGGGATAG	TTCTAGAACT	CAATGGTGTG	CTCTGTGCAA	CTCCCTCAT	TTTTATCATT	1020
CCATCAGCCT	GTATCTGAA	ACTGTCTGAA	GAACCAAGGA	CACACTCCGA	TAAGATTATG	1080
TCTTGTGTCA	TGCTTCCCAT	TGGTGCTGTG	GTGATGGTTT	TTGGATTGCT	CATGGCTATT	1140
ACAAATACTC	AAGACTGCAC	CCATGGGCAG	GAAATGTTCT	ACTGCTTCC	TGACAATTTC	1200
TCTCTCACA	ATACCTCAGA	GTCTCATGTT	CAGCAGACAA	CACAACCTTC	TACTTTAAAT	1260
ATTAGTATCT	TTCAACTCGA	GTAA				

50 Seq ID NO: 671 Protein sequence
Protein Accession #: Eos sequence

1	11	21	31	41	51	
MGYQRQEPVI	PPQRGLPYSM	KQAGFPLGIL	LLFWVSYYTD	PSLVLLIKGG	ALSGTDTYQS	60
LVNKTFGPPG	YLLLSVLQPL	YPIAMISYN	IIAGDTLSKV	FORIPGVDP	NVFIGRHFII	120
GLSTVFTPLP	LSLVRNIAKL	GKVSLLISTGL	TTLILGIVMA	RAISLGPHE	KTEDAWVFAK	180
PNAIQAVGVM	SFAFICHNS	FLVYSLEEF	TVAKWSRLIH	MSIVISVFIC	IFFATCGYLT	240
FTGFTQGLDF	ENYCRNDDL	TGFRFCYGV	VILTYPMECF	VTREIVANVF	PGNLSVSVF	300
IVVTVMVITV	ATLVSLIDIC	LGIVLELNGV	LCATPLIPII	PSACYLKLSE	EPRTHSKIM	360
SCVMLPIGAV	VMVFGFVMAI	TNTQDCTHGQ	EMFYCFPDNF	SLTNTSESHV	QQTTLSTLN	420
ISIFQLE						

65 Seq ID NO: 672 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..1203

1	11	21	31	41	51	
ATGGGCTACC	AGAGGCAGGA	GCCTGTCATC	CCGCCGCGAGT	TTTCCCTTGT	TTATTGATA	60
AAAGGAGGGG	CCCTCTCTGG	AACAGATACC	TACCACTCTT	TGGTCAATAA	AACCTTCGGC	120
TTTCCAGGGT	ATCTGCTCCT	CTCTGTTCTT	CAGTTTTTGT	ATCCTTTTAT	AGCAATGATA	180
AGTTACAATA	TAATAGCTGG	AGATACTTTG	AGCAAAGTTT	TTCAAAGAAT	CCCAGGAGTT	240
GATCCTGAAA	ACGTGTTTAT	TGGTCGCCAC	TTCATTATTG	GACTTTCAC	AGTTACCTTT	300
ACTCTGCCTT	TATCCTTGTA	CCGAAATATA	GCAAAGCTTG	GAAAGGTCTC	CCTCATCTCT	360
ACAGGTTTAA	CAACTCTGAT	TCTTGGAAAT	GTAATGGCAA	GGGCAATTC	ACTGGGTCCA	420
CACATACCAA	AAACAGAAGA	CGCTTGGGTA	TTTGCAAAGC	CCAATGCCAT	TCAAGCGGTC	480
GGGGTTATGT	CTTTTGCAAT	TATTTGCCAC	CATAACTCCT	TCTTAGTTTA	CAGTTCTCTA	540
GAAGAACCCA	CAGTAGCTAA	GTGGTCCCGC	CTTATCCATA	TGTCATCGT	GATTCTGTGA	600
TTTATCTGTA	TATCTTTTGC	TACATGTGGA	TACTTGACAT	TTACTGGCTT	CACCCAAGGG	660
GACTTATTTG	AAAATTACTG	CAGAAATGAT	GACCTGGTAA	CATTTGGAAG	ATTTTGTATT	720
GGTGTCATCT	ATCTTTTGAC	ATACCTATG	GAATGCTTTG	TGACAAGAGA	GGTAATTGCC	780
AATGTGTTTT	TGGTGGGAA	TCTTTCATCG	GTTTTCACCA	TTGTGTGAAC	AGTGATGGTC	840
ATCACTGTAG	CCAGGCTTGT	GTCAATGCTG	ATTGATTGCC	TCGGGATAGT	TCTAGAACTC	900
AATGGTGTGC	TCTGTGCAAC	TCCCTCATTT	TTTATCATTC	CATCAGCCTG	TTATCTGAAA	960
CTGTCTGAAG	AACCAAGGAC	ACACTCCGAT	AAGATTATGT	CTTGTGTCAT	GCTTCCCAT	1020
GOTGCTGTGG	TGATGGTTTT	TGGATTCGTC	ATGGCTATTA	CAAATACTCA	AGACTGCACC	1080
CATGGGCAGG	AAATGTTCTA	CTGCTTTCCT	GACAATTTCT	CTCTCACAAA	TACCTCAGAG	1140
TCTCATGTTT	AGCAGACAAC	ACAACCTTCT	ACTTTAAATA	TTAGTATCTT	TCAACTCGAG	1200

TAA

Seq ID NO: 673 Protein sequence
Protein Accession #: Eos sequence

```

1      11      21      31      41      51
|      |      |      |      |      |
MGYQRQEPVI PPQFSLVLLI KGGALSGTDT YQSLVNKTFG FPGYLLLSVL QPLYPFIAMI 60
SYNIIAGDTL SKVFQRIPIV DPENVFIGRH FIIGLSTVTF TLPLSLYRNI AKLGRVSLIS 120
TGLTLLILGI VMARAIISLP HIPKTEDAWV FAKPNAIQAV GVMSPAFICH HNSFLVYSSL 180
EEPTVAKWSR LIHMSIVISV PICIFPATCG YLFTGTPTQG DLFENYCRND DLVTFGRFCY 240
GVTVLITYPM ECFVTREIVN NVFFGGNLSS VFHIVVTVMV ITVATLVSLI IDCLGIVLEL 300
NGVLCATPLI FIIPSACYLK LSEEPRTSHD KIMSCVMLPI GAVVMVFGFV MAITNTQDCT 360
HGQEMFYCFP DNFSLTNTSE SHVQQTQLS TLNISIFQLE

```

Seq ID NO: 674 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..1140

```

1      11      21      31      41      51
|      |      |      |      |      |
ATGGGCTACC AGAGGCAGGA GCCTGTCATC CCGCCGCAGG TCAATAAAAC TTTCGGCTTT 60
CCAGGGTATC TGCTCCTCTC TGTTCTTCAG TTTTGTATC CTTTATAGC AATGATAAGT 120
TACAAATATA TAGCTGGAGA TACTTTGAGC AAAGTTTTC AAAGAATCCC AGGAGTTGAT 180
CCTGAAAACG TGTTTATGCG TGCCCACTTC ATTATTGGAC TTCCACAGT TACCTTTACT 240
CTGCCCTTAT CCTTTGACCG AATATAGCA AAGCTTGGAA AGGTCTCCCT CATCTCTACA 300
GGTTTAAACA CTCGTATTCT TGGAAATGTA ATGGCAAGGG CAATTTCACT GGGTCCACAC 360
ATACCAAAAA CAGAAGACGC TTGGGTATTG GCAAAGCCCA ATGCCATTCA AGCGGTCGGG 420
GTTATGTCTT TTGCAATTAT TTGCCACCAT AACTCCTTCT TAGTTTACAG TTCTCTAGAA 480
GAACCCACAG TACTTAAGTG GTCCCGCCTT ATCCATATGT CCATCGTGAT TTCTGTATTT 540
ATCTGTATAT TCCTTGTCTAC ATGTGGATAC TTGACATTTA CTGGCTTCAC CCAAGGGGAC 600
TTATTGTAAA ATTACTGCAG AATATGATAC CTGGTAACAT TTGGAAGATT TTGTTATGGT 660
GTCACGTGCA TTTTGACATA CCTATGGAA TGCTTTGTGA CAAGAGAGGT AATTGCCAAT 720
GTGTTTTTTG GTGGGAATCT TTCATCGGTT TTCCACATTG TTGTAACAGT GATGGTCATC 780
ACTGTAGCCA CGCTTGTGTC ATTGCTGATT GATTGCCTCG GGATAGTTCT AGAACTCAAT 840
GGGTGTGCTT GCTCACTCC CCTCATTTT ATCATTCCAT CAGCCTGTTA TCTGAAACTG 900
TCTGAAGAAC CAGGACACA CTCGATAAG ATTATGCTT GTGTCATGCT TCCCATTGGT 960
GCTGTGGTGA TGGTTTTTGG ATTGCTCATG GCTATTACAA ATACTCAAGA CTCACCCAT 1020
GGGCAGGAAA TGTCTACTG CTTTCTGAC AATTCTCTC TCACAAATAC CTCAGAGTCT 1080
CATGTTTCAGC AGACAACACA ACTTTCTACT TTAATATTA GTATCTTTCA ACTCGAGTAA

```

Seq ID NO: 675 Protein sequence
Protein Accession #: Eos sequence

```

1      11      21      31      41      51
|      |      |      |      |      |
MGYQRQEPVI PPQVNKTGFG PLYLLLSVLQ FLYPFIAMIS YNIIAGDTLS KVFQRIPIVD 60
PENVFGRHF IIGLSTVTF LPLSLYRNIA KLGRVSLIST GLTLLILGIV MARAISLGP 120
IPKTEDAWVF AKPNAIQAVG VMSFAFICH NSFLVYSSLE EPTVAKWSRL IHMSIVISVF 180
ICIFPATCGY LFTGTPTQGD LFNENYCRND LVTFGRCYCG VTVILTYPME CFTVTREIVN 240
VFFGGNLSSV FHVIVVTMVI TVATLVSLI DCLGIVLELN GVLCAATPLIF IIPSACYLKL 300
SEEPRTSHDK IMSCVMLPIG AVVMVFGFVM AITNTQDCTH GQEMFYCFPD NPSLTNTSES 360
HVQQTQLST LNISIFQLE

```

Seq ID NO: 676 DNA sequence
Nucleic Acid Accession #: NM_006853.1
Coding sequence: 26..874

```

1      11      21      31      41      51
|      |      |      |      |      |
AGGAATCTGC GCTCGGGTTC CGCAGATGCA GAGGTGAGG TGGCTGCGGG ACTGGAAGTC 60
ATCGGGCAGA GGTCTCACAG CAGCCAAGGA ACCTGGGGCC CGCTCCTCCC CCTCCAGGC 120
CATGAGGATT CTGCAGTTAA TCCTGCTTGC TCTGGCAACA GGGCTTGTAG GGGAGAGAC 180
CAGGATCATC AAGGGGTTCG AGTGCAAGCC TCACTCCAGC CCTGGCAGG CAGCCCTGTT 240
CGAGAAGACG CGGCTACTCT GTGGGCGGAC GCTCATCGCC CCCAGATGGC TCCTGACAGC 300
AGCCCACTGC CTCAGGCCCC GCTACATAGT TCACCTGGGG CAGCACAAAC TCCAGAAGGA 360
GGAGGGCTGT GAGCAGACCC GGACAGCCAC TGAGTCTCTC CCCCACCCCG GCTTCAACAA 420
CAGCCTCCCC AACAAAGACC ACCGCAATGA CATCATGCTG GTGAAGATGG CATCGCCAGT 480
CTCCATCACC TGGGCTGTGC GACCCCTCAC CCTCTCTCA CGCTGTGTCA CTGCTGGCAC 540
CAGCTGCCTC ATTTCCGGCT GGGGCGGAC GTCCAGCCCC CAGTTAGGCC TGCTTCACAC 600
CTTGCGATGC GCCAATATCA CCATCATTGA GCACCAAGG TGTGAGAAGC CCTACCCCGG 660
CAACATCACA GACACCATGG TGTGTGCCAG CGTGACGAA GGGGGCAAGG ACTCCTGCCA 720
GGGTGACTCC GAGGGCCCTC TGGTCTGTAA CCAGTCTCTT CAAGGCATTA TCTCTGGGG 780
CCAGGATCCG TGTGCGATCA CCGGAAAGCC TGGTGTCTAC ACGAAAGTCT GCAAAATATG 840
GGACTGGATC CAGGAGACGA TGAAGAACAA TTAGACTGGA CCCACCCACC ACAGCCCATC 900
ACCCTCCATT TCCACTTGGT GTTTGGTCC TGTTCATCT GTTAATAAGA AACCTTAAGC 960
CAAGACCCTC TACGAACATT CTTTGGGCTT CCTGGACTAC AGGAGATGCT GTCATTAAAT 1020
AATCAACCTG TGGTTCGAAA TCAGTGAGAC CTGGATTCAA ATTCTGCCTT GAAATATTGT 1080
GACTCTGGGA ATGACAACAC CTGGTTTGT CTCTGTTGTA TCCCCAGCCC CAAAGACAGC 1140
TCCTGGCCAT ATATCAAGGT TTCAATAAAT ATTTGCTAAA TGAGTG

```

Seq ID NO: 677 Protein sequence
Protein Accession #: NP_006844.1

```

1      11      21      31      41      51
|      |      |      |      |      |
MRILQLILLA LATGLVGGET RIIGKFECKP HSQPWQAALF EKTRLLCGAT LIAPRWLLTA 60

```

AHCLKPRYIV HLGQHNLOKE EGCEQTRTAT ESPPHPGFNN SLPNKDHRND IMLVKMASPV 120
SITWAVRPLT LSSRCVTAGT SCLISGWST SSPQLRLPHT LRCANITIE HOKCENAYPG 180
NITDTMVCAS VQEGGKDSQ GDSGGPLVCN QSLQGIISWG QDPCAITRKP GVTYKVKYV 240
DWIETMKNN

Seq ID NO: 678 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..933

1 11 21 31 41 51
| | | | | |
ATGTGCACGA ATGGACGGTG CATCCCGGGC GCCTGGCAGT GTGACGGGCT GCCTGACTGC 60
TTGACAAAGA GTGATGAGAA GGAGTGCCCC AAGGCTAAGT CGAAATGTGG CCCGACCTTC 120
TTCCCTCTGT CCAGCGGCAT CCATTGCATC ATTGGTCTGT TCCGGTGCAA TGGGTTTGAG 180
GACTGTCCCG ATGGCAGCGA TGAAGAGAAC TGCACAGCAA ACCCTCTGCT TTGCTCCACC 240
GCCCCGTACC ACTGCAAGAA CGGCCTCTGT ATTGACAAGA GCTTCATCTG CGATGGACAG 300
AATAACTGTC AAGACAACAG TGATGAGGAA AGCTGTGAAA GTTCTCAAGA ACCGGGCACT 360
GGGCAGGTGT TTGTGACTTC AGAGAACCAG CTGTGTGATT ACCCCAGCAT CACCTATGCC 420
ATCATCGGCA GCTCCGTCAT TTTGTGCTGT GTGGTGGCCC TGCTGGCACT GGTCTTGAC 480
CACCAGCGGA AGCGGAACAA CCTCATGACG CTGCCCCGTG ACCGGCTGCA GCACCCTGTG 540
CTGTGTCTCC GCCTGGTGGT CCTGGACCAC CCCCACTACT GCAACGTAC CACCAACGTC 600
AATAATGGCA TCCAGTATGT GGCCAGCCAG GCGGAGCAGA ATGCGTCGGA AGTAGGCTCC 660
CCACCCTCCT ACTCCGAGGC CTGTGTGGAC CAGAGGCGCTG CGTGGTATGA CCTTCTCTCA 720
CCGCCCTACT CTCTTGACAC GGAATCTCTG AACCAGCCCG ACCTGCCCCC CTACCGCTCC 780
CGGTCCGGGA GTGCCAGTCC TGCCAGCTCC CAGGCAGCCA GCAGCTCTCT GAGCTGGGAA 840
GACACCAAGC ACAGCCCGGG GCAGCTGGC CCCAGGAGG GCACTGCTGA GCCCAGGGAC 900
TCTGAGCCCA GCCAGGGCAC TGAAGAAGTA TAA

Seq ID NO: 679 Protein sequence
Protein Accession #: Eos sequence

1 11 21 31 41 51
| | | | | |
MCSNRCIPG AWQCDGLPDC FDKSDEKECP KAKSKCGPTF FPCASGIHCI IGRFRNGFE 60
DCPDGSDEN CTANPLLCST ARYHCKNGLC IDKSFICDQ NNCQDNDSE SCSSQEPGS 120
GQVFVTSBNQ LVVYPSITYA IIGSSVIFVL VVALLALVLH HQKRNNLMT LPVHRLQHPV 180
LLSRLVVLHD PHHCNVYINV NNGIQYVASQ AEQNAEVSQ PPSYSEALD QRPANYDLFP 240
PPYSSDTESL NQADLPYRS RSGSANSASS QAASSLLSVE DTSHPGQPG PQEGTAEPED 300
SEPSQGTTEE

Seq ID NO: 680 DNA sequence
Nucleic Acid Accession #: S78203.1
Coding sequence: 1..2190

1 11 21 31 41 51
| | | | | |
ATGAATCCTT TCCAGAAAAA TGAGTCCAAG GAAACTCTTT TTTACCTGT CTCCATTGAA 60
GAGGTACCAC CTCGACCACC TAGCCCTCCA AAGAAGCCAT CTCGACAAT CTGTGGCTCC 120
AACTATCCAC TGAGCATTGC CTTCATTGTG GTGAATGAAT TCTGCGAGCG CTTTTCCTAT 180
TATGGAATGA AAGCTGTGCT GATCCTGTAT TTCTGTATT TCCTGCACTG GAATGAAGAT 240
ACCTCCACAT CTATATACCA TGCCCTCAGC AGCCTCTGTT ATTTTACTCC CATCCTGGGA 300
GCAGCCATTG CTGACTCGTG GTTGGGAAAA TTCAAGACAA TCATCTATCT CTCTTGGTG 360
TATGTGCTTG GCCATGTGAT CAAGTCCTTG GGTGCCTTAC CAATACTGGG AGGACAAGTG 420
GTACACACAG TCCTATCATT GATCGGCGTG AGTCTAATAG CTTTGGGAGC AGGAGGCATC 480
AAAACCTGTG TGGCAGCTTT TGGTGGAGAC CAGTTTGAAG AAAACATGCG AGAGGAACCG 540
ACTAGATACT TCTCAGTCTT CTACCTGTCC ATCAATGCAG GGAGCTTGAT TTCTACATT 600
ATCACACCCA TGCTGAGAGG AGATGTGCAA TGTTTTGGAG AAGACTGCTA TGCAATTGGCT 660
TTTGGAGTTC CAGGACTGCT CATGGTAATT GCACTTGTG TGTITGCAAT GGGGAAGCAA 720
ATATACAATA AACCAACCCC TGAAGGAAAC ATAGTGGCTC AAGTTTTCAT ATGTATCTGG 780
TTTGCTATT CCAATCGTTT CAAGAACCCT TCTGGAGACA TTCCAAAGCG ACAGCACTGG 840
CTAGACTGGG CAGCTGAGAA ATATCCAAAG CAGCTCATT TGGATGTAAA GGCAGTGACC 900
AGGTACTAT CTCTTTATAT CCCATTGCC ATGTTCTGGG CTCTTTTGA TCAGCAGGGT 960
TCACGATGGA CTTTGCAAGC CATCAGGATG AATAGGAATT TGGGGTTTT TGTGCTTCAG 1020
CCGACACAGA TGCAGGTTCT AAATCCCTTT CTGGTTCTTA TCTTCATCCC GTTGTGTTGAC 1080
TTTGTCAATT ATCGTCTGGT CTCCAAGTGT GGAATTAACT TCTCATCACT TAGGAAAATG 1140
CTGTGTGGTA TGATCCTAGC GTGCCTGGCA TTTGCAGTTG CGGCAGCTGT AGAGATAAAA 1200
ATAAATGAAA TGGCCCCAGC CCAGTCAGGT CCCCAGGAGG TTTTCTACA AGTCTTGAAT 1260
CTGGCAGATG ATGAGGTGAA GGTGACAGTG GTGGGAAATG AAAACAATTC TCTGTTGATA 1320
GAGTCCATCA AATCCTTTCA GAAAACACCA CACTATTCCA AACTGCACCT GAAAACAAAA 1380
AGCCAGGATT TTCATTCCA CCTGAAATAT CACAATTGT CTCTCTACAC TGAGCATTCT 1440
GTGCAGGAGA AGAAGTGGTA CAGTCTGTGC ATTGCTGAAG ATGGGAACAG TATCTCCAGC 1500
ATGATGGTAA AGGATACAGA AAGCAAAACA ACCAATGGGA TGACAACCGT GAGGTTTGGT 1560
AACACTTTGC ATAAAGATGT CAACATCTCC CTGAGTACAG ATACCTCTCT CAATGTTGGT 1620
GAAGACTATG GTGTGCTGCT TTATAGAACT GTGCAAGAG GAGAATACCC TGCACTGCAC 1680
TGTAAGACAG AAGATAAGAA CTTTCTCTCT AATTGCGGTC TTCTAGACTT TGGTGCAGCA 1740
TATCTGTTTG TTATTACTAA TAACACCAAT CAGGGTCTTC AGGCCTGGAA GATTGAAGAC 1800
ATCCAGCCA ACAAAATGTC CATTGCGTGG CAGCTACCAC AATATGCCCT GGTACAGCT 1860
GGGAGGTCA TGTTCTCTGT CACAGGTCTT GAGTTTCTT ATTCTCAGGC TCCCTCTAGC 1920
ATGAAATCTG TGCTCCAGGC AGCTTGGCTA TTGACAATTG CAGTTGGGAA TATCATCGTG 1980
CTGTGTGGG CACAGTTTCAG TGGCCTGGTA CAGTGGGCGG AATTCAATTT GTTTCTCTGC 2040
CTCCTGCTGG TGATCTGCCT GATCTTCTCC ATCATGGGCT ACTACTATGT TCCTGTAAG 2100
ACAGAGGATA TGGGGGTCC AGCAGATAAG CACATTCTCT ACATCCAGGG GAACATGATC 2160
AAACTAGAGA CCAAGAGAC AAAACTCTGA

Seq ID NO: 681 Protein sequence
Protein Accession #: AAB34388.1

1 11 21 31 41 51
| | | | | |
MNPFQKNESE ETLFSPVSE EVPPRPPSP KKPSPPTICGS NYPLSIAFIV VNEPCERFSY 60
YGMKAVLILY FLYFLHWNED TSTSIYHAFS SLCYFTPILO AAIADSWLQK FKTIYLSLV 120
5 YVLGHVILKSL GALPILGGQV VHTVLSLIGL SLIALGTGGI KPCVAAFGGD QPEEKHABER 180
TRYFSVFLYS INAGSLISTF ITPMLRGDVO CFGEDCYALA FGVPGLLMVI ALVVPAMGSK 240
IYNKPPPEGN IVAQVFKCIW PAISNRFKNR SGDIPKRQHW LDWAAEKYFK QLMIDVKALT 300
RVLFYLIPLP MFWALLDQGG SRWTLQAI RM NRNLGPFVLO PDQMQVLNPF LVLIFIPLFD 360
10 FVIYRLVSKC GINFSRLRM AVGMILACLA FAVAAVEIK INEMAPAQSG PQEVFLQVLN 420
LADDEVKTVV VGNENNSLLI ESIKSFQKTP HYSKLHLKTK SQDPHFLKY HNLSTLYEHS 480
VQEKNWYSLV IREDGNSISS MMVKDTESKT TNGMTTVRFV NTLHKOVNIS LSTDTSLNVG 540
EDYGVSAIRT VQGEYPAVH CRTEDKNFSL NLGLLDFGAA YLFVITNNTN QGLQAWKIED 600
IPANKMSIAW QLPQYALVTA GEVMSFTVGL EFSYSQAPSS MKSVLQAANL LTIAGVNIIV 660
15 LVVAQFSGLV QWAEFILFSC LLLVICLIFS IMGYVYPVK TEDMRGPADK HIPHIQGNMI 720
KLETKKTKL

Seq ID NO: 682 DNA sequence
Nucleic Acid Accession #: NM_016077.1
Coding sequence: 128..667

1 11 21 31 41 51
| | | | | |
TCGCTTTGTG ATTCTTGATC CGGAACCTTG TCACCCAGGA ACCCCGGAAG AGGTAGCTCA 60
CGCGATAGAA ACCTGTTCGC TTGCCAGAA GAAGGGAAGG CGCGAGTGAG GAAAGGAGGT 120
25 ACTGTAGATG CCTCCAAAT CCTTGGTTAT GGAATATTG GCTCATCCCA GTACACTCGG 180
CTTGGCTGTT GGAGTTGCTT GTGGCATGTG CCTGGGCTGG AGCCTTCGAG TATGCTTTGG 240
GATGCTCCCC AAAAGCAAGA CGAGCAAGAC ACACACAGAT ACTGAAAGTG AAGCAAGCAT 300
CTTGGGAGAC AGCGGGGAGT ACAAGATGAT TCTTGTGGTT CGAAATGACT TAAAGATGGG 360
30 AAAAGGGAAG GTGGCTGCC AGTGCTCTCA TGCTGCTGTT TCAGCCTACA AGCAGATTCA 420
AAGAAGAAAT CCTGAAATGC TCAACAATG GGAATACTGT GGCCAGCCCA AGGTGGTGGT 480
CAAAGCTCCT GATGAAGAAA CCTGATTGC ATTATTGGCC CATGCAAAAA TGCTGGGACT 540
GACTGTAAGT TTAATTCAAG ATGCTGGACG TACTCAGATT GCACCAAGCT CTCAAACTGT 600
CCTAGGGATT GGGCCAGGAC CAGCAGACCT AATTGACAAA GTCACTGGTC ACCTAAACT 660
35 TTACTAGTGT GACTTTGATA TGACAAACAC CCTCCATCA CAAGTGTGTT AAGCCTGTCA 720
GATTCTAACA ACAAAGCTG AATTCTTCA CCCAACTTAA ATGTTCTTGA GATGAAAAATA 780
AAACCTATTC CCATGTTCTA AAAAAA

Seq ID NO: 683 Protein sequence
Protein Accession #: NP_057161.1

1 11 21 31 41 51
| | | | | |
MPSKSLVMEY LAHPSTLGLA VGVACGMCLG WSLRVCFGML PKSKTSKTH TDESEASILG 60
45 DSGEYKMLLV VRNDLRKMGK KVAAQCASHA VSAYKQIQRR NPEMLKQWEY CGQPKVVVKA 120
PDEETLIALL AHAKMLGLTV SLIQDAGRTO IAPGSQTVLG IGPFPADLID KVTGHLRLY

Seq ID NO: 684 DNA sequence
Nucleic Acid Accession #: NM_004864.1
Coding sequence: 26..952

1 11 21 31 41 51
| | | | | |
CGGAACGAGG GCAACCTGCA CAGCCATGCC CGGGCAAGAA CTCAGGACGG TGAATGGCTC 60
TCAGATGCTC CTGGTGTGTC TGGTGCTCTC GTGGCTGCCG CATGGGGGCG CCCTGTCTCT 120
55 GGCCGAGGCG AGCCGCGCAA GTTCCCGGG ACCCTCAGAG TTGCACTCCG AAGACTCCAG 180
ATTCGAGAGG TTGCGGAAAC GCTACGAGGA CCTGTAAACC AGGCTGCGGG CCAACACAG 240
CTGGGAAGAT TCGAACACCG ACCTCGTCCC GGCCCGTCCA GTCCGGATAC TCACGCCAGA 300
AGTGGCGCTG GATCGCGCG GCGACCTGCA CTGCGGTATC TCTCGGGCCG CCCTTCCGCA 360
60 GGGGCTCCCC GAGGCTCTCC GCCTTCACCG GGCTCTGTTC CGGCTGTCCC CGACGGCGTC 420
AAGGTCTGTG GAGGTGACAC GACCGCTGCG GCGTCAGCTC AGCCTTGCAA GACCCCAAGC 480
GCCCGCGCTG CACCTGCGAC TGTGCGCGCC GCGTCCGAG TCGGACCAAC TGCTGGCAGA 540
ATCTTCGTCC GCACGCGCCC AGCTGGAGTT GCACTTGCGG CCGCAAGCCG CCAGGGGGCG 600
CGCAGAGCGG CGTGCAGCGA ACGGGGAAGA CTGTCCGCTC GGGCCCGGGC GTTGTGCGCG 660
65 TCTGCACACG GTCGCGCGGT CGCTGGAAGA CCTGGGCTGG GCCGATTGGG TGCTGTGCGC 720
ACGGGAGGTG CAAGTGACCA TGTGCATCGG CGCGTGCCCG AGCCAGTTCC GGGCGGCAAA 780
CATGCACGCG CAGATCAAGA CGAGCCTGCA CCGCCTGAAG CCGGACACCG AGCCAGCGCC 840
CTGCTGCGTG CCCGCCAGCT ACAATCCCAT GGTGCTCATT CAAAAGACCG ACACGGGGGT 900
GTCGCTCCAG ACCTATGATG ACTTGTAGC CAAAGACTGC CACTGCATAT GAGCAGTCTC 960
70 GGTCTTCCA CTGTGCACCT GCGCGGGGGA GCGACCTCA GTTGTCTGCT CCTGTGGAAT 1020
GGGCTCAAGG TTCTGTAGAC ACCCGATTCC TGCCCAAACA GCTGTATTTA TATAAGTCTG 1080
TTATTATTA TTAATTTATT GGGGTGACCT TCTTGGGGAC TCGGGGGCTG GTCTGATGGA 1140
ACTGTGTATT TATTTAAAC TCTGTGATA AAAATAAAGC TGCTGAACT GTTAAAAAAA 1200
AAAA

Seq ID NO: 685 Protein sequence
Protein Accession #: NP_004855.1

1 11 21 31 41 51
| | | | | |
80 MPQQLRLTVN QSQMLLVLLV LSWLPHGGAL SLAEASRAS FPGSELHSED SRFRELKRY 60
EDLLTRLRAN QSWEDSNTDL VPAPAVRILT PEVRLGSGGH LHLRISRAAL PEGLEASRL 120
HRLRRLSPT ASRSWDVTRP LRRQLSLARF QAPALHLRLS PPSQSDQLL AESSSARPL 180
ELHLRFPQAR GRRRARARG DDCLGPGRC CRLHTVRASL EDLGDWADWL SPREVQVTC 240
85 IGACPSQFRA ANMHAQIKTS LHRLKPDTEP APCCVPASYN PMVLIQKTDI GVSQTYDDL 300
LAKDCHCI

Seq ID NO: 686 DNA sequence

Nucleic Acid Accession #: NM_002423.2
Coding sequence: 48..851

```

5      1      11      21      31      41      51
      |      |      |      |      |      |
      ACCAAATCAA CCATAGGTCC AAGAACAATT GTCTCTGGAC GGCAGCTATG CGACTCACCG      60
      TGCCTGTGTC TGTGTGCTGT CTGCCTGGCA GCCTGGCCCT GCCGCTGCCT CAGGAGGCGG      120
      GAGGCATGAG TGAGCTACAG TGGGAACAGG CTCAGGACTA TCTCAAGAGA TTTTATCTCT      180
      ATGACTCAGA AACAAAAAAT GCCAACAGTT TAGAAGCCAA ACTCAAGGAG ATGCAAAAAT      240
10     TCTTTGGCCT ACCTATAACT GGAATGTTAA ACTCCGCGT CATAGAAATA ATGCAGAAGC      300
      CCAGATGTGG AGTGCCAGAT GTTGCAGAAAT ACTCACTATT TCCAAATAGC CCAAAATGGA      360
      CTTCCAAAGT GGTCACTTAC AGGATCGTAT CATATACTCG AGACTTACCG CATATTACAG      420
      TGGATCGATT AGTGTCAAAG GCTTTAAACA TGTGGGGCAA AGAGATCCCC CTGCATTTCA      480
      GGAAAGTTGT ATGGGGAACT GCTGACATCA TGATTGGCTT TGCGCGAGGA GTCATGGGG      540
15     ACTCTTACCC ATTTGATGGG CCAGGAAACA CGCTGGCTCA TGCCTTTGCG CCGGGACAG      600
      GTCTCGAGG AGATGCTCAC TTCGATGAGG ATGAACGCTG GACGGATGGT AGCAGTCTAG      660
      GGATTAACTT CCTGTATGCT GCAACTCATG AACTTGGCCA TTCTTTGGGT ATGGGACATT      720
      CCTCTGATCC TAATGCAATG ATGTATCCAA CCTATGGAAA TGGAGATCCC CAAAATTTTA      780
      AACTTTCCCA GGATGATATT AAAGGCATTC AGAAACTATA TGGAAAGAGA AGTAATTCAA      840
20     GAAAGAAATA GAAACTTCAG GCAGAACATC CATTATTCA TTCAATTGGT TGTATATCAT      900
      TGTTCACAA TCAGAAATGA TAAGCACTGT TCCTCCACTC CATTAGCAA TTATGTCACC      960
      CTTTTTTATT GCAGTTGGTT TTTGAATGTC TTTCACTCCT TTTATTGGTT AAACCTCCTT      1020
      ATGGTGTGAC TGTGTCTTAT TCCATCTATG AGCTTTGTCA GTGCGCGTAG ATGTCAATAA      1080
25     ATGTTACATA CACAAATAAA TAAATGTTT ATTCCATGST AAATTTA

```

Seq ID NO: 687 Protein sequence
Protein Accession #: NP_002414.1

```

30     1      11      21      31      41      51
      |      |      |      |      |      |
      MRLTVLCAVC LLPGSLALPL PQEAGGMSLE QWEQAQDYLK RPYLYDSETK NANSLEAKLK      60
      EMQKFFGLPI TGMLNSRVIE IMQKPRCGVP DVAEYSLFPN SPKWTISKVVT YRIVSYTRDL      120
      PHITVDRLVS KALNMWGKEI PLHFRKVVWG TADIMIGFAR GAHGDSPFPD GPGNTLAHAF      180
35     APGTGLGGDA HFDEDERWTD GSSLGINFLY AATHELGHSL GMGHSSDPNA VMYPTYNGND      240
      PQNFKLSQDD IKGIQKLYGK RSNSRKK

```

Seq ID NO: 688 DNA sequence
Nucleic Acid Accession #: NM_005221.3
Coding sequence: 1..870

```

40     1      11      21      31      41      51
      |      |      |      |      |      |
      ATGACAGGAG TGGTTGACAG AAGGGTCCCC AGCATCCGAT CCGGCGACTT CCAAGCTCCG      60
      TTCCAGACGT CCGCAGCTAT GCACCATCCG TCTCAGGAAT CGCCAACTTT GCCCGAGTCT      120
45     TCAGCTACCG ATTCTGACTA CTACAGCCCT ACGGGGGGAG CCCCGCACGG CTAAGTCTCT      180
      CCTACCTCGG CTCTCTATGG CAAAGCTCTC AACCCCTACC AGTATCAGTA TCACGGCGTG      240
      AACGGCTCCG CCGGGAGCTA CCCAGCCAAA GCTTATGCCG ACTATAGTA CGTAGCTCC      300
      TACCACCACT ACGCGGGCGC CTACAACCGC GTCCCAAGCG CCACCAACCA GCCAGAGAAA      360
50     GAAGTGACCG AGCCCGAGGT GAGAATGGTG AATGGCAAAC CAAAGAAAGT TCGTAAACCC      420
      AGGACTATTT ATTCCAGCTT TCAGCTGGCC GCATTACAGA GAAGGTTTCA GAAGACTCAG      480
      TACCTCGCTT TGCCGGAACG CGCCGAGCTG GCCGCTCGC TGGGATTGAC ACAAAACACAG      540
      GTGAAAATCT GGTTCAGAA CAAAAGATCC AAGATCAAGA AGATCATGAA AAACGGGGAG      600
      ATGCCCCCGG AGCACAGTCC CAGCTCCAGC GACCCATGCG CGTGTAACTC GCCGCACTCT      660
55     CCAGCGGTGT GGGAGCCCCA GGGCTCGTCC CGCTCGCTCA GCCACCACCC TCATGCCCAC      720
      CCTCCGACCT CCAACCAATC CCCAGCGTCC AGCTACCTGG AGAACTCTGC ATCCTGGTAC      780
      ACAAGTGACG CCAAGCTCAAT CAATCCCACG CTGCCGCCGC CGGCTCCTT ACAGCACCCG      840
      CTGGCGCTGG CCTCCGGGAC ACTCTATTAG

```

Seq ID NO: 689 Protein sequence
Protein Accession #: NP_005212.1

```

60     1      11      21      31      41      51
      |      |      |      |      |      |
      MTGVFDRRVF SIRSGDFQAP FQTSAAHHP SQESPTLPES SATDSDYISP TGGAPHGYS      60
65     PTSASYGKAL NPYQYQYHGV NGSAGSYPK AYADYSYASS YHQYGGAYNR VPSATNQPEK      120
      EVTEPEVRMV NGKPKVKRKP RTIYSSFOLA ALQRRFQKTQ YLALPERAEL AASLGLTQTO      180
      VKIWFQNKRS KIKKIMKNKE MPPEHSPSSS DPMACNSPQS PAVWEPQSSS RSLSHPHAH      240
      PPTSNQSPAS SYLENSASWY TSAASSINSH LPPPGSLQHP LALASGTLTY

```

It is understood that the examples described above in no way serve to limit the true scope of this invention, but rather are presented for illustrative purposes. All publications, sequences of accession numbers, and patent applications cited in this specification are herein incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference.

WHAT IS CLAIMED IS:

- 1 1. A method of detecting a lung cancer-associated transcript in a cell
2 from a patient, the method comprising contacting a biological sample from the patient with a
3 polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence
4 as shown in Tables 1A-16.
- 1 2. The method of claim 1, wherein the polynucleotide selectively
2 hybridizes to a sequence at least 95% identical to a sequence as shown in Tables 1A-16.
- 1 3. The method of claim 1, wherein the biological sample is a tissue
2 sample.
- 1 4. The method of claim 1, wherein the biological sample comprises
2 isolated nucleic acids.
- 1 5. The method of claim 4, wherein the nucleic acids are mRNA.
- 1 6. The method of claim 4, further comprising the step of amplifying
2 nucleic acids before the step of contacting the biological sample with the polynucleotide.
- 1 7. The method of claim 1, wherein the polynucleotide comprises a
2 sequence as shown in Tables 1A-16.
- 1 8. The method of claim 1, wherein the polynucleotide is labeled.
- 1 9. The method of claim 8, wherein the label is a fluorescent label.
- 1 10. The method of claim 1, wherein the polynucleotide is immobilized on
2 a solid surface.
- 1 11. The method of claim 1, wherein the patient is undergoing a therapeutic
2 regimen to treat lung cancer.
- 1 12. The method of claim 1, wherein the patient is suspected of having lung
2 cancer.
- 1 13. A method of monitoring the efficacy of a therapeutic treatment of lung
2 cancer, the method comprising the steps of:

- 3 (i) providing a biological sample from a patient undergoing the therapeutic
4 treatment; and
5 (ii) determining the level of a lung cancer-associated transcript in the
6 biological sample by contacting the biological sample with a polynucleotide that selectively
7 hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16,
8 thereby monitoring the efficacy of the therapy.

1 14. The method of claim 13, further comprising the step of: (iii) comparing
2 the level of the lung cancer-associated transcript to a level of the lung cancer-associated
3 transcript in a biological sample from the patient prior to, or earlier in, the therapeutic
4 treatment.

1 15. The method of claim 13, wherein the patient is a human.

1 16. A method of monitoring the efficacy of a therapeutic treatment of lung
2 cancer, the method comprising the steps of:

- 3 (i) providing a biological sample from a patient undergoing the therapeutic
4 treatment; and
5 (ii) determining the level of a lung cancer-associated antibody in the biological
6 sample by contacting the biological sample with a polypeptide encoded by a polynucleotide
7 that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in
8 Tables 1A-16, wherein the polypeptide specifically binds to the lung cancer-associated
9 antibody, thereby monitoring the efficacy of the therapy.

1 17. The method of claim 16, further comprising the step of: (iii) comparing
2 the level of the lung cancer-associated antibody to a level of the lung cancer-associated
3 antibody in a biological sample from the patient prior to, or earlier in, the therapeutic
4 treatment.

1 18. The method of claim 16, wherein the patient is a human.

1 19. A method of monitoring the efficacy of a therapeutic treatment of lung
2 cancer, the method comprising the steps of:

- 3 (i) providing a biological sample from a patient undergoing the therapeutic
4 treatment; and

5 (ii) determining the level of a lung cancer-associated polypeptide in the
6 biological sample by contacting the biological sample with an antibody, wherein the antibody
7 specifically binds to a polypeptide encoded by a polynucleotide that selectively hybridizes to
8 a sequence at least 80% identical to a sequence as shown in Tables 1A-16, thereby
9 monitoring the efficacy of the therapy.

1 20. The method of claim 19, further comprising the step of: (iii) comparing
2 the level of the lung cancer-associated polypeptide to a level of the lung cancer-associated
3 polypeptide in a biological sample from the patient prior to, or earlier in, the therapeutic
4 treatment.

1 21. The method of claim 19, wherein the patient is a human.

1 22. An isolated nucleic acid molecule consisting of a polynucleotide
2 sequence as shown in Tables 1A-16.

1 23. The nucleic acid molecule of claim 22, which is labeled.

1 24. The nucleic acid of claim 23, wherein the label is a fluorescent label

1 25. An expression vector comprising the nucleic acid of claim 22.

1 26. A host cell comprising the expression vector of claim 25.

1 27. An isolated polypeptide which is encoded by a nucleic acid molecule
2 having polynucleotide sequence as shown in Tables 1A-16.

1 28. An antibody that specifically binds a polypeptide of claim 27.

1 29. The antibody of claim 28, further conjugated to an effector component.

1 30. The antibody of claim 29, wherein the effector component is a
2 fluorescent label.

1 31. The antibody of claim 29, wherein the effector component is a
2 radioisotope or a cytotoxic chemical.

1 32. The antibody of claim 29, which is an antibody fragment.

- 1 33. The antibody of claim 29, which is a humanized antibody
- 1 34. A method of detecting a lung cancer cell in a biological sample from a
2 patient, the method comprising contacting the biological sample with an antibody of claim
3 28.
- 1 35. The method of claim 34, wherein the antibody is further conjugated to
2 an effector component.
- 1 36. The method of claim 35, wherein the effector component is a
2 fluorescent label.
- 1 37. A method of detecting antibodies specific to lung cancer in a patient,
2 the method comprising contacting a biological sample from the patient with a polypeptide
3 encoded by a nucleic acid comprises a sequence from Tables 1A-16.
- 1 38. A method for identifying a compound that modulates a lung cancer-
2 associated polypeptide, the method comprising the steps of:
3 (i) contacting the compound with a lung cancer-associated polypeptide, the
4 polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least
5 80% identical to a sequence as shown in Tables 1A-16; and
6 (ii) determining the functional effect of the compound upon the polypeptide.
- 1 39. The method of claim 38, wherein the functional effect is a physical
2 effect.
- 1 40. The method of claim 38, wherein the functional effect is a chemical
2 effect.
- 1 41. The method of claim 38, wherein the polypeptide is expressed in a
2 eukaryotic host cell or cell membrane.
- 1 42. The method of claim 38, wherein the functional effect is determined by
2 measuring ligand binding to the polypeptide.
- 1 43. The method of claim 38, wherein the polypeptide is recombinant.

1 44. A method of inhibiting proliferation of a lung cancer-associated cell to
2 treat lung cancer in a patient, the method comprising the step of administering to the subject a
3 therapeutically effective amount of a compound identified using the method of claim 38.

1 45. The method of claim 44, wherein the compound is an antibody.

1 46. The method of claim 45, wherein the patient is a human.

1 47. A drug screening assay comprising the steps of
2 (i) administering a test compound to a mammal having lung cancer or a cell
3 isolated therefrom;
4 (ii) comparing the level of gene expression of a polynucleotide that selectively
5 hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16 in a
6 treated cell or mammal with the level of gene expression of the polynucleotide in a control
7 cell or mammal, wherein a test compound that modulates the level of expression of the
8 polynucleotide is a candidate for the treatment of lung cancer.

1 48. The assay of claim 47, wherein the control is a mammal with lung
2 cancer or a cell therefrom that has not been treated with the test compound.

1 49. The assay of claim 47, wherein the control is a normal cell or mammal.

1 50. A method for treating a mammal having lung cancer comprising
2 administering a compound identified by the assay of claim 47.

1 51. A pharmaceutical composition for treating a mammal having lung
2 cancer, the composition comprising a compound identified by the assay of claim 47 and a
3 physiologically acceptable excipient.

REVISED VERSION

(19) World Intellectual Property
Organization
International Bureau



(43) International Publication Date
31 October 2002 (31.10.2002)

PCT

(10) International Publication Number
WO 2002/086443 A2

(51) International Patent Classification⁷: **C07H 21/02**,
21/04, C12Q 1/68

(21) International Application Number:
PCT/US2002/012476

(22) International Filing Date: 18 April 2002 (18.04.2002)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
60/284,770 18 April 2001 (18.04.2001) US
60/290,492 10 May 2001 (10.05.2001) US
60/339,245 9 November 2001 (09.11.2001) US
60/350,666 13 November 2001 (13.11.2001) US
60/334,370 29 November 2001 (29.11.2001) US
60/372,246 12 April 2002 (12.04.2002) US

(81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW.

(84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Declaration under Rule 4.17:
— of inventorship (Rule 4.17(iv)) for US only

(71) Applicant (*for all designated States except US*): PRO-TEIN DESIGN LABS, INC [US/US]; 225A Gateway Boulevard, South San Francisco, CA 94080 (US).

Published:
— with declaration under Article 17(2)(a); without abstract; title not checked by the International Searching Authority

(72) Inventors; and

(75) Inventors/Applicants (*for US only*): AZIZ, Natasha [US/US]; 411 California Avenue, Palo Alto, CA 94306 (US). MURRAY, Richard [US/US]; 22643 Woodbridge Court, Cupertino, CA 95014 (US).

(48) Date of publication of this revised version: 17 June 2004

(15) Information about Correction:
see PCT Gazette No. 25/2004 of 17 June 2004, Section II

(74) Agent: HALLUIN, Albert, P.; HOWREY SIMON ARNOLD & WHITE LLP, 301 Ravenswood Avenue, Box 34, Menlo Park, CA 94025 (US).

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: METHODS OF DIAGNOSIS OF LUNG CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF LUNG CANCER

(57) Abstract:



WO 2002/086443 A2

PATENT COOPERATION TREATY

PCT

DECLARATION OF NON-ESTABLISHMENT OF INTERNATIONAL SEARCH REPORT

(PCT Article 17(2)(a), Rule 13ter.1(c) and 39)

Applicant's or agent's file reference 18501-15-3PC	IMPORTANT DECLARATION	Date of mailing (day/month/year) 15 AUG 2003
International application No. PCT/US02/12476	International filing date (day/month/year) 18 April 2002 (18.04.2002)	(Earliest) Priority date (day/month/year) 10 May 2001 (10.05.2001)
International Patent Classification (IPC) or both national classification and IPC IPC(7): C07H 21/02, 21/04; C12Q 1/68 and US Cl.: 435/6, 536/23.1, 23.5		
Applicant EOS BIOTECHNOLOGY, INC		

This International Searching Authority hereby declares, according to Article 17(2)(a), that no international search report will be established on the international application for the reasons indicated below.

1. ☐ The subject matter of the international application relates to:
 - a. ☐ scientific theories.
 - b. ☐ mathematical theories
 - c. ☐ plant varieties.
 - d. ☐ animal varieties.
 - e. ☐ essential biological processes for the production of plants and animals, other than microbiological processes and the products of such processes.
 - f. ☐ schemes, rules or methods of doing business.
 - g. ☐ schemes, rules or methods of performing purely mental acts.
 - h. ☐ schemes, rules or methods of playing games.
 - i. ☐ methods for treatment of the human body by surgery or therapy.
 - j. ☐ methods for treatment of the animal body by surgery or therapy.
 - k. ☐ diagnostic methods practised on the human or animal body.
 - l. ☐ mere presentations of information.
 - m. ☐ computer programs for which this International Searching Authority is not equipped to search prior art.
2. ☐ The failure of the following parts of the international application to comply with prescribed requirements prevents a meaningful search from being carried out:

☐ the description
☐ the claims
☐ the drawings
3. ☒ The failure of the nucleotide and/or amino acid sequence listing to comply with the standard provided for in Annex C of the Administrative Instructions prevents a meaningful search from being carried out:

☐ the written form has not been furnished or does not comply with the standard.
☒ the computer readable form has not been furnished or does not comply with the standard.
4. Further comments:

Name and mailing address of the ISA/US Mail Stop PCT, Attn: ISA/US Commissioner for Patents P.O. Box 1450 Alexandria, Virginia 22313-1450 Facsimile No. (703)305-3230	Authorized officer <div style="text-align: center;"> CARLA J. MYERS PRIMARY EXAMINER </div> Telephone No. 703-308-0196
--	---

PATENT COOPERATION TREATY

From the INTERNATIONAL SEARCHING AUTHORITY

To:
TOWNSEND AND TOWNSEND AND CREW LLP
TWO EMBARCADERO CENTER
EIGHTH FLOOR
SAN FRANCISCO, CA 94111-3834

PCT

NOTIFICATION OF TRANSMITTAL OF THE INTERNATIONAL SEARCH REPORT OR THE DECLARATION

(PCT Rule 44.1)

Date of Mailing (day/month/year) 15 AUG 2003	
Applicant's or agent's file reference 18501-15-3PC	FOR FURTHER ACTION See paragraphs 1 and 4 below
International application No. PCT/US02/12476	International filing date (day/month/year) 18 April 2002 (18.04.2002)
Applicant EOS BIOTECHNOLOGY, INC	

1. ☐ The applicant is hereby notified that the international search report has been established and is transmitted herewith.

Filing of amendments and statement under Article 19:

The applicant is entitled, if he so wishes, to amend the claims of the international application (see Rule 46):

When? The time limit for filing such amendments is normally two months from the date of transmittal of the international search report.

Where? Directly to the International Bureau of WIPO, 34, chemin des Colombettes
1211 Geneva 20, Switzerland, Facsimile No.: (41-22) 740.14.35

For more detailed instructions, see the notes on the accompanying sheet.

2. ☒ The applicant is hereby notified that no international search report will be established and that the declaration under Article 17(2)(a) to that effect is transmitted herewith.

3. ☐ With regard to the protest against payment of (an) additional fee(s) under Rule 40.2, the applicant is notified that:

☐ the protest together with the decision thereon has been transmitted to the International Bureau together with the applicant's request to forward the texts of both the protest and the decision thereon to the designated Offices.

☐ no decision has been made yet on the protest; the applicant will be notified as soon as a decision is made.

4. Reminders

Shortly after 18 months from the priority date, the international application will be published by the International Bureau. If the applicant wishes to avoid or postpone publication, a notice of withdrawal of the international application, or of the priority claim, must reach the International Bureau as provided in Rules 90 bis.1 and 90 bis.3, respectively, before the completion of the technical preparations for international publication.

Within 19 months from the priority date, but only in respect of some designated Offices, a demand for international preliminary examination must be filed if the applicant wishes to postpone the entry into the national phase until 30 months from the priority date (in some Offices even later); otherwise the applicant must, within 20 months from the priority date, perform the prescribed acts for entry into the national phase before those designated Offices.

In respect of other designated Offices, the time limit of 30 months (or later) will apply even if no demand is filed within 19 months.

See the Annex to Form PCT/IB/301 and, for details about the applicable time limits, Office by Office, see the *PCT Applicant's Guide*, Volume II, National Chapters and the WIPO Internet site.

Name and mailing address of the ISA/US
Mail Stop PCT, Attn: ISA/US
Commissioner for Patents
P.O. Box 1450
Alexandria, Virginia 22313-1450
Facsimile No. (703)305-3230

Authorized officer

Valerie Bell-Harris
Carla Myers

Telephone No. 703-308-0196